



C 107	42	4.2	51	1	AA177521	Human silent SNP c	180	36.2	3.7	41	1	ABZ46915	Human ATP-binding
C 108	42	4.2	51	1	AA179584	Human silent SNP c	C 181	36.2	3.7	41	1	ABZ49747	Human cerebroside
C 109	42	4.2	51	1	AA178039	Human silent SNP c	C 182	35.8	3.6	40	1	AAH91201	Human inflammatory
C 110	42	4.2	51	1	AA178300	Human silent SNP c	C 183	35.8	3.6	41	1	ABZ50133	Human NDUPF1 gene
C 111	42	4.2	51	1	AA173860	Human silent SNP c	C 184	35.8	3.6	41	1	ABZ44123	Human NDUPF1 gene
C 112	42	4.2	51	1	AA173760	Human silent SNP c	C 185	35.2	3.6	40	1	AA179407	Synthetic oligomer
C 113	42	4.2	51	1	AA177806	Human silent SNP c	C 186	35.2	3.6	40	1	AAV19045	Alu PCR primer 2.
C 114	42	4.2	51	1	AA173533	Human silent SNP c	C 187	35.2	3.6	40	1	ABL59101	Nucleotide sequenc
C 115	42	4.2	51	1	ABL00195	Human silent nonco	C 188	35.2	3.6	41	1	AAH49727	Human DNA mismatch
C 116	42	4.2	48	1	AD112525	Human BRCA1 DNA ju	C 189	35.2	3.6	41	1	ABL40963	Transcription regu
C 117	41.6	4.2	51	1	AA175849	Human silent SNP c	C 190	35.2	3.6	41	1	ABL40964	Transcription regu
C 118	41.6	4.2	51	1	ABL00141	Human silent nonco	C 191	35.2	3.6	41	1	ABZ20666	Human G protein su
C 119	41.4	4.2	51	1	AA177442	Human AluSubfamily	C 192	35.2	3.6	41	1	ABQ77547	Human red blood ce
C 120	41.4	4.2	51	1	AA176988	Human clone CG4292	C 193	35.2	3.6	41	1	ABV77328	Human protein 10.0
C 121	41.4	4.2	51	1	AA177021	Human clone CG4308	C 194	35.2	3.6	41	1	ACC00156	Probe #1 for guano
C 122	41.4	4.2	51	1	AD016930	Human single nucle	C 195	35	3.5	35	1	AAO27391	Inter-Alu specific
C 123	41.4	4.2	51	1	AA176193	Human silent SNP c	C 196	34.6	3.5	41	1	ABQ83633	Human mper3-10.01
C 124	41.4	4.2	51	1	AA173061	Human silent SNP c	C 197	34.6	3.5	41	1	ABQ83634	Human mper3-10.01
C 125	41.4	4.2	51	1	AA174775	Human silent SNP c	C 198	34.6	3.5	41	1	ABL52955	Serine proteinase
C 126	41.4	4.2	51	1	AA173736	Human silent SNP c	C 199	34.6	3.5	41	1	ABZ49715	Human sulphotransf
C 127	41.4	4.2	51	1	AA176185	Human silent SNP c	C 200	34.6	3.5	41	1	ABZ43958	Human glutathione-
C 128	41.4	4.2	51	1	AA174502	Human silent SNP c	C 201	34.6	3.5	41	1	ABZ49550	Human glutathione-
C 129	41.4	4.2	51	1	AA176499	Human silent SNP c	C 202	34.6	3.5	41	1	ABZ49230	Human aldehyde deh
C 130	41.4	4.2	51	1	AA179533	Human silent SNP c	C 203	34.6	3.5	41	1	ABZ45236	Human aldehyde deh
C 131	41.4	4.2	51	1	AA179539	Human silent SNP c	C 204	34.6	3.5	41	1	ABZ43562	Human sulphotransf
C 132	41.4	4.2	51	1	AA176814	Human silent SNP c	C 205	34.6	3.5	41	1	ADP75520	Human ADAM19 gene,
C 133	41.4	4.2	51	1	AA176092	Human silent SNP c	C 206	34.6	3.5	41	1	ADP64137	Human single nucle
C 134	41.4	4.2	51	1	AA179838	Human nonconservat	C 207	34.6	3.5	41	1	ADL64139	Human single nucle
C 135	41.4	4.2	51	1	AA176541	Human silent SNP c	C 208	34.6	3.5	41	1	ADL64284	Human single nucle
C 136	41.4	4.2	51	1	AA179697	Human conservative	C 209	34.6	3.4	40	1	AA197406	Synthetic oligomer
C 137	41.4	4.2	51	1	AA174778	Human silent SNP c	C 210	33.6	3.4	40	1	ADK41334	Human chromosome 1
C 138	41.4	4.2	51	1	AA173250	Human silent SNP c	C 211	33.6	3.4	41	1	AAH49728	Human DNA mismatch
C 139	41.4	4.2	51	1	AA179700	Human conservative	C 212	33.6	3.4	41	1	ABL49776	Human tyrosinase 1
C 140	41.4	4.2	51	1	AA178386	Human silent SNP c	C 213	33.6	3.4	41	1	ABL49775	Human tyrosinase 1
C 141	41.4	4.2	51	1	AA173862	Human silent SNP c	C 214	33.6	3.4	41	1	ABZ20657	Human G protein su
C 142	41.4	4.2	51	1	AA179783	Human nonconservat	C 215	33.6	3.4	41	1	ABA94091	Human tumour suppr
C 143	41.4	4.2	51	1	AAH90585	Human clone CG4308	C 216	33.6	3.4	41	1	AA143826	Human oncogene pro
C 144	41.4	4.2	51	1	AAH89405	Human coding seque	C 217	33.6	3.4	41	1	AA143827	Human oncogene pro
C 145	41.4	4.2	51	1	AAH89485	Human coding seque	C 218	33.6	3.4	41	1	ABZ44551	Human glycosyltran
C 146	41.4	4.2	51	1	AAH89519	Human coding seque	C 219	33.6	3.4	41	1	ABZ50762	Human glycosyltran
C 147	41.4	4.2	51	1	AAH89519	Human coding seque	C 220	33.6	3.4	41	1	ABV77329	Human protein 10.0
C 148	41.4	4.2	51	1	AAH89467	Human coding seque	C 221	33.6	3.4	41	1	ACC00157	Probe #2 for guano
C 149	41.4	4.2	51	1	AAH89553	Human coding seque	C 222	33.6	3.4	41	1	ABZ57114	Human KIA0608 pro
C 150	41.4	4.2	51	1	AAH89472	Human coding seque	C 223	33.6	3.4	41	1	ADL64136	Human single nucle
C 151	41.4	4.2	51	1	ADK19818	Human mannosyl tra	C 224	33.2	3.4	41	1	ABZ45510	Human ATP-binding
C 152	41.2	4.2	51	1	AA179589	Human silent SNP c	C 225	33.2	3.4	41	1	ABZ46916	Human ATP-binding
C 153	41	4.1	49	1	AD112532	Mutant human BRCA1	C 226	33	3.3	33	1	ACC84461	NTP peptide encodi
C 154	41	4.1	51	1	AA176816	Human silent SNP c	C 227	33	3.3	41	1	AA197976	Human eukaryotic a
C 155	41	4.1	51	1	AA179093	Human silent SNP c	C 228	33	3.3	41	1	ABL52956	Serine proteinase
C 156	41	4.1	51	1	AA173524	Human silent SNP c	C 229	33	3.3	41	1	ABZ44124	Human NDUPF1 gene
C 157	41	4.1	51	1	AAH89516	Human coding seque	C 230	33	3.3	41	1	ABZ45508	Human ATP-binding
C 158	41	4.1	51	1	AAH38408	Human SNP flanking	C 231	33	3.3	41	1	ABZ49572	Human glutathione-
C 159	41	4.1	51	1	AAH40504	Human SNP flanking	C 232	33	3.3	41	1	ABZ49713	Human sulphotransf
C 160	41	4.1	51	1	ABL00045	Human silent nonco	C 233	33	3.3	41	1	ABZ50134	Human NDUPF1 gene
C 161	40.6	4.1	49	1	AAZ68649	Human map-related	C 234	33	3.3	41	1	ABZ43960	Human sulphotransf
C 162	40.6	4.1	47	1	ADZ77198	KALPFA SNP CV61660	C 235	33	3.3	41	1	ABZ43980	Human glutathione-
C 163	40.4	4.1	42	1	AD112523	Human BRCA1 DNA ju	C 236	33	3.3	41	1	ABZ46914	Human ATP-binding
C 164	40.4	4.1	50	1	ABZ07627	Human leukocyte ge	C 237	33	3.3	41	1	ABZ47296	Human ATP-binding
C 165	40	4.0	40	1	AAV19044	Alu PCR primer 1.	C 238	33	3.3	41	1	ABA94080	Human multi-copper
C 166	40	4.0	40	1	ABL59100	Nucleotide sequenc	C 239	33	3.3	41	1	AA155590	Human DNA mismatch
C 167	40	4.0	41	1	ABZ49631	Human sulphotransf	C 240	33	3.3	41	1	ADL64285	Human single nucle
C 168	40	4.0	41	1	ABZ43598	Human sulphotransf	C 241	33	3.3	41	1	ADL64286	Human single nucle
C 169	40	4.0	50	1	AAH89619	Human coding seque	C 242	32	3.2	40	1	ABZ48532	Human oligopeptide
C 170	39	3.9	39	1	ACC84472	NTP peptide encodi	C 243	31.8	3.2	35	1	AAO45257	Alu primer PDJ34 t
C 171	39	3.9	39	1	ACC84471	NTP peptide encodi	C 244	31.8	3.2	35	1	ABA93847	Human GAS1 PCR pr
C 172	37.8	3.8	41	1	ABA96813	Human uteroglobin	C 245	31.4	3.2	35	1	AAQ27392	Inter-Alu specific
C 173	37.8	3.8	41	1	ABA96812	Human uteroglobin	C 246	30.4	3.1	32	1	ADE14248	Optineurin promote
C 174	37.8	3.8	41	1	ABZ44526	Human neuropathy t	C 247	30.2	3.1	36	1	AAH91142	Human inflammatory
C 175	37.8	3.8	41	1	ABZ50785	Human neuropathy t	C 248	30	3.0	32	1	ACC84462	NTP peptide encodi
C 176	37.8	3.8	42	1	AD112521	Human BRCA1 DNA ju	C 249	29.4	3.0	32	1	ADE14029	Optineurin promote
C 177	37.6	3.8	47	1	AAZ68006	Human map-related	C 250	29	2.9	31	1	AAQ73572	Enhancer element e
C 178	36.2	3.7	41	1	ABZ43589	Human cerebroside	C 251	27.6	2.8	29	1	AAH04659	Polymorphic fragme
C 179	36.2	3.7	41	1	ABZ45509	Human ATP-binding	C 252	27.4	2.8	29	1	AAH37977	SNP specific upper



C 253	27.4	2.8	31	1	AAK06467	Human biallelic po
C 254	27.4	2.8	32	1	AAQ27389	Inter-Alu specific
C 255	27.4	2.8	32	1	ADRI4206	Optineurin promote
C 256	27.2	2.7	33	1	AAI62688	Human breast or ov
C 257	27.2	2.7	33	1	AAI06897	Human reproductive
C 258	27.2	2.7	33	1	ABLA0976	HOMO glandulae mam
C 259	27	2.7	37	1	ACC84460	NTP peptide encodi
C 260	27	2.7	29	1	AAA04371	Polymorphic fragme
C 261	27	2.7	29	1	AAA04506	Polymorphic fragme
C 262	27	2.7	29	1	AAA04303	Polymorphic fragme
C 263	27	2.7	29	1	AAA04500	Polymorphic fragme
C 264	27	2.7	29	1	AAA03996	Polymorphic fragme
C 265	27	2.7	32	1	AAQ03570	Enhancer element e
C 266	27	2.7	32	1	AAQ3570	Human digestive by
C 267	26.8	2.7	32	1	AAK32075	Human liver associ
C 268	26.8	2.7	32	1	ABN90430	Human liver antige
C 269	26.8	2.7	32	1	ADJ15343	Human liver-relate
C 270	26.8	2.7	32	1	AAQ77890	Neural thread prot
C 271	26.4	2.7	30	1	AAQ77890	Neural thread prot
C 272	26.4	2.7	30	1	AAI27744	Human inflammatory
C 273	26.2	2.6	32	1	AAA04663	Polymorphic fragme
C 274	26	2.6	29	1	AAA03961	Polymorphic fragme
C 275	26	2.6	29	1	AAA03961	Polymorphic fragme
C 276	26	2.6	29	1	AAQ03993	Neural thread prot
C 277	25.8	2.6	30	1	AAQ77889	Neural thread prot
C 278	25.8	2.6	30	1	AAI27743	Enhancer element e
C 279	25.8	2.6	31	1	AAQ73573	Human genomic DNA
C 280	25.8	2.6	31	1	AAI78748	Human tandem tag D
C 281	25.6	2.6	32	1	AAAD63091	Polymorphic fragme
C 282	25.4	2.6	29	1	AAA04017	Polymorphic fragme
C 283	25.4	2.6	29	1	AAA04065	Polymorphic fragme
C 284	25.4	2.6	29	1	AAA03995	Polymorphic fragme
C 285	25.4	2.6	29	1	AAA04512	Polymorphic fragme
C 286	25.4	2.6	29	1	AAA04499	Polymorphic fragme
C 287	25.4	2.6	29	1	AAA03984	Polymorphic fragme
C 288	25.4	2.6	29	1	AAA04645	Polymorphic fragme
C 289	25.4	2.6	30	1	AAH38989	SNP specific upper
C 290	25.2	2.5	30	1	AAH40734	SNP specific lower
C 291	25	2.5	25	1	AAQ25353	Sequence of probe
C 292	25	2.5	25	1	AAH40799	SNP specific SNPB
C 293	25	2.5	25	1	AAH51700	Human Alu sequence
C 294	25	2.5	25	1	ABT03658	Human Med-6 gene p
C 295	24.8	2.5	29	1	AAH91598	Human inflammatory
C 296	24.6	2.5	29	1	AAA03985	Polymorphic fragme
C 297	24.4	2.5	26	1	ABK66984	Human gene specifi
C 298	24.4	2.5	26	1	AAH91530	Human inflammatory
C 299	24.4	2.5	28	1	AAA04000	Polymorphic fragme
C 300	24.4	2.5	29	1	AAA04507	Polymorphic fragme
C 301	24.4	2.5	29	1	AAA04507	Polymorphic fragme
C 302	24.4	2.5	29	1	AAA04369	Polymorphic fragme
C 303	24.4	2.5	29	1	AAA03994	Polymorphic fragme
C 304	24.4	2.5	29	1	AAA04389	Polymorphic fragme
C 305	24.4	2.5	29	1	AAA04314	Polymorphic fragme
C 306	24.4	2.5	30	1	AD182609	Prostate-specific
C 307	24.2	2.4	25	1	AAQ29012	Alu family consens
C 308	24.2	2.4	30	1	AAH91549	Human inflammatory
C 309	24.2	2.4	30	1	AAH91549	Human inflammatory
C 310	24	2.4	24	1	AAH45830	Telomere size dete
C 311	24	2.4	24	1	AAH45828	Telomere size dete
C 312	24	2.4	24	1	ADL07545	Sec24 protein-31.3
C 313	23.8	2.4	28	1	AAH91303	Human inflammatory
C 314	23.8	2.4	29	1	AAA03956	Polymorphic fragme
C 315	23.8	2.4	29	1	AAA03956	Polymorphic fragme
C 316	23.8	2.4	29	1	AAA04662	Polymorphic fragme
C 317	23.8	2.4	29	1	AAA04486	Polymorphic fragme
C 318	23.8	2.4	29	1	AAH03878	Polymorphic fragme
C 319	23.8	2.4	29	1	AAA04600	Polymorphic fragme
C 320	23.8	2.4	29	1	AAA04502	Polymorphic fragme
C 321	23.8	2.4	29	1	AAA04601	Polymorphic fragme
C 322	23.4	2.4	25	1	AAZ09548	Human Apo E oligon
C 323	23.4	2.4	25	1	AAH16609	Interleukin 1 (441
C 324	23.4	2.4	25	1	AAH14584	Human SNRP23 SNP r
C 325	23.4	2.4	25	1	AAH14584	Human SNRP23 SNP r

In-situ analysis s  
PCR primer #1, use  
Human MD27 scannin  
Human interleukin-  
PCR primer for SGR  
SNP specific SNPE  
Reverse primer ill  
NTP peptide encodi  
RT-PCR primer 2 re  
Polymorphic fragme  
Human inflammatory  
PCR primer F1209 u  
Human inflammatory  
X-T-D oligonucleot  
Inter-Alu region p  
Human NOV-associat  
Human NOV20a RTQ-P  
SNP specific SNPE  
SNP specific SNPE  
SNP specific SNPE  
SNP specific SNPE  
Human inflammatory  
Human ABC1 transcr  
Human transglutami  
PCR primer #2, use  
Zinc finger protei  
Human arginase 9  
Human breast susc  
Human PSF promoter  
Human genomic DNA  
Human TGNP promote  
PCR primer SEQ ID  
Human VRI exon 1d  
Human IL-1 genotyp  
SNP specific SNPE  
Human MD27 scannin  
Human MD27 scannin  
Single multiplex p  
Single multiplex p  
Nucleotide sequenc  
AHRECSAPO transge  
Human Alu sequence  
Human thyroid mal  
NTP peptide encodi  
Mouse SNM5, untra  
SNP specific SNPE  
Human MD27 scannin  
Human MD27 scannin  
Human MD27 scannin  
Primer sequence R2  
Human inflammatory  
SNP specific SNPE  
SNP specific SNPE  
Human inflammatory  
Primer B2C to isol  
Human zinc finger  
RT-PCR primer #1 f  
RT-PCR primer #2 f  
Human alkylation D  
Human acid phospho  
PCR primer #1 used  
RT-PCR primer #1 f  
SNP specific SNPE  
Oligonucleotide us  
Human NOV3 Exon 1i  
Human gene specifi  
Human PEFT1 PCR pr  
Mutant human BRCAl  
Primer Alu-S binds  
Human gene single  
Human Alu sequence

399	21	2.1	21	1	ABSG8163	Human multidrug re	472	20	2.0	20	1	AAZ35378	Interspersed repea
C 400	21	2.1	21	1	ADFG8789	Human TNF-alpha in	C 473	20	2.0	20	1	AAAI945	PCR primer SRI use
C 401	21	2.1	21	1	ADDS5495	HIV gene expressio	C 474	20	2.0	20	1	AAAD14808	Human glycogen syn
C 402	21	2.1	23	1	ADHI3395	Human malignant ne	C 475	20	2.0	20	1	AAK95176	Human cDNA clone-s
C 403	20.8	2.1	24	1	AAV19046	Alu PCR primer 3.	C 476	20	2.0	20	1	AAFB0866	Human mdm2 phospho
C 404	20.8	2.1	24	1	AAAZ7181	Reverse primer p2	C 477	20	2.0	20	1	AAFB0891	Human mdm2 phospho
C 405	20.8	2.1	24	1	AAI65251	Human dihydroorota	C 478	20	2.0	20	1	AAFB0890	Human mdm2 phospho
C 406	20.8	2.1	24	1	AAAF24627	Primer for a polym	C 479	20	2.0	20	1	AAFB38246	SNP specific lower
C 407	20.8	2.1	24	1	AAAF24635	Primer for polymer	C 480	20	2.0	20	1	AAAS29506	Human mdm2 antisen
C 408	20.8	2.1	24	1	AAAF75870	Human reverse tran	C 481	20	2.0	20	1	AAAS29505	Human mdm2 antisen
C 409	20.8	2.1	24	1	AAAI2447	Ribosome size prot	C 482	20	2.0	20	1	AAAS29481	Human mdm2 antisen
C 410	20.8	2.1	24	1	AAI65332	Human pterin-molyb	C 483	20	2.0	20	1	AAK96932	Human Beta-globin
C 411	20.8	2.1	24	1	AAI71673	Human myosin heavy	C 484	20	2.0	20	1	ABSS59253	Human CAS gene ant
C 412	20.8	2.1	24	1	AAAF69782	Human IL4alpha ge	C 485	20	2.0	20	1	ABSF67840	Human casein kinase
C 413	20.8	2.1	24	1	AAI68386	Human ATP-dependen	C 486	20	2.0	20	1	AAI40355	Human caspase 6 an
C 414	20.8	2.1	24	1	ABAB82841	Human protective D	C 487	20	2.0	20	1	AAI40351	Human caspase 6 an
C 415	20.8	2.1	24	1	ABIS59102	PCR primer used to	C 488	20	2.0	20	1	AAI40354	Human caspase 6 an
C 416	20.8	2.1	24	1	ABKI4186	Human splicing fac	C 489	20	2.0	20	1	ABLI44512	Human chromosome 1
C 417	20.8	2.1	24	1	ABKI2860	Human topoisomeras	C 490	20	2.0	20	1	ABAI44004	Human chromosome 1
C 418	20.8	2.1	24	1	ABZ25248	Human peroxidase 9	C 491	20	2.0	20	1	ABAI92187	Polymorphisim 506B1
C 419	20.8	2.1	24	1	ABAO2134	Human zinc ion tra	C 492	20	2.0	20	1	ABAI92208	Reverse PCR primer
C 420	20.8	2.1	24	1	ABSI6055	Human microtubulin	C 493	20	2.0	20	1	AAAS6659	Telomerase reverse
C 421	20.8	2.1	24	1	ABBS7470	Human plasminogen	C 494	20	2.0	20	1	ABK91100	PCR primer Alu3. f
C 422	20.8	2.1	24	1	ABZ21093	Starch precursor p	C 495	20	2.0	20	1	ACC40946	Human superoxide d
C 423	20.8	2.1	24	1	ACA90126	Human kinesin gene	C 496	20	2.0	20	1	ABZ79385	Acetyl-Coenzyme A-
C 424	20.8	2.1	24	1	ACCA90127	Human kinesin gene	C 497	20	2.0	20	1	AAI60008	Human GH-1 gene am
C 425	20.8	2.1	24	1	ACCS7313	Zinc finger protei	C 498	20	2.0	20	1	ADD21702	Human mdm2 antisen
C 426	20.8	2.1	24	1	ADGB3872	Human SLG6A14 forw	C 499	20	2.0	20	1	ADD21701	Human mdm2 antisen
C 427	20.8	2.1	25	1	AAZ24391	Chemokine receptor	C 500	20	2.0	20	1	ABD21677	Human RANTES oligo
C 428	20.8	2.1	25	1	ABD04739	Human MD27 scannin	C 501	20	2.0	20	1	ABZ97911	Human RANTES oligo
C 429	20.8	2.1	25	1	ABD04618	Human MD27 scannin	C 502	20	2.0	20	1	ABZ99076	Human PDE4C oligon
C 430	20.8	2.1	25	1	ABD04738	Human MD27 scannin	C 503	20	2.0	20	1	ABZ98014	Human RANTES oligo
C 431	20.8	2.1	25	1	ABD04740	Human MD27 scannin	C 504	20	2.0	20	1	ABZ99055	Human PDE4C oligon
C 432	20.8	2.1	25	1	ABD04617	Human MD27 scannin	C 505	20	2.0	20	1	ABZ99075	Human PDE4C oligon
C 433	20.8	2.1	25	1	ABD04578	Human MD27 scannin	C 506	20	2.0	20	1	ABZ92715	Human oligonucleot
C 434	20.8	2.1	25	1	ABD04746	Human MD27 scannin	C 507	20	2.0	20	1	ABZ92716	Human oligonucleot
C 435	20.8	2.1	25	1	ABD04580	Human MD27 scannin	C 508	20	2.0	20	1	ABZ99068	Human PDE4C oligon
C 436	20.8	2.1	25	1	AD011741	Single multiplex P	C 509	20	2.0	20	1	ABX94882	Human MBH1K recep
C 437	20.4	2.1	22	1	AAZ25152	Human short inters	C 510	20	2.0	20	1	ADL25066	Intestinal epithel
C 438	20.4	2.1	22	1	AAZ25149	Human short inters	C 511	20	2.0	20	1	ADM65742	Human Y chromosome
C 439	20.4	2.1	22	1	AAZ25146	Human short inters	C 512	20	2.0	20	1	ADM65739	Human Y chromosome
C 440	20.4	2.1	22	1	AAZ25146	Human short inters	C 513	20	2.0	20	1	ADM65575	NK1 polymorphisim d
C 441	20.4	2.1	22	1	AAZ25146	Human ABC1 BAC con	C 514	20	2.0	20	1	ADM65745	Human Y chromosome
C 442	20.4	2.1	22	1	AAZ25146	Primer #66. Homo	C 515	20	2.0	20	1	ADM65578	NK1 polymorphisim d
C 443	20.4	2.1	22	1	ADL66997	Multiplex PCR prim	C 516	20	2.0	20	1	ADM34330	Human cryopyrin cd
C 444	20.4	2.1	23	1	AAO30457	Human novel GPCR p	C 517	20	2.0	20	1	ABD33099	Human PDE4C-deriv
C 445	20.4	2.1	24	1	AAH49787	Human IL4alpha ge	C 518	20	2.0	20	1	ABD31045	Human RANTES-deriv
C 446	20.4	2.1	24	1	ABBS6869	Human uncoiling en	C 519	20	2.0	20	1	ABD30942	Human RANTES-deriv
C 447	20.4	2.1	25	1	AAH40563	SNP specific SNPE	C 520	20	2.0	20	1	ABD32107	Human PDE4C-deriv
C 448	20.2	2.0	25	1	AAH38991	SNP specific SNPE	C 521	20	2.0	20	1	ABD28946	NS473-derived oli
C 449	20.2	2.0	25	1	AAH40899	SNP specific SNPE	C 522	20	2.0	20	1	ABD32106	Human PDE4C-deriv
C 450	20.2	2.0	25	1	AAH37979	SNP specific SNPE	C 523	20	2.0	20	1	ABD32086	Human PDE4C-deriv
C 451	20.2	2.0	25	1	AAH37611	SNP specific SNPE	C 524	20	2.0	20	1	ABD28945	NS473-derived oli
C 452	20.2	2.0	25	1	AAH39587	SNP specific SNPE	C 525	20	2.0	20	1	ADT80086	Human transforming
C 453	20.2	2.0	25	1	AAH39123	SNP specific SNPE	C 526	20	2.0	20	1	ADT80087	Human transforming
C 454	20.2	2.0	25	1	AAH40067	SNP specific SNPE	C 527	20	2.0	20	1	ADT80087	Human transforming
C 455	20.2	2.0	25	1	AAH40295	SNP specific SNPE	C 528	20	2.0	20	1	ADT80221	Human transforming
C 456	20.2	2.0	25	1	ABD04682	Human MD27 scannin	C 529	20	2.0	20	1	ADJ53542	Human PPI3CB DNA a
C 457	20.2	2.0	25	1	ABD04614	Human MD27 scannin	C 530	20	2.0	20	1	ADJ53600	Human PPI3CB DNA a
C 458	20.2	2.0	25	1	ABD04577	Human MD27 scannin	C 531	20	2.0	20	1	ADJ60953	Oligonucleotide as
C 459	20.2	2.0	25	1	ABD04684	Human MD27 scannin	C 532	20	2.0	20	1	ADJ60960	Oligonucleotide as
C 460	20.2	2.0	25	1	ABD04683	Human MD27 scannin	C 533	20	2.0	20	1	ADJ59879	Oligonucleotide as
C 461	20.2	2.0	25	1	ABD04576	Human MD27 scannin	C 534	20	2.0	20	1	ADJ60940	Oligonucleotide as
C 462	20.2	2.0	25	1	ABD04581	Human MD27 scannin	C 535	20	2.0	20	1	ADJ60961	Oligonucleotide as
C 463	20.2	2.0	25	1	ADJ70378	Probe used to anly	C 536	20	2.0	20	1	ADJ59776	Oligonucleotide as
C 464	20	2.0	20	1	AAAT7304	PCR primer used to	C 537	20	2.0	20	1	ADL23339	Primer #1 for ampl
C 465	20	2.0	20	1	AAAT7303	PCR primer SRI use	C 538	20	2.0	20	1	ADL32388	Clone specific PCR
C 466	20	2.0	20	1	AAV85582	LRP5 PCR primer Gp	C 539	20	2.0	20	1	ADL61592	Human protein tyro
C 467	20	2.0	20	1	AAV69963	Human c-fos protei	C 540	20	2.0	20	1	ADM14394	Human mPGES-1 chim
C 468	20	2.0	20	1	AAZ37736	Human mdm2 phospho	C 541	20	2.0	20	1	ADM14746	Human mPGES-1 chim
C 469	20	2.0	20	1	AAZ37712	Human mdm2 phospho	C 542	20	2.0	20	1	ADM14277	Human mPGES-1 chim
C 470	20	2.0	20	1	AAZ37737	Human mdm2 phospho	C 543	20	2.0	20	1	ADM14482	Human mPGES-1 chim
C 471	20	2.0	20	1	AAA96410	Primer used to amp	C 544	20	2.0	20	1	ADM15309	Human mPGES-1 chim

C 545	20	2.0	20	1	ADM15160	Human mPGES-1 chim	C 618	19.4	2.0	22	1	AAF93028	Polymorphic sequen
C 546	20	2.0	20	1	ADM14957	Human mPGES-1 chim	C 619	19.4	2.0	22	1	ADC24360	PCR primer for amp
C 547	20	2.0	20	1	ADM15553	Human mPGES-1 chim	C 620	19.4	2.0	24	1	AAQ73576	Enhancer element e
C 548	20	2.0	20	1	ADM15081	Human mPGES-1 chim	C 621	19.4	2.0	24	1	AAQ73577	Enhancer element e
C 549	20	2.0	20	1	ADM15268	Human mPGES-1 chim	C 622	19.2	1.9	20	1	AA763214	Primer Alu 5' used
C 550	20	2.0	20	1	ADM14958	Human oligonucleot	C 623	19.2	1.9	24	1	AAA35956	Human genomic SNP
C 551	20	2.0	20	1	ADM45369	Human oligonucleot	C 624	19.2	1.9	24	1	AA427180	Forward primer P2
C 552	20	2.0	20	1	ADO46449	Human oligonucleot	C 625	19.2	1.9	24	1	AA45660	PCR primer specifici
C 553	20	2.0	20	1	ADO46442	Human oligonucleot	C 626	19.2	1.9	24	1	AA46154	Cysteine protease
C 554	20	2.0	20	1	ADO45266	Human oligonucleot	C 627	19.2	1.9	24	1	AA47565	Human Pax protein
C 555	20	2.0	20	1	ADO46449	Human oligonucleot	C 628	19.2	1.9	24	1	AA48397	Human ABC1 transcr
C 556	20	2.0	20	1	ADO46450	Human oligonucleot	C 629	19.2	1.9	24	1	AA492846	Fumarate 9 PCR pri
C 557	20	2.0	20	1	ADO81016	Human prion protei	C 630	19.2	1.9	24	1	AA48397	Primer #7. Uniden
C 558	20	2.0	20	1	ADO52209	Human inhibitor of	C 631	19.2	1.9	24	1	AAH37609	SNP specific lower
C 559	20	2.0	20	1	ADO52273	Human inhibitor of	C 632	19.2	1.9	24	1	AAH37609	SNP specific upper
C 560	20	2.0	20	1	AAV27991	Ataxia telangiecta	C 633	19.2	1.9	24	1	AAH37609	PCR primer used to
C 561	20	2.0	20	1	AAZ25145	Human short inters	C 634	19.2	1.9	24	1	AA164727	Human line 1-12 PC
C 562	20	2.0	20	1	AAZ25143	Human short inters	C 635	19.2	1.9	24	1	ABO83629	Human mper3-10.01
C 563	20	2.0	20	1	AAZ25144	Human short inters	C 636	19.2	1.9	24	1	ABV76754	Human sailer trans
C 564	20	2.0	20	1	AAZ25144	Human short inters	C 637	19.2	1.9	24	1	ABQ84159	Human alpha 2,3-si
C 565	20	2.0	20	1	ADG70428	REN-34 SNP binding	C 638	19.2	1.9	24	1	ABQ84159	Human G protein su
C 566	20	2.0	20	1	ADG70427	REN-34 SNP binding	C 639	19.2	1.9	24	1	ABV72841	Guanosine triphosp
C 567	20	2.0	20	1	ADG70427	Single multiplex p	C 640	19.2	1.9	24	1	ABE20663	Ras GTP enzyme-act
C 568	20	2.0	20	1	ADG70427	Human short inters	C 641	19.2	1.9	24	1	ABX14631	Human natruietic
C 569	20	2.0	20	1	ADG70427	Human short inters	C 642	19.2	1.9	24	1	ABV96633	Human phytochrome
C 570	20	2.0	20	1	AAZ25151	Human short inters	C 643	19.2	1.9	24	1	AAZ20139	Human phosphatidic
C 571	20	2.0	20	1	AAZ25151	Human short inters	C 644	19.2	1.9	24	1	AB199962	Human cytokine rec
C 572	20	2.0	20	1	AAZ25147	Human short inters	C 645	19.2	1.9	24	1	AA172742	Human oncoegene pro
C 573	20	2.0	20	1	ABLS55369	Human leucine zipp	C 646	19.2	1.9	24	1	AA143822	Human SOX3 protein
C 574	20	2.0	20	1	ADG56863	RT-PCR primer Seq	C 647	19.2	1.9	24	1	ABSS5854	Human SOX3 protein
C 575	20	2.0	20	1	AAH77559	Human dihydroxyrio	C 648	19.2	1.9	24	1	ABL40967	Polyptide-1-hexoki
C 576	20	2.0	20	1	AAH77559	Primer #14. Homo	C 649	19.2	1.9	24	1	ABSS57191	Amylase 9.35 speci
C 577	20	2.0	20	1	AAH77559	Primer #13 forward	C 650	19.2	1.9	24	1	ABO81233	Human 14273 probe.
C 578	20	2.0	20	1	AAH77559	Primer #1 to ampli	C 651	19.2	1.9	24	1	ABA04729	Human Parkinson B
C 579	20	2.0	20	1	ADG47348	Human SORBS1 gene	C 652	19.2	1.9	24	1	ABO77823	Human ubiquitin-bi
C 580	20	2.0	20	1	ADG47348	PCR primer for hum	C 653	19.2	1.9	24	1	ABO77823	Human protein phos
C 581	20	2.0	20	1	AAH46454	Oligonucleotide pr	C 654	19.2	1.9	24	1	ADG14009	Optineurin promote
C 582	20	2.0	20	1	AAH46454	SNP specific upper	C 655	19.2	1.9	24	1	AA794773	Human progestatone
C 583	20	2.0	20	1	AAH46454	Enolpyruvate phosp	C 656	19.2	1.9	24	1	AA184754	FISH primer for hu
C 584	20	2.0	20	1	AAH46454	Human RNA helicase	C 657	19.2	1.9	24	1	AA184754	SNP specific upper
C 585	20	2.0	20	1	ABLA1338	Human TRIID subun	C 658	19.2	1.9	24	1	AAH38421	SNP specific upper
C 586	20	2.0	20	1	AAH38421	Human phosphatidy	C 659	19.2	1.9	24	1	AAH38421	Presenilin-1 gene
C 587	20	2.0	20	1	AAH38421	Human GDD DNA ampl	C 660	19.2	1.9	24	1	AAH38421	Human chromosome 1
C 588	20	2.0	20	1	AAH38421	Primer #2 relatin	C 661	19.2	1.9	24	1	AAH38421	Intestinal epithel
C 589	20	2.0	20	1	AAH38421	Human RNA polymera	C 662	19.2	1.9	24	1	AAH38421	Human interleukin-
C 590	20	2.0	20	1	AAH38421	Human protein phos	C 663	19.2	1.9	24	1	AAH38421	CENPc1 extend prim
C 591	20	2.0	20	1	AAH38421	Single multiplex p	C 664	19.2	1.9	24	1	AAH38421	LRP5 exon primer 5
C 592	20	2.0	20	1	AAH38421	PCR primer for and	C 665	19.2	1.9	24	1	AAH38421	Human mdm2 phospho
C 593	20	2.0	20	1	AAH38421	SNP specific lower	C 666	19.2	1.9	24	1	AAH38421	Human mdm2 phospho
C 594	20	2.0	20	1	AAH38421	SNP specific upper	C 667	19.2	1.9	24	1	AAH38421	Human mdm2 phospho
C 595	20	2.0	20	1	AAH38421	Human polymorphic	C 668	19.2	1.9	24	1	AAH38421	Human mdm2 antisen
C 596	20	2.0	20	1	AAH38421	Human polymorphic	C 669	19.2	1.9	24	1	AAH38421	Human mdm2 antisen
C 597	20	2.0	20	1	AAH38421	Primer #84. Homo	C 670	19.2	1.9	24	1	AAH38421	Human mdm2 antisen
C 598	20	2.0	20	1	AAH38421	Human DISC1/DISC2	C 671	19.2	1.9	24	1	AAH38421	Human mdm2 antisen
C 599	20	2.0	20	1	AAH38421	Human multidrug re	C 672	19.2	1.9	24	1	AAH38421	Human caspase 8 nk
C 600	20	2.0	20	1	AAH38421	Human FANCD2 PCR p	C 673	19.2	1.9	24	1	AAH38421	Human TGF-beta rec
C 601	20	2.0	20	1	AAH38421	Optineurin promote	C 674	19.2	1.9	24	1	AAH38421	Human mdm2 antisen
C 602	20	2.0	20	1	AAH38421	Non-nucleotide pro	C 675	19.2	1.9	24	1	AAH38421	Human mdm2 antisen
C 603	20	2.0	20	1	AAH38421	Non-nucleotide pro	C 676	19.2	1.9	24	1	AAH38421	Human mdm2 antisen
C 604	20	2.0	20	1	AAH38421	Non-nucleotide pro	C 677	19.2	1.9	24	1	AAH38421	Human mdm2 antisen
C 605	20	2.0	20	1	AAH38421	Non-nucleotide pro	C 678	19.2	1.9	24	1	AAH38421	Human mdm2 antisen
C 606	20	2.0	20	1	AAH38421	Non-nucleotide pro	C 679	19.2	1.9	24	1	AAH38421	Human mdm2 antisen
C 607	20	2.0	20	1	AAH38421	Human NF-kappaB as	C 680	19.2	1.9	24	1	AAH38421	Human mdm2 antisen
C 608	20	2.0	20	1	AAH38421	Human LpLIR PCR pr	C 681	19.2	1.9	24	1	AAH38421	Human mdm2 antisen
C 609	20	2.0	20	1	AAH38421	Single multiplex p	C 682	19.2	1.9	24	1	AAH38421	Human mdm2 antisen
C 610	20	2.0	20	1	AAH38421	Human short inters	C 683	19.2	1.9	24	1	AAH38421	Human mdm2 antisen
C 611	20	2.0	20	1	AAH38421	Human short inters	C 684	19.2	1.9	24	1	AAH38421	Human mdm2 antisen
C 612	20	2.0	20	1	AAH38421	Human short inters	C 685	19.2	1.9	24	1	AAH38421	Human mdm2 antisen
C 613	20	2.0	20	1	AAH38421	Human short inters	C 686	19.2	1.9	24	1	AAH38421	Human mdm2 antisen
C 614	20	2.0	20	1	AAH38421	Human short inters	C 687	19.2	1.9	24	1	AAH38421	Human mdm2 antisen
C 615	20	2.0	20	1	AAH38421	Human short inters	C 688	19.2	1.9	24	1	AAH38421	Human mdm2 antisen
C 616	20	2.0	20	1	AAH38421	Human short inters	C 689	19.2	1.9	24	1	AAH38421	Human mdm2 antisen
C 617	20	2.0	20	1	AAH38421	Human CYP2B6 allel	C 690	19.2	1.9	24	1	AAH38421	Human mdm2 antisen

C 691	19	1.9	20	1	ADN15184	Human mPGES-1 chim	C 764	18.4	1.9	20	1	ABZ71056	Human HKR1 phospho
692	19	1.9	20	1	AD045265	Human oligonucleot	C 765	18.4	1.9	20	1	ADA20921	Human BAX chimeric
693	19	1.9	20	1	AD045357	Human oligonucleot	766	18.4	1.9	20	1	ACF33682	MHC class II trans
694	19	1.9	20	1	ADP08716	Extend primer 53 u	767	18.4	1.9	20	1	ABT44432	Chimeric antisense
C 695	19	1.9	20	1	ADG30202	PKR-targeted siNA	C 768	18.4	1.9	20	1	ADD21681	Human mdm2 antisen
C 696	19	1.9	21	1	ADL25334	Intestinal epithel	C 769	18.4	1.9	20	1	ADD21703	Human mdm2 antisen
697	19	1.9	22	1	AAZ25156	Human short inters	C 770	18.4	1.9	20	1	ADDE43606	Human KNSL1 sequen
698	19	1.9	22	1	AAZ25157	Human short inters	C 771	18.4	1.9	20	1	ADDE46781	Human KNSL1 sequen
699	19	1.9	22	1	AAZ25158	Human short inters	772	18.4	1.9	20	1	AD161628	GATA primer #1. H
700	19	1.9	22	1	AAZ25170	Human short inters	773	18.4	1.9	20	1	ABZ97965	Human SAP-1 gene t
701	19	1.9	22	1	AAZ25172	Human short inters	C 774	18.4	1.9	20	1	ABZ89864	Human oligonucleot
702	19	1.9	22	1	AAZ25159	Human short inters	775	18.4	1.9	20	1	ABZ97964	Human RANTES oligo
703	19	1.9	22	1	AAZ25163	Human short inters	776	18.4	1.9	20	1	ABZ97909	Human RANTES oligo
704	19	1.9	22	1	AAZ25169	Human short inters	C 777	18.4	1.9	20	1	ABZ89861	Human oligonucleot
705	19	1.9	22	1	AAZ25171	Human short inters	778	18.4	1.9	20	1	ABZ97902	Human RANTES oligo
706	19	1.9	22	1	AAZ25160	Human short inters	779	18.4	1.9	20	1	ABZ97724	Human oligonucleot
707	19	1.9	22	1	AAZ25164	Human short inters	780	18.4	1.9	20	1	ABZ98012	Human RANTES oligo
708	19	1.9	22	1	AAZ25165	Human short inters	781	18.4	1.9	20	1	ABZ98015	Human RANTES oligo
709	19	1.9	22	1	ADG30198	PKR-targeted siNA	782	18.4	1.9	20	1	ABZ97908	Human RANTES oligo
710	18.8	1.9	22	1	AAZ39493	Steroidogenesis ac	783	18.4	1.9	20	1	ABZ98003	Human RANTES oligo
711	18.8	1.9	22	1	AAZ83018	Primer K to isolat	784	18.4	1.9	20	1	ABZ97903	Human RANTES oligo
C 712	18.8	1.9	22	1	AAZ69375	Human ABC1 BAC con	785	18.4	1.9	20	1	ABZ99062	Human PDE4C oligon
C 713	18.8	1.9	22	1	AAZ32938	Sequence tagged si	786	18.4	1.9	20	1	ABZ99105	Human PDE4C oligon
C 714	18.8	1.9	22	1	AAZ84349	Human CYP2C181 PCR	787	18.4	1.9	20	1	ABZ98013	Human RANTES oligo
C 715	18.8	1.9	22	1	AAZ29797	Preseniline-1 gene	788	18.4	1.9	20	1	ABZ99071	Human PDE4C oligon
C 716	18.8	1.9	22	1	AAZ31453	Human chromosome 1	C 789	18.4	1.9	20	1	ABZ89844	Human oligonucleot
C 717	18.8	1.9	22	1	AAZ31457	Human chromosome 1	790	18.4	1.9	20	1	ABZ92736	Human oligonucleot
C 718	18.8	1.9	22	1	AD166998	Multiplex PCR prim	791	18.4	1.9	20	1	ABZ99077	Human PDE4C oligon
C 719	18.8	1.9	22	1	AAZ37708	Human Rad51 antis	C 792	18.4	1.9	20	1	ACA88928	Selection and ampl
720	18.8	1.9	23	1	AAZ501201	Human RAD51 antis	C 793	18.4	1.9	20	1	ADA26875	Human PR-3 forwar
721	18.8	1.9	23	1	AD43247	Antisense oligonuc	794	18.4	1.9	20	1	ADL24948	Intestinal epithel
C 722	18.8	1.9	23	1	ADH26585	Human hUNC93B1 pool	795	18.4	1.9	20	1	ADL25083	Intestinal epithel
C 723	18.4	1.9	20	1	AAZ10907	Human cytochrome P	796	18.4	1.9	20	1	ABD31093	Human RANTES-deriv
C 724	18.4	1.9	20	1	AAZ66010	Primer #1 to ampli	797	18.4	1.9	20	1	ABD31043	Human RANTES-deriv
C 725	18.4	1.9	20	1	AAZ66017	Primer #2 to ampli	798	18.4	1.9	20	1	ABD32136	Human PDE4C-deriv
C 726	18.4	1.9	20	1	AAZ94341	Human DPC4 sequenc	799	18.4	1.9	20	1	ABD31044	Human RANTES-deriv
C 727	18.4	1.9	20	1	AAZ85762	LRPS exon primer 5	800	18.4	1.9	20	1	ABD28966	Human PDE4C-deriv
C 728	18.4	1.9	20	1	AAZ85840	LRPS SNP primer 57	801	18.4	1.9	20	1	ABD30933	Human RANTES-deriv
729	18.4	1.9	20	1	AAZ85801	LRPS exon primer 5	C 802	18.4	1.9	20	1	ABD26091	AA463249-derived o
730	18.4	1.9	20	1	AAZ85879	LRPS SNP primer 58	C 803	18.4	1.9	20	1	ABD26094	Human RANTES-deriv
C 731	18.4	1.9	20	1	AAZ90795	Human 7SL RNA spec	804	18.4	1.9	20	1	ABD30934	Human RANTES-deriv
732	18.4	1.9	20	1	AAZ86546	Primer r6617 used	805	18.4	1.9	20	1	ABD31046	Human RANTES-deriv
C 733	18.4	1.9	20	1	AAZ37738	Human mdm2 phospho	806	18.4	1.9	20	1	ABD32108	Human PDE4C-deriv
C 734	18.4	1.9	20	1	AAZ37736	Human mdm2 phospho	807	18.4	1.9	20	1	ABD32093	Human PDE4C-deriv
735	18.4	1.9	20	1	AAA28013	Uncoupling protein	C 808	18.4	1.9	20	1	ABD26074	AA463249-derived o
736	18.4	1.9	20	1	AAA11943	Human MDX antis	809	18.4	1.9	20	1	ABD30995	Human RANTES-deriv
737	18.4	1.9	20	1	AAZ52253	Primer ZC12502 for	810	18.4	1.9	20	1	ABD31034	Human RANTES-deriv
C 738	18.4	1.9	20	1	AAZ31822	Human RANK antis	811	18.4	1.9	20	1	ABD30940	Human RANTES-deriv
C 739	18.4	1.9	20	1	AAZ31823	Human RANK antis	812	18.4	1.9	20	1	ABD30996	Human RANTES-deriv
C 740	18.4	1.9	20	1	AAZ14819	Human glycogen syn	813	18.4	1.9	20	1	ABD28954	NS8473-derived oli
C 741	18.4	1.9	20	1	AAZ14817	Human glycogen syn	814	18.4	1.9	20	1	ABD32102	Human PDE4C-deriv
C 742	18.4	1.9	20	1	AAZ95122	Human CDNA clone-s	C 815	18.4	1.9	20	1	ADH70951	Human Vbeta PCR pr
743	18.4	1.9	20	1	AAH02356	Human AKAP10 codin	C 816	18.4	1.9	20	1	ADH54084	Human neurodegener
C 744	18.4	1.9	20	1	AAZ92892	Human ABC1 transcr	817	18.4	1.9	20	1	ADL25029	Human ZNF9 exon 1
745	18.4	1.9	20	1	AAZ18044	PCR primer for a m	C 818	18.4	1.9	20	1	ADH76733	MCCHR1 genomic sequ
C 746	18.4	1.9	20	1	AAZ80892	Human mdm2 phospho	819	18.4	1.9	20	1	ADH76678	MCCHR1 locus SNP pr
C 747	18.4	1.9	20	1	AAZ80870	Human mdm2 phospho	820	18.4	1.9	20	1	ADH76813	MCCHR1 locus SNP pr
748	18.4	1.9	20	1	AAZ38602	SNP specific lower	C 821	18.4	1.9	20	1	ADJ46556	Human requiem targ
C 749	18.4	1.9	20	1	AAH37610	SNP specific lower	822	18.4	1.9	20	1	ADJ46607	Human requiem anti
C 750	18.4	1.9	20	1	AAH40090	SNP specific lower	823	18.4	1.9	20	1	ADJ59878	Oligonucleotide as
C 751	18.4	1.9	20	1	AAZ28586	Epo-R PCR primer #	824	18.4	1.9	20	1	ADJ59868	Oligonucleotide as
C 752	18.4	1.9	20	1	AAZ28587	Primer JNF14 to is	825	18.4	1.9	20	1	ADJ59877	Oligonucleotide as
C 753	18.4	1.9	20	1	AAH20704	Human telomeric re	826	18.4	1.9	20	1	ADJ60947	Oligonucleotide as
C 754	18.4	1.9	20	1	AAH20699	Human telomeric re	827	18.4	1.9	20	1	ADJ59768	Oligonucleotide as
C 755	18.4	1.9	20	1	AAZ29507	Human mdm2 antis	828	18.4	1.9	20	1	ADJ60990	Oligonucleotide as
C 756	18.4	1.9	20	1	AAZ29485	Human mdm2 antis	829	18.4	1.9	20	1	ADJ59767	Oligonucleotide as
757	18.4	1.9	20	1	AAZ28754	Target specific PC	830	18.4	1.9	20	1	ADJ59830	Oligonucleotide as
758	18.4	1.9	20	1	AAZ40357	Human caspase 6 an	831	18.4	1.9	20	1	ADJ59829	Oligonucleotide as
C 759	18.4	1.9	20	1	ABK68939	Human phosphorylas	832	18.4	1.9	20	1	ADJ60962	Oligonucleotide as
C 760	18.4	1.9	20	1	AAJ38181	Human BH3 interact	833	18.4	1.9	20	1	ADJ59773	Oligonucleotide as
C 761	18.4	1.9	20	1	AAJ38190	Human BH3 interact	834	18.4	1.9	20	1	ADJ59774	Oligonucleotide as
C 762	18.4	1.9	20	1	ABQ74794	Human TNFR2 antis	835	18.4	1.9	20	1	ADJ59880	Oligonucleotide as
C 763	18.4	1.9	20	1	ACC55324	Human ADAMTS13 SFS	836	18.4	1.9	20	1	ADJ60956	Oligonucleotide as

837	18.4	1.9	20	1	ADJ96297	Human breast cance	C 910	18.2	1.8	19	1	AA048683	Human Alu segment
C 838	18.4	1.9	20	1	ADJ96333	Human breast cance	C 911	18.2	1.8	19	1	AA085677	PCR primer alu 2 f
839	18.4	1.9	20	1	ADJ96393	Human breast cance	C 912	18.2	1.8	19	1	AA085676	PCR primer alu 1 f
C 840	18.4	1.9	20	1	ADJ96457	Human breast cance	C 913	18.2	1.8	19	1	AA076249	Generic Alu consen
C 841	18.4	1.9	20	1	ADJ10233	Clonase specific PCR	C 914	18.2	1.8	19	1	AA076247	Generic primer fro
842	18.4	1.9	20	1	ADJ10232	Phosphorothioate a	C 915	18.2	1.8	19	1	AA076247	PCR primer used to
C 843	18.4	1.9	20	1	ADJ10783	Primer of the inve	C 916	18	1.8	18	1	AA076247	Human biallelic po
C 844	18.4	1.9	20	1	ADJ10783	Primer of the inve	C 917	18	1.8	18	1	AA076247	Human FLAME-1 PCR
C 845	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 918	18	1.8	18	1	AA076247	Human FLAME-1 PCR
C 846	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 919	18	1.8	18	1	AA076247	Human CREL mRNA in
C 847	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 920	18	1.8	18	1	AA076247	SNP specific lower
C 848	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 921	18	1.8	18	1	AA076247	SNP specific lower
C 849	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 922	18	1.8	18	1	AA076247	Human FLAME-1 spec
C 850	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 923	18	1.8	18	1	AA076247	Human FLAME-1 spec
C 851	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 924	18	1.8	18	1	AA076247	Murine TRPV trans
C 852	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 925	18	1.8	18	1	AA076247	Non-nucleotide pro
C 853	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 926	18	1.8	18	1	AA076247	Non-nucleotide pro
C 854	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 927	18	1.8	18	1	AA076247	NTP peptide encodi
C 855	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 928	18	1.8	18	1	AA076247	SNP specific lower
C 856	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 929	18	1.8	18	1	AA076247	Human inflammatory
C 857	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 930	18	1.8	18	1	AA076247	Forward PCR primer
C 858	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 931	18	1.8	18	1	AA076247	Human familial bip
C 859	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 932	18	1.8	18	1	AA076247	Human cancer supp
C 860	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 933	18	1.8	18	1	AA076247	Human POLYX PCR pr
C 861	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 934	18	1.8	18	1	AA076247	Human interleukin-
C 862	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 935	18	1.8	18	1	AA076247	Extend primer 86 u
C 863	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 936	18	1.8	18	1	AA076247	SNP specific lower
C 864	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 937	18	1.8	18	1	AA076247	Human telomeric re
C 865	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 938	18	1.8	18	1	AA076247	Human hepatocellul
C 866	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 939	18	1.8	18	1	AA076247	Human RANTES oligo
C 867	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 940	18	1.8	18	1	AA076247	Human oligonucleot
C 868	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 941	18	1.8	18	1	AA076247	NS473-derived oli
C 869	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 942	18	1.8	18	1	AA076247	Human RANTES-deriv
C 870	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 943	18	1.8	18	1	AA076247	Human RPTN12 antis
C 871	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 944	18	1.8	18	1	AA076247	Oligonucleotide as
C 872	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 945	18	1.8	18	1	AA076247	Human mPGEs-1 chim
C 873	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 946	18	1.8	18	1	AA076247	Human oligonucleot
C 874	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 947	18	1.8	18	1	AA076247	Polyomorph ic fragme
C 875	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 948	18	1.8	18	1	AA076247	Human ASTH1J 5' re
C 876	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 949	18	1.8	18	1	AA076247	SNP specific upper
C 877	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 950	18	1.8	18	1	AA076247	Single nucleotide
C 878	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 951	18	1.8	18	1	AA076247	Primer specific fo
879	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 952	18	1.8	18	1	AA076247	Biomarker UC band
880	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 953	18	1.8	18	1	AA076247	Human chromosome 1
881	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 954	18	1.8	18	1	AA076247	Human Alu-specific
882	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 955	18	1.8	18	1	AA076247	Human Alu-specific
883	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 956	18	1.8	18	1	AA076247	Reverse transcript
884	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 957	18	1.8	18	1	AA076247	Reverse transcript
885	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 958	18	1.8	18	1	AA076247	Reverse transcript
886	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 959	18	1.8	18	1	AA076247	Human beta-globin
887	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 960	18	1.8	18	1	AA076247	Primer G to isolat
888	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 961	18	1.8	18	1	AA076247	Primer used when o
889	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 962	18	1.8	18	1	AA076247	Sense primer used
890	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 963	18	1.8	18	1	AA076247	Human TSC gene exo
891	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 964	18	1.8	18	1	AA076247	Human polymorphic
892	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 965	18	1.8	18	1	AA076247	PCR amplification
C 893	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 966	18	1.8	18	1	AA076247	Primer 1 for human
C 894	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 967	18	1.8	18	1	AA076247	Human beta-globin
895	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 968	18	1.8	18	1	AA076247	SNP specific lower
896	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 969	18	1.8	18	1	AA076247	SNP specific upper
C 897	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 970	18	1.8	18	1	AA076247	Human polymorphis
C 898	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 971	18	1.8	18	1	AA076247	Human chymotrypsin
C 899	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 972	18	1.8	18	1	AA076247	Microsatellite typ
C 900	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 973	18	1.8	18	1	AA076247	Human multilidng re
C 901	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 974	18	1.8	18	1	AA076247	Human multilidng re
C 902	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 975	18	1.8	18	1	AA076247	Human multilidng re
C 903	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 976	18	1.8	18	1	AA076247	Human CYP4501A2 pr
C 904	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 977	18	1.8	18	1	AA076247	Human cytochrome-1
C 905	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 978	18	1.8	18	1	AA076247	Human tumour-associ
C 906	18.4	1.9	20	1	ADJ10783	Human mPGEs-1 chim	C 979	18	1.8	18	1	AA076247	NOV14 probe, SEQ 1
C 907	18.2	1.8	19	1	AA025869	5' Alu primer. SY	C 980	17.8	1.8	21	1	ADH47846	Novel human protei
908	18.2	1.8	19	1	AA025868	Human Alu segment	C 981	17.8	1.8	21	1	ABX97680	
909	18.2	1.8	19	1	AA048682	Human Alu segment	C 982	17.8	1.8	21	1	ABX97680	

c 983	17.8	1.8	21	1	ACF64055	1056	17.4	1.8	19	1	ADO80022	CENPC1 extend prim
984	17.8	1.8	21	1	ACF64053	c1057	17.4	1.8	20	1	AAZ07267	Human telomerase R
c 985	17.8	1.8	21	1	ADP11633	c1058	17.4	1.8	20	1	AAZ37719	Human mdm2 phospho
c 986	17.8	1.8	21	1	ADP11652	c1059	17.4	1.8	20	1	AAZ37727	Human mdm2 phospho
c 987	17.8	1.8	21	1	ADP12370	c1060	17.4	1.8	20	1	AAZ37726	Human mdm2 phospho
c 988	17.8	1.8	21	1	ADP12525	c1061	17.4	1.8	20	1	AAZ21805	Exemplary oligonuc
c 989	17.8	1.8	21	1	ADH59601	c1062	17.4	1.8	20	1	AAAF31821	Human RANK antisen
c 990	17.8	1.8	21	1	ADH59613	c1063	17.4	1.8	20	1	AAAF80881	Human mdm2 phospho
991	17.8	1.8	21	1	ADJ95339	c1064	17.4	1.8	20	1	AAAF80873	Human mdm2 phospho
992	17.8	1.8	21	1	ADK01282	c1065	17.4	1.8	20	1	AAAF80880	Human mdm2 phospho
993	17.8	1.8	21	1	ADK01329	c1066	17.4	1.8	20	1	AAH40109	SNP specific upper
c 994	17.8	1.8	21	1	ADP68377	c1067	17.4	1.8	20	1	AAAC86127	Primer UNP15 to is
c 995	17.8	1.8	21	1	ADP68416	c1068	17.4	1.8	20	1	AAAS01235	Reverse PCR primer
c 996	17.8	1.8	21	1	ADK41377	c1069	17.4	1.8	20	1	AAAF74118	Primer #52. Homo
c 997	17.8	1.8	21	1	ADK41351	c1070	17.4	1.8	20	1	AAH20696	Human telomeric re
c 998	17.8	1.8	21	1	ADM32366	c1071	17.4	1.8	20	1	AAAS29495	Human mdm2 antisen
c 999	17.8	1.8	21	1	ADL25728	c1072	17.4	1.8	20	1	AAAS29488	Human mdm2 antisen
c1000	17.8	1.8	21	1	ADM94155	c1073	17.4	1.8	20	1	AAAS29496	Human mdm2 antisen
c1001	17.8	1.8	22	1	AAAT71928	c1074	17.4	1.8	20	1	AAAS67842	Human casein kinase
c1002	17.8	1.8	22	1	AAAT71942	c1075	17.4	1.8	20	1	AAAL40350	Human casein kinase
c1003	17.8	1.8	22	1	AAAT71925	c1076	17.4	1.8	20	1	AAAL40285	Caspase 6 antisens
c1004	17.8	1.8	22	1	AAAT72000	c1077	17.4	1.8	20	1	AAAL38206	Human BH3 interact
c1005	17.8	1.8	22	1	AAAT71997	c1078	17.4	1.8	20	1	AAAL38189	Human BH3 interact
c1006	17.8	1.8	22	1	AAAT72014	c1079	17.4	1.8	20	1	AAAD29949	Human PL2, group
c1007	17.8	1.8	22	1	AAAX0910	c1080	17.4	1.8	20	1	AAAS96658	Telomerase reverse
c1008	17.8	1.8	22	1	AAAX89393	c1081	17.4	1.8	20	1	AAAS65070	Human casein kinase
c1009	17.8	1.8	22	1	AAH40206	c1082	17.4	1.8	20	1	AAAC40949	Human superoxide d
c1010	17.8	1.8	22	1	AAAD31451	c1083	17.4	1.8	20	1	AAAL61497	Human ARF3 antisen
c1011	17.8	1.8	22	1	AAK65937	c1084	17.4	1.8	20	1	AAAD47544	Human Artemis exon
c1012	17.8	1.8	22	1	AAK43557	c1085	17.4	1.8	20	1	AAAD20977	Mouse BAX chimeric
c1013	17.8	1.8	22	1	AAAD63370	c1086	17.4	1.8	20	1	AAAL61525	Human inhibitor-ka
c1014	17.8	1.8	22	1	AD123730	c1087	17.4	1.8	20	1	AAAD21684	Human mdm2 antisen
c1015	17.6	1.8	41	1	AAAT66003	c1088	17.4	1.8	20	1	AAAD21691	Human mdm2 antisen
c1016	17.4	1.8	19	1	AAAT66003	c1089	17.4	1.8	20	1	AAAD21692	Human mdm2 antisen
c1017	17.4	1.8	19	1	AAAT66003	c1090	17.4	1.8	20	1	AAAD21693	Human mdm2 antisen
c1018	17.4	1.8	19	1	AAAT66003	c1091	17.4	1.8	20	1	AAAD21694	Human mdm2 antisen
c1019	17.4	1.8	19	1	AAAT66003	c1092	17.4	1.8	20	1	AAAD21695	Human mdm2 antisen
c1020	17.4	1.8	19	1	AAAT66003	c1093	17.4	1.8	20	1	AAAD21696	Human mdm2 antisen
c1021	17.4	1.8	19	1	AAAT66003	c1094	17.4	1.8	20	1	AAAD21697	Human mdm2 antisen
c1022	17.4	1.8	19	1	AAAT66003	c1095	17.4	1.8	20	1	AAAD21698	Human mdm2 antisen
c1023	17.4	1.8	19	1	AAAT66003	c1096	17.4	1.8	20	1	AAAD21699	Human mdm2 antisen
c1024	17.4	1.8	19	1	AAAT66003	c1097	17.4	1.8	20	1	AAAD21700	Human mdm2 antisen
c1025	17.4	1.8	19	1	AAAT66003	c1098	17.4	1.8	20	1	AAAD21701	Human mdm2 antisen
c1026	17.4	1.8	19	1	AAAT66003	c1099	17.4	1.8	20	1	AAAD21702	Human mdm2 antisen
c1027	17.4	1.8	19	1	AAAT66003	c1100	17.4	1.8	20	1	AAAD21703	Human mdm2 antisen
c1028	17.4	1.8	19	1	AAAT66003	c1101	17.4	1.8	20	1	AAAD21704	Human mdm2 antisen
c1029	17.4	1.8	19	1	AAAT66003	c1102	17.4	1.8	20	1	AAAD21705	Human mdm2 antisen
c1030	17.4	1.8	19	1	AAAT66003	c1103	17.4	1.8	20	1	AAAD21706	Human mdm2 antisen
c1031	17.4	1.8	19	1	AAAT66003	c1104	17.4	1.8	20	1	AAAD21707	Human mdm2 antisen
c1032	17.4	1.8	19	1	AAAT66003	c1105	17.4	1.8	20	1	AAAD21708	Human mdm2 antisen
c1033	17.4	1.8	19	1	AAAT66003	c1106	17.4	1.8	20	1	AAAD21709	Human mdm2 antisen
c1034	17.4	1.8	19	1	AAAT66003	c1107	17.4	1.8	20	1	AAAD21710	Human mdm2 antisen
c1035	17.4	1.8	19	1	AAAT66003	c1108	17.4	1.8	20	1	AAAD21711	Human mdm2 antisen
c1036	17.4	1.8	19	1	AAAT66003	c1109	17.4	1.8	20	1	AAAD21712	Human mdm2 antisen
c1037	17.4	1.8	19	1	AAAT66003	c1110	17.4	1.8	20	1	AAAD21713	Human mdm2 antisen
c1038	17.4	1.8	19	1	AAAT66003	c1111	17.4	1.8	20	1	AAAD21714	Human mdm2 antisen
c1039	17.4	1.8	19	1	AAAT66003	c1112	17.4	1.8	20	1	AAAD21715	Human mdm2 antisen
c1040	17.4	1.8	19	1	AAAT66003	c1113	17.4	1.8	20	1	AAAD21716	Human mdm2 antisen
c1041	17.4	1.8	19	1	AAAT66003	c1114	17.4	1.8	20	1	AAAD21717	Human mdm2 antisen
c1042	17.4	1.8	19	1	AAAT66003	c1115	17.4	1.8	20	1	AAAD21718	Human mdm2 antisen
c1043	17.4	1.8	19	1	AAAT66003	c1116	17.4	1.8	20	1	AAAD21719	Human mdm2 antisen
c1044	17.4	1.8	19	1	AAAT66003	c1117	17.4	1.8	20	1	AAAD21720	Human mdm2 antisen
c1045	17.4	1.8	19	1	AAAT66003	c1118	17.4	1.8	20	1	AAAD21721	Human mdm2 antisen
c1046	17.4	1.8	19	1	AAAT66003	c1119	17.4	1.8	20	1	AAAD21722	Human mdm2 antisen
c1047	17.4	1.8	19	1	AAAT66003	c1120	17.4	1.8	20	1	AAAD21723	Human mdm2 antisen
c1048	17.4	1.8	19	1	AAAT66003	c1121	17.4	1.8	20	1	AAAD21724	Human mdm2 antisen
c1049	17.4	1.8	19	1	AAAT66003	c1122	17.4	1.8	20	1	AAAD21725	Human mdm2 antisen
c1050	17.4	1.8	19	1	AAAT66003	c1123	17.4	1.8	20	1	AAAD21726	Human mdm2 antisen
c1051	17.4	1.8	19	1	AAAT66003	c1124	17.4	1.8	20	1	AAAD21727	Human mdm2 antisen
c1052	17.4	1.8	19	1	AAAT66003	c1125	17.4	1.8	20	1	AAAD21728	Human mdm2 antisen
c1053	17.4	1.8	19	1	AAAT66003	c1126	17.4	1.8	20	1	AAAD21729	Human mdm2 antisen
c1054	17.4	1.8	19	1	AAAT66003	c1127	17.4	1.8	20	1	AAAD21730	Human mdm2 antisen
c1055	17.4	1.8	19	1	AAAT66003	c1128	17.4	1.8	20	1	AAAD21731	Human mdm2 antisen

1129	17.4	1.8	20	1	AD052207	Human inhibitor of
c1130	17.4	1.8	20	1	AD052271	Human inhibitor of
1131	17.4	1.8	20	1	AD052203	Human inhibitor of
1132	17.4	1.8	20	1	ADP45826	Extend primer 18 u
1133	17.4	1.8	21	1	AAQ10789	Probe for identity
c1134	17.4	1.8	21	1	AAH37857	SNP specific upper
c1135	17.4	1.8	21	1	AAH38405	SNP specific upper
1136	17.4	1.8	21	1	AAAF24290	Complementary nucl
c1137	17.4	1.8	21	1	ABR68537	Human cholesteryl
c1138	17.4	1.8	21	1	ABSG0598	Human polymorphism
c1139	17.4	1.8	21	1	ABSG0817	Human polymorphism
c1140	17.4	1.8	21	1	ABSG0599	Human polymorphism
c1141	17.4	1.8	21	1	ABSG0816	Human polymorphism
1142	17.4	1.8	21	1	ABX79794	EST polymorphic DN
1143	17.4	1.8	21	1	ADG79161	Calineurin A cata
1144	17.4	1.8	21	1	ABZ58551	PCR primer MR for
c1145	17.4	1.8	21	1	ADP08769	Extend primer 106
1146	17.2	1.7	18	1	AD056549	Human cyclin-depen
1147	17.2	1.7	18	1	AD056979	Human CdkK/PPG pr
c1148	17.2	1.7	18	1	AD056537	Human cyclin-depen
c1149	17.2	1.7	19	1	AAQ76248	Generic primer fto
1150	17.2	1.7	20	1	ABX93649	Human Alu-specific
1151	17.2	1.7	20	1	ABX95025	Human Alu specific
c1152	17.2	1.7	17	1	AAV29284	Nucleotide sequenc
1153	17	1.7	17	1	AAA22861	Integrin subunit b
1154	17	1.7	17	1	AAA22744	Integrin subunit b
1155	17	1.7	17	1	AAA22747	Integrin subunit b
1156	17	1.7	17	1	AAA22759	Integrin subunit b
1157	17	1.7	17	1	AAA22860	Integrin subunit b
1158	17	1.7	17	1	AAA22741	Integrin subunit b
1159	17	1.7	17	1	AAA22722	Integrin subunit b
c1160	17	1.7	17	1	AAA22959	Integrin subunit b
c1161	17	1.7	17	1	AAA22958	Integrin subunit b
1162	17	1.7	17	1	AAA22746	Integrin subunit b
1163	17	1.7	17	1	AAA22745	Integrin subunit b
1164	17	1.7	17	1	AAA22831	Integrin subunit b
c1165	17	1.7	17	1	AAAC87597	Human Alu sequence
1166	17	1.7	17	1	ADBO4439	Human MD27 scannin
1167	17	1.7	17	1	ADBO4442	Human MD27 scannin
1168	17	1.7	17	1	ADBO4282	Human MD27 scannin
1169	17	1.7	17	1	ADBO4440	Human MD27 scannin
1170	17	1.7	17	1	ADBO4314	Human MD27 scannin
1171	17	1.7	17	1	ADBO4283	Human MD27 scannin
1172	17	1.7	17	1	ADBO4441	Human MD27 scannin
1173	17	1.7	17	1	ABZ60587	Human K-Ras DNazym
1174	17	1.7	17	1	ABZ60584	Human K-Ras DNazym
1175	17	1.7	17	1	ADBA3523	Tumour suppression
c1176	17	1.7	17	1	ADBA14243	Optineurin promote
c1177	17	1.7	17	1	ADH59606	Non-nucleotide pro
1178	17	1.7	17	1	ADH59604	Non-nucleotide pro
1179	17	1.7	17	1	ADH59616	Non-nucleotide pro
1180	17	1.7	17	1	ADH59618	Non-nucleotide pro
c1181	17	1.7	17	1	ACCS1496	Human tumour suppr
1182	17	1.7	17	1	ACCS4017	Human tumour suppr
1183	17	1.7	17	1	ADL49972	Human PKR substrat
1184	17	1.7	17	1	ADL50424	Human PKR substrat
1185	17	1.7	17	1	ADL50732	Human PKR substrat
1186	17	1.7	17	1	ADL49423	Human PKR substrat
1187	17	1.7	17	1	ADL50218	Human PKR substrat
1188	17	1.7	17	1	ADL50751	Human PKR substrat
1189	17	1.7	17	1	ADL49453	Human PKR substrat
1190	17	1.7	17	1	ADL49460	Human PKR substrat
1191	17	1.7	17	1	ADL49928	Human PKR substrat
1192	17	1.7	17	1	ADL49956	Human PKR substrat
1193	17	1.7	17	1	ADL49968	Human PKR substrat
1194	17	1.7	17	1	ADL49969	Human PKR substrat
1195	17	1.7	17	1	ADL49454	Human PKR substrat
1196	17	1.7	17	1	ADL50220	Human PKR substrat
1197	17	1.7	17	1	ADL50739	Human PKR substrat
1198	17	1.7	17	1	ADL50219	Human PKR substrat
1199	17	1.7	17	1	ADL50750	Human PKR substrat
1200	17	1.7	17	1	ADL49933	Human PKR substrat
1201	17	1.7	17	1	ADL49953	Human PKR substrat
1202	17	1.7	17	1	ADL49971	Human PKR substrat
1203	17	1.7	17	1	ADL49955	Human PKR substrat
1204	17	1.7	17	1	ADL50733	Human PKR substrat
1205	17	1.7	17	1	ADL50752	Human PKR substrat
1206	17	1.7	17	1	ADL49954	Human PKR substrat
1207	17	1.7	17	1	ADL49970	Human PKR substrat
1208	17	1.7	17	1	ADL49945	Human PKR substrat
1209	17	1.7	17	1	ADL49967	Human PKR substrat
1210	17	1.7	17	1	ADL50753	Human PKR substrat
c1211	17	1.7	17	1	ADL50755	Human PKR substrat
c1212	17	1.7	17	1	ADL50757	Human PKR substrat
c1213	17	1.7	17	1	ADL82338	Human glioma endoc
1214	17	1.7	17	1	ADL82338	Human glioma endoc
1215	17	1.7	17	1	ADP08674	Human ER+ breast c
1216	17	1.7	17	1	ADP08783	Extend primer 60 u
1217	17	1.7	17	1	ADP08783	Extend primer 11 u
1218	17	1.7	17	1	ADP08783	Extend primer 120
c1219	17	1.7	17	1	ADP08783	Extend primer 124
c1220	17	1.7	17	1	ADP08783	Extend primer 124
1221	17	1.7	17	1	ADP08783	Extend primer 124
1222	17	1.7	17	1	ADP08783	Extend primer 124
c1223	17	1.7	17	1	ADP08783	Extend primer 124
c1224	17	1.7	17	1	ADP08783	Extend primer 124
1225	17	1.7	17	1	ADP08783	Extend primer 124
1226	17	1.7	17	1	ADP08783	Extend primer 124
1227	17	1.7	17	1	ADP08783	Extend primer 124
1228	17	1.7	17	1	ADP08783	Extend primer 124
1229	17	1.7	17	1	ADP08783	Extend primer 124
1230	17	1.7	17	1	ADP08783	Extend primer 124
1231	17	1.7	17	1	ADP08783	Extend primer 124
1232	17	1.7	17	1	ADP08783	Extend primer 124
1233	17	1.7	17	1	ADP08783	Extend primer 124
1234	17	1.7	17	1	ADP08783	Extend primer 124
1235	17	1.7	17	1	ADP08783	Extend primer 124
1236	17	1.7	17	1	ADP08783	Extend primer 124
1237	17	1.7	17	1	ADP08783	Extend primer 124
c1238	17	1.7	17	1	ADP08783	Extend primer 124
c1239	17	1.7	17	1	ADP08783	Extend primer 124
c1240	17	1.7	17	1	ADP08783	Extend primer 124
c1241	17	1.7	17	1	ADP08783	Extend primer 124
c1242	17	1.7	17	1	ADP08783	Extend primer 124
1243	17	1.7	17	1	ADP08783	Extend primer 124
c1244	17	1.7	17	1	ADP08783	Extend primer 124
c1245	17	1.7	17	1	ADP08783	Extend primer 124
1246	17	1.7	17	1	ADP08783	Extend primer 124
1247	17	1.7	17	1	ADP08783	Extend primer 124
1248	17	1.7	17	1	ADP08783	Extend primer 124
c1249	17	1.7	17	1	ADP08783	Extend primer 124
c1250	17	1.7	17	1	ADP08783	Extend primer 124
c1251	17	1.7	17	1	ADP08783	Extend primer 124
1252	17	1.7	17	1	ADP08783	Extend primer 124
1253	17	1.7	17	1	ADP08783	Extend primer 124
1254	17	1.7	17	1	ADP08783	Extend primer 124
1255	17	1.7	17	1	ADP08783	Extend primer 124
c1256	17	1.7	17	1	ADP08783	Extend primer 124
1257	17	1.7	17	1	ADP08783	Extend primer 124
1258	17	1.7	17	1	ADP08783	Extend primer 124
c1259	17	1.7	17	1	ADP08783	Extend primer 124
c1260	17	1.7	17	1	ADP08783	Extend primer 124
c1261	17	1.7	17	1	ADP08783	Extend primer 124
1262	17	1.7	17	1	ADP08783	Extend primer 124
1263	17	1.7	17	1	ADP08783	Extend primer 124
1264	17	1.7	17	1	ADP08783	Extend primer 124
1265	17	1.7	17	1	ADP08783	Extend primer 124
1266	17	1.7	17	1	ADP08783	Extend primer 124
c1267	17	1.7	17	1	ADP08783	Extend primer 124
1268	17	1.7	17	1	ADP08783	Extend primer 124
1269	17	1.7	17	1	ADP08783	Extend primer 124
1270	17	1.7	17	1	ADP08783	Extend primer 124
1271	17	1.7	17	1	ADP08783	Extend primer 124
1272	17	1.7	17	1	ADP08783	Extend primer 124
c1273	17	1.7	17	1	ADP08783	Extend primer 124
c1274	17	1.7	17	1	ADP08783	Extend primer 124



1275	16.8	1.7	20	1	AA053171	Familial dysautono	1348	16.8	1.7	20	1	ABX75089	Human gene 216 pol
1276	16.8	1.7	20	1	AA047775	Antisense oligonuc	1349	16.8	1.7	20	1	ACC86803	Human VEGFR-1 chim
1277	16.8	1.7	20	1	AA063001	Hyertension/ACE 1	1350	16.8	1.7	20	1	ABZ71057	Human HKR1 phospho
1278	16.8	1.7	20	1	AA075579	Reverse transcript	1351	16.8	1.7	20	1	ABZ71059	Human HKR1 phospho
1279	16.8	1.7	20	1	AA075581	Reverse transcript	1352	16.8	1.7	20	1	ADA20923	Human BAX chimeric
1280	16.8	1.7	20	1	AA074147	Human gene signatu	1353	16.8	1.7	20	1	ADA20924	Human BAX chimeric
1281	16.8	1.7	20	1	AA071831	BRCA1 gene mapping	1354	16.8	1.7	20	1	ADB16959	Human BAX chimeric
1282	16.8	1.7	20	1	AA071832	Primer #1 for land	1355	16.8	1.7	20	1	ADA27318	Human microsatelli
1283	16.8	1.7	20	1	AA073260	BRCA1 gene mapping	1356	16.8	1.7	20	1	ABT44385	Human microsatelli
1284	16.8	1.7	20	1	AA073260	Antisense oligonuc	1357	16.8	1.7	20	1	ADB81564	Chimeric antisense
1285	16.8	1.7	20	1	AA077752	Phosphorothioate o	1358	16.8	1.7	20	1	ADB81567	Antisense oligo (S
1286	16.8	1.7	20	1	AA073398	Primer for human g	1359	16.8	1.7	20	1	ADB90595	Human pituitary pr
1287	16.8	1.7	20	1	AA085807	LRP5 exon primer 5	1360	16.8	1.7	20	1	ADC89590	Human COREST antls
1288	16.8	1.7	20	1	AA085885	LRP5 SNP primer 58	1361	16.8	1.7	20	1	ADC89591	Human COREST antls
1289	16.8	1.7	20	1	AA090920	Phosphorothioate o	1362	16.8	1.7	20	1	ADD21697	Human mdm2 antisen
1290	16.8	1.7	20	1	AA090920	Human mdm2 phospho	1363	16.8	1.7	20	1	ADD21700	Human mdm2 antisen
1291	16.8	1.7	20	1	AA090920	Human mdm2 phospho	1364	16.8	1.7	20	1	ADD21693	Human mdm2 antisen
1292	16.8	1.7	20	1	AA090920	Human mdm2 phospho	1365	16.8	1.7	20	1	ADD21698	Human mdm2 antisen
1293	16.8	1.7	20	1	AA090920	Human mdm2 phospho	1366	16.8	1.7	20	1	ADD21698	Human mdm2 antisen
1294	16.8	1.7	20	1	AA090920	Sense primer of PC	1367	16.8	1.7	20	1	ADG28968	PCR primer SEQ ID
1295	16.8	1.7	20	1	AA090920	Primer intefr for S	1368	16.8	1.7	20	1	ABZ97914	Human RANTES oligo
1296	16.8	1.7	20	1	AA090920	Exonic primer PMW	1369	16.8	1.7	20	1	ABZ97915	Human RANTES oligo
1297	16.8	1.7	20	1	AA090920	Primer for ASTH1 p	1370	16.8	1.7	20	1	ABZ97901	Human RANTES oligo
1298	16.8	1.7	20	1	AA090920	Alzheimer's disease	1371	16.8	1.7	20	1	ABZ89546	Human oligonucleot
1299	16.8	1.7	20	1	AA090920	Primer used to amp	1372	16.8	1.7	20	1	ABZ99069	Human PDE4C oligon
1300	16.8	1.7	20	1	AA090920	Human familial dys	1373	16.8	1.7	20	1	ABZ89880	Human oligonucleot
1301	16.8	1.7	20	1	AA090920	PCR primer used to	1374	16.8	1.7	20	1	ABZ89179	Human oligonucleot
1302	16.8	1.7	20	1	AA090920	Antisense oligonuc	1375	16.8	1.7	20	1	ABZ89863	Human oligonucleot
1303	16.8	1.7	20	1	AA090920	Human growth hormo	1376	16.8	1.7	20	1	ABZ97264	Human nucleic acid
1304	16.8	1.7	20	1	AA090920	Human MDMX antisen	1377	16.8	1.7	20	1	ABZ97912	Human RANTES oligo
1305	16.8	1.7	20	1	AA090920	Human MDMX antisen	1378	16.8	1.7	20	1	ABZ99070	Human PDE4C oligon
1306	16.8	1.7	20	1	AA090920	ASTH1 polymorphic	1379	16.8	1.7	20	1	ABZ97383	Human IL4-R oligon
1307	16.8	1.7	20	1	AA090920	PCR primer used fo	1380	16.8	1.7	20	1	ABZ99801	Human RANTES oligo
1308	16.8	1.7	20	1	AA090920	Human CDNA clone-s	1381	16.8	1.7	20	1	ABZ99803	Human PDE4C oligon
1309	16.8	1.7	20	1	AA090920	Human CDNA clone-s	1382	16.8	1.7	20	1	ABZ89846	Human oligonucleot
1310	16.8	1.7	20	1	AA090920	SPINK5 gene sequen	1383	16.8	1.7	20	1	ABZ99109	Human PDE4C oligon
1311	16.8	1.7	20	1	AA090920	Human ABC1 transcr	1384	16.8	1.7	20	1	ABZ99108	Human PDE4C oligon
1312	16.8	1.7	20	1	AA090920	S. aureus groE ope	1385	16.8	1.7	20	1	ABZ99058	Human PDE4C oligon
1313	16.8	1.7	20	1	AA090920	S. aureus groE ope	1386	16.8	1.7	20	1	ABZ99804	Human RANTES oligo
1314	16.8	1.7	20	1	AA090920	Human mdm2 phospho	1387	16.8	1.7	20	1	ABZ97925	Human oligonucleot
1315	16.8	1.7	20	1	AA090920	Human mdm2 phospho	1388	16.8	1.7	20	1	ABZ97905	Human RANTES oligo
1316	16.8	1.7	20	1	AA090920	Human mdm2 phospho	1389	16.8	1.7	20	1	ABZ99064	Human PDE4C oligon
1317	16.8	1.7	20	1	AA090920	Human mdm2 phospho	1390	16.8	1.7	20	1	ABZ99099	Human PDE4C oligon
1318	16.8	1.7	20	1	AA090920	PCR primer #1 for	1391	16.8	1.7	20	1	ABZ99729	Human oligonucleot
1319	16.8	1.7	20	1	AA090920	SNP specific upper	1392	16.8	1.7	20	1	ABZ99730	Human oligonucleot
1320	16.8	1.7	20	1	AA090920	Human PIR1 promote	1393	16.8	1.7	20	1	ABZ99808	Human PDE4C oligon
1321	16.8	1.7	20	1	AA090920	Presentiline-1 gene	1394	16.8	1.7	20	1	ABZ89865	Human oligonucleot
1322	16.8	1.7	20	1	AA090920	Human growth hormo	1395	16.8	1.7	20	1	ABZ99061	Human PDE4C oligon
1323	16.8	1.7	20	1	AA090920	Mouse Survivin ant	1396	16.8	1.7	20	1	ABZ99087	Human PDE4C oligon
1324	16.8	1.7	20	1	AA090920	Human mdm2 antisen	1397	16.8	1.7	20	1	ABZ97900	Human RANTES oligo
1325	16.8	1.7	20	1	AA090920	Human mdm2 antisen	1398	16.8	1.7	20	1	ABZ89853	Human oligonucleot
1326	16.8	1.7	20	1	AA090920	Human mdm2 antisen	1399	16.8	1.7	20	1	ABZ89860	Human oligonucleot
1327	16.8	1.7	20	1	AA090920	Human mdm2 antisen	1400	16.8	1.7	20	1	ACB88890	Selection and ampl
1328	16.8	1.7	20	1	AA090920	Gene 216 SSP seque	1401	16.8	1.7	20	1	ADM65766	Human Y chromosome
1329	16.8	1.7	20	1	AA090920	Human RECD2 antls	1402	16.8	1.7	20	1	ABD32139	Human PDE4C-deri
1330	16.8	1.7	20	1	AA090920	Human Proteoln Phos	1403	16.8	1.7	20	1	ABD32140	Human PDE4C-deri
1331	16.8	1.7	20	1	AA090920	Human casein kinas	1404	16.8	1.7	20	1	ABD32094	Human PDE4C-deri
1332	16.8	1.7	20	1	AA090920	Human casein kinas	1405	16.8	1.7	20	1	ABD32118	Human PDE4C-deri
1333	16.8	1.7	20	1	AA090920	Human LINC-1 DNA a	1406	16.8	1.7	20	1	ABD28955	Human PDE4C-deri
1334	16.8	1.7	20	1	AA090920	Human chromosome 2	1407	16.8	1.7	20	1	ABD30930	Human RANTES-deri
1335	16.8	1.7	20	1	AA090920	Human chromosome 1	1408	16.8	1.7	20	1	ABD25409	Human PDE4C-deri
1336	16.8	1.7	20	1	AA090920	Human chromosome 1	1409	16.8	1.7	20	1	ABD32100	Human PDE4C-deri
1337	16.8	1.7	20	1	AA090920	Human chromosome 1	1410	16.8	1.7	20	1	ABD28959	Human PDE4C-deri
1338	16.8	1.7	20	1	AA090920	Human phosphorilas	1411	16.8	1.7	20	1	ABD25083	Human PDE4C-deri
1339	16.8	1.7	20	1	AA090920	Human B33 interact	1412	16.8	1.7	20	1	ABD30943	Human RANTES-deri
1340	16.8	1.7	20	1	AA090920	Forward PCR primer	1413	16.8	1.7	20	1	ABD25110	Human RANTES-deri
1341	16.8	1.7	20	1	AA090920	Human casein kinas	1414	16.8	1.7	20	1	ABD30932	Human RANTES-deri
1342	16.8	1.7	20	1	AA090920	Human D9S58 gene1	1415	16.8	1.7	20	1	ABD32095	Human PDE4C-deri
1343	16.8	1.7	20	1	AA090920	Human NF-kappa ac	1416	16.8	1.7	20	1	ABD25776	Human PDE4C-deri
1344	16.8	1.7	20	1	AA090920	Human cathepsin B	1417	16.8	1.7	20	1	ABD25792	Human PDE4C-deri
1345	16.8	1.7	20	1	AA090920	Human PKR antisen	1418	16.8	1.7	20	1	ABD30931	Human RANTES-deri
1346	16.8	1.7	20	1	AA090920	Acetyl-Coenzyme A-	1419	16.8	1.7	20	1	ABD31032	Human RANTES-deri
1347	16.8	1.7	20	1	AA090920	7S cloning forward	1420	16.8	1.7	20	1	ABD28965	Human RANTES-deri



c1421	16.8	1.7	20	1	ABD30414	Human IL4-R derive	c1494	16.8	1.7	20	1	ADM13851	Human mPGES-1 chim
c1422	16.8	1.7	20	1	ABD26076	AA463249-derived o	c1495	16.8	1.7	20	1	ADM14695	Human mPGES-1 chim
c1423	16.8	1.7	20	1	ABD26090	AA463249-derived o	c1496	16.8	1.7	20	1	ADM13899	Human mPGES-1 chim
c1424	16.8	1.7	20	1	ABD26093	AA463249-derived o	c1497	16.8	1.7	20	1	ADM14111	Human mPGES-1 chim
1425	16.8	1.7	20	1	ABD30936	Human RANTES-deriv	c1498	16.8	1.7	20	1	ADM14491	Human mPGES-1 chim
1426	16.8	1.7	20	1	ABD31035	Human RANTES-deriv	c1499	16.8	1.7	20	1	ADM14603	Human mPGES-1 chim
1427	16.8	1.7	20	1	ABD32101	Human PDE4C-deriv	c1500	16.8	1.7	20	1	ADM14641	Human mPGES-1 chim
1428	16.8	1.7	20	1	ABD30945	Human RANTES-deriv	c1501	16.8	1.7	20	1	ADM14769	Human mPGES-1 chim
1429	16.8	1.7	20	1	ABD32130	Human PDE4C-deriv	c1502	16.8	1.7	20	1	ADM15380	Human mPGES-1 chim
1430	16.8	1.7	20	1	ABD28960	N58473-derived o	c1503	16.8	1.7	20	1	ADM14342	Human mPGES-1 chim
c1431	16.8	1.7	20	1	ABD26095	AA463249-derived o	c1504	16.8	1.7	20	1	ADM13854	Human mPGES-1 chim
1432	16.8	1.7	20	1	ABD32089	Human PDE4C-deriv	c1505	16.8	1.7	20	1	ADM13854	Human mPGES-1 chim
1433	16.8	1.7	20	1	ABD32119	Human PDE4C-deriv	c1506	16.8	1.7	20	1	ADM14675	Human mPGES-1 chim
1434	16.8	1.7	20	1	ADP86417	VLA4 antagonist-re	c1507	16.8	1.7	20	1	ADM14425	Human mPGES-1 chim
1435	16.8	1.7	20	1	ADG86786	Human PPAR antisen	c1508	16.8	1.7	20	1	ADM14469	Human mPGES-1 chim
c1436	16.8	1.7	20	1	ADG86939	Human PPAR antisen	c1509	16.8	1.7	20	1	ADM14642	Human mPGES-1 chim
1437	16.8	1.7	20	1	ADH56917	Human CARD4 DNA ol	c1510	16.8	1.7	20	1	ADM14763	Human mPGES-1 chim
c1438	16.8	1.7	20	1	ADH73294	Human ALU sequence	c1511	16.8	1.7	20	1	ADM14262	Human mPGES-1 chim
1439	16.8	1.7	20	1	ADH330044	Human dual specif	c1512	16.8	1.7	20	1	ADM14410	Human mPGES-1 chim
1440	16.8	1.7	20	1	ADH76711	MCHR1 genomic sequ	c1513	16.8	1.7	20	1	ADM14596	Human mPGES-1 chim
c1441	16.8	1.7	20	1	ADH76713	MCHR1 genomic sequ	c1514	16.8	1.7	20	1	ADM14660	Human mPGES-1 chim
c1442	16.8	1.7	20	1	ADH77272	Human PAZ/PIWI dom	c1515	16.8	1.7	20	1	ADM14676	Human mPGES-1 chim
1443	16.8	1.7	20	1	ADH77198	Human PAZ/PIWI dom	c1516	16.8	1.7	20	1	ADM14829	Human mPGES-1 chim
c1444	16.8	1.7	20	1	ADH18181	Human PEX4 gene-ep	c1517	16.8	1.7	20	1	ADM14269	Human mPGES-1 chim
1445	16.8	1.7	20	1	ADJ36817	Human gene 216 SNP	c1518	16.8	1.7	20	1	ADM14328	Human mPGES-1 chim
1446	16.8	1.7	20	1	ADJ60954	Oligonucleotide as	c1519	16.8	1.7	20	1	ADM14470	Human mPGES-1 chim
1447	16.8	1.7	20	1	ADJ59777	Oligonucleotide as	c1520	16.8	1.7	20	1	ADM15246	Human mPGES-1 chim
1448	16.8	1.7	20	1	ADJ59866	Oligonucleotide as	c1521	16.8	1.7	20	1	ADM15325	Human mPGES-1 chim
1449	16.8	1.7	20	1	ADJ60948	Oligonucleotide as	c1522	16.8	1.7	20	1	ADM15564	Human mPGES-1 chim
1450	16.8	1.7	20	1	ADJ59764	Oligonucleotide as	c1523	16.8	1.7	20	1	ADM14146	Human mPGES-1 chim
1451	16.8	1.7	20	1	ADJ60955	Oligonucleotide as	c1524	16.8	1.7	20	1	ADM14674	Human mPGES-1 chim
1452	16.8	1.7	20	1	ADJ60984	Oligonucleotide as	c1525	16.8	1.7	20	1	ADM14776	Human mPGES-1 chim
1453	16.8	1.7	20	1	ADJ59766	Oligonucleotide as	c1526	16.8	1.7	20	1	ADM14800	Human mPGES-1 chim
1454	16.8	1.7	20	1	ADJ60973	Oligonucleotide as	c1527	16.8	1.7	20	1	ADM14814	Human mPGES-1 chim
1455	16.8	1.7	20	1	ADJ61656	TL4RA receptor #1	c1528	16.8	1.7	20	1	ADM15362	Human mPGES-1 chim
1456	16.8	1.7	20	1	ADJ59779	Oligonucleotide as	c1529	16.8	1.7	20	1	ADM15526	Human mPGES-1 chim
1457	16.8	1.7	20	1	ADJ60946	Oligonucleotide as	c1530	16.8	1.7	20	1	ADM15526	Human mPGES-1 chim
1458	16.8	1.7	20	1	ADJ60949	Oligonucleotide as	c1531	16.8	1.7	20	1	ADO46482	Human mPGES-1 chim
1459	16.8	1.7	20	1	ADJ60972	Oligonucleotide as	c1532	16.8	1.7	20	1	ADO44692	Human mPGES-1 chim
1460	16.8	1.7	20	1	ADJ59202	Oligonucleotide as	c1533	16.8	1.7	20	1	ADO46473	Human mPGES-1 chim
1461	16.8	1.7	20	1	ADJ59765	Oligonucleotide as	c1534	16.8	1.7	20	1	ADO45336	Human mPGES-1 chim
1462	16.8	1.7	20	1	ADJ59770	Oligonucleotide as	c1535	16.8	1.7	20	1	ADO46432	Human mPGES-1 chim
1463	16.8	1.7	20	1	ADJ60943	Oligonucleotide as	c1536	16.8	1.7	20	1	ADO46461	Human mPGES-1 chim
1464	16.8	1.7	20	1	ADJ59869	Oligonucleotide as	c1537	16.8	1.7	20	1	ADO46483	Human mPGES-1 chim
1465	16.8	1.7	20	1	ADJ60993	Oligonucleotide as	c1538	16.8	1.7	20	1	ADO45260	Human mPGES-1 chim
1466	16.8	1.7	20	1	ADJ60994	Oligonucleotide as	c1539	16.8	1.7	20	1	ADO46435	Human mPGES-1 chim
c1467	16.8	1.7	20	1	ADK41378	Human chromosome 1	c1540	16.8	1.7	20	1	ADO46462	Human mPGES-1 chim
c1468	16.8	1.7	20	1	ADK41252	Human chromosome 1	c1541	16.8	1.7	20	1	ADO46443	Human mPGES-1 chim
1469	16.8	1.7	20	1	ADJ96296	Human breast cancer	c1542	16.8	1.7	20	1	ADO45286	Human mPGES-1 chim
c1470	16.8	1.7	20	1	ADJ96332	Human breast cancer	c1543	16.8	1.7	20	1	ADO45286	Human mPGES-1 chim
c1471	16.8	1.7	20	1	ADJ96345	Human breast cancer	c1544	16.8	1.7	20	1	ADO45269	Human mPGES-1 chim
1472	16.8	1.7	20	1	ADJ96392	Human breast cancer	c1545	16.8	1.7	20	1	ADO47047	Human mPGES-1 chim
1473	16.8	1.7	20	1	ADL14967	Human glaucoma-rel	c1546	16.8	1.7	20	1	ADO45254	Human mPGES-1 chim
c1474	16.8	1.7	20	1	ADL23335	Primer #1 for ampl	c1547	16.8	1.7	20	1	ADO45287	Human mPGES-1 chim
1475	16.8	1.7	20	1	ADL81396	Gene 216 polymorph	c1548	16.8	1.7	20	1	ADO45285	Human mPGES-1 chim
1476	16.8	1.7	20	1	ADL74414	Chimeric phosphoro	c1549	16.8	1.7	20	1	ADO45339	Human mPGES-1 chim
1477	16.8	1.7	20	1	ADL32377	Clone specific PCR	c1550	16.8	1.7	20	1	ADO46444	Human mPGES-1 chim
1478	16.8	1.7	20	1	ADL32402	Clone specific PCR	c1551	16.8	1.7	20	1	ADO46437	Human mPGES-1 chim
c1479	16.8	1.7	20	1	ADL34877	Human PPAR-delta t	c1552	16.8	1.7	20	1	ADO11743	Human mPGES-1 chim
1480	16.8	1.7	20	1	ADL34724	Antisense oligonuc	c1553	16.8	1.7	20	1	ADO52208	Human mPGES-1 chim
c1481	16.8	1.7	20	1	ADM14052	Human mPGES-1 chim	c1554	16.8	1.7	20	1	ADO52272	Human mPGES-1 chim
c1482	16.8	1.7	20	1	ADM15037	Human mPGES-1 chim	c1555	16.8	1.7	20	1	ADP45835	Human mPGES-1 chim
c1483	16.8	1.7	20	1	ADM15443	Human mPGES-1 chim	c1556	16.8	1.7	20	1	ADP46278	Human mPGES-1 chim
c1484	16.8	1.7	20	1	ADM15456	Human mPGES-1 chim	c1557	16.8	1.7	20	1	AAQ75719	Human mPGES-1 chim
c1485	16.8	1.7	20	1	ADM14625	Human mPGES-1 chim	c1558	16.8	1.7	20	1	AAQ75730	Human mPGES-1 chim
c1486	16.8	1.7	20	1	ADM14799	Human mPGES-1 chim	c1559	16.8	1.7	20	1	AAQ75728	Human mPGES-1 chim
c1487	16.8	1.7	20	1	ADM15381	Human mPGES-1 chim	c1560	16.8	1.7	20	1	AAQ75727	Human mPGES-1 chim
c1488	16.8	1.7	20	1	ADM14381	Human mPGES-1 chim	c1561	16.8	1.7	20	1	AAQ75722	Human mPGES-1 chim
c1489	16.8	1.7	20	1	ADM14481	Human mPGES-1 chim	c1562	16.8	1.7	20	1	AAQ75712	Human mPGES-1 chim
c1490	16.8	1.7	20	1	ADM14501	Human mPGES-1 chim	c1563	16.8	1.7	20	1	AAQ75721	Human mPGES-1 chim
c1491	16.8	1.7	20	1	ADM15122	Human mPGES-1 chim	c1564	16.8	1.7	20	1	AAQ96626	Human mPGES-1 chim
c1492	16.8	1.7	20	1	ADM15136	Human mPGES-1 chim	c1565	16.8	1.7	20	1	AAZ72283	Human mPGES-1 chim
c1493	16.8	1.7	20	1	ADM15147	Human mPGES-1 chim	c1566	16.8	1.7	20	1	AAH39786	Human mPGES-1 chim

c1567	16.8	1.7	21	1	AB560534	Human polymorphism	1640	16.4	1.7	20	1	ADP56753	Antisense 2'-MOE g
c1568	16.8	1.7	21	1	AB560764	Human polymorphism	c1641	16.4	1.7	20	1	ADP56830	Human AMACR DNA ta
c1569	16.8	1.7	21	1	AB560765	Human polymorphism	c1642	16.4	1.7	20	1	AAF88161	Human thymoid malif
c1570	16.8	1.7	21	1	AB560535	Human polymorphism	1643	16	1.6	16	1	AB597400	Human cyclooxigena
1571	16.8	1.7	21	1	AB593617	Human DISC1/DISC2	c1644	16	1.6	16	1	AB598039	Human multidrug re
1572	16.8	1.7	21	1	AB158478	HPT probe generat	c1645	16	1.6	16	1	ACA62885	Repeated nucleic a
c1573	16.8	1.7	21	1	AB566754	Human MRP-1 polyom	1646	16	1.6	16	1	ACA62878	Repeated nucleic a
c1574	16.8	1.7	21	1	AB566755	Human MRP-1 polyom	1647	16	1.6	16	1	ACA62880	Repeated nucleic a
c1575	16.8	1.7	21	1	ADC42667	Human FANCD2 PCR p	1648	16	1.6	16	1	ACA62882	Repeated nucleic a
1576	16.8	1.7	21	1	ADC42667	Hypoxanthine phosph	1649	16	1.6	16	1	ACA62879	Repeated nucleic a
1577	16.8	1.7	21	1	ADK01281	Rat DNA microarray	c1650	16	1.6	16	1	AD63080	Human tandem tag D
1578	16.8	1.7	21	1	ADK01284	Rat DNA microarray	c1651	16	1.6	16	1	AD63081	Human tandem tag D
1579	16.8	1.7	21	1	ADK01341	Rat DNA microarray	c1652	16	1.6	16	1	AD63078	Human tandem tag D
1580	16.8	1.7	21	1	ADK01283	Rat DNA microarray	c1653	16	1.6	16	1	AD63084	Human tandem tag D
1581	16.8	1.7	21	1	ADK01331	Rat DNA microarray	c1654	16	1.6	16	1	AD63086	Human tandem tag D
1582	16.8	1.7	21	1	ADK01330	Rat DNA microarray	1655	16	1.6	17	1	AAA23740	Integrin subunit b
1583	16.8	1.7	21	1	ADK01332	Rat DNA microarray	1656	16	1.6	17	1	AAA23748	Integrin subunit b
1584	16.8	1.7	21	1	AD123739	Human LPDIR PCR pr	1657	16	1.6	17	1	AAA22736	Integrin subunit b
c1585	16.6	1.7	19	1	AAV83938	PCR primer used to	1658	16	1.6	17	1	AAA22742	Integrin subunit b
c1586	16.4	1.7	18	1	AAZ89776	Human RIP-1 antisense	1659	16	1.6	17	1	AAA22957	Integrin subunit b
c1587	16.4	1.7	18	1	AAZ89747	Human RIP-1 antisense	c1660	16	1.6	17	1	AA664147	Primer #89. Homo
c1588	16.4	1.7	18	1	AAZ39625	Human CREL mRNA in	c1661	16	1.6	17	1	AA683022	Acacia telangiecta
c1589	16.4	1.7	18	1	AAH40733	SNP specific upper	c1662	16	1.6	17	1	AA683108	Tumour suppression
c1590	16.4	1.7	18	1	AAH38918	SNP specific lower	1663	16	1.6	17	1	AA683067	Tumour suppression
c1591	16.4	1.7	18	1	AAH39265	SNP specific upper	1664	16	1.6	17	1	AA683067	Tumour suppression
1592	16.4	1.7	18	1	AAH47615	Human Her-3 mRNA i	1665	16	1.6	17	1	ADB04313	Human MD27 scannin
1593	16.4	1.7	18	1	AAH47615	Human Her-3 mRNA i	1666	16	1.6	17	1	ADB04443	Human MD27 scannin
c1594	16.4	1.7	18	1	AB882413	Zmax1 gene region	1667	16	1.6	17	1	ADB04438	Human MD27 scannin
c1595	16.4	1.7	18	1	AB882413	Zmax1 gene region	1668	16	1.6	17	1	ADB04281	Human MD27 scannin
1596	16.4	1.7	18	1	AB898053	Human multidrug re	1669	16	1.6	17	1	ADB04315	Human MD27 scannin
c1597	16.4	1.7	18	1	ABK22992	Human Zmax1 cDNA r	1670	16	1.6	17	1	AB260605	Human K-Ras DNazym
1598	16.4	1.7	18	1	ABK22992	Human Zmax1 cDNA r	1671	16	1.6	17	1	AB260605	Human K-Ras DNazym
1599	16.4	1.7	18	1	ACC49483	Human GAPDH revers	c1672	16	1.6	17	1	ACC63031	Murine oligonucleo
1600	16.4	1.7	18	1	ACC45793	Human HBM STS mark	c1673	16	1.6	17	1	ADB44260	Tumour suppression
c1601	16.4	1.7	18	1	ACC45575	Human HBM STS mark	1674	16	1.6	17	1	ACC54382	Human tumour supp
c1602	16.4	1.7	18	1	ACC45283	Human GAPDH PCR pr	c1675	16	1.6	17	1	ACC51495	Human tumour supp
c1603	16.4	1.7	18	1	ACA62881	Repeated nucleic a	1676	16	1.6	17	1	ADL50194	Human PKR substrat
1604	16.4	1.7	18	1	ADB98491	Sequence tagged si	1677	16	1.6	17	1	ADL50204	Human PKR substrat
c1605	16.4	1.7	18	1	ADB98491	Sequence tagged si	1678	16	1.6	17	1	ADL49433	Human PKR substrat
1606	16.4	1.7	18	1	ADH59603	Non-nucleotide pro	1679	16	1.6	17	1	ADL49459	Human PKR substrat
c1607	16.4	1.7	18	1	ADH59615	Non-nucleotide pro	1680	16	1.6	17	1	ADL50215	Human PKR substrat
c1608	16.4	1.7	18	1	ADH71082	Human Vbeta mltros	1681	16	1.6	17	1	ADL49914	Human PKR substrat
1609	16.4	1.7	18	1	ADH71082	MCHRI genomic sequ	1682	16	1.6	17	1	ADL49909	Human PKR substrat
1610	16.4	1.7	18	1	ADP08780	Extend primer 117	1683	16	1.6	17	1	ADL49932	Human PKR substrat
c1611	16.4	1.7	18	1	ADP46226	Extend primer 7 us	1684	16	1.6	17	1	ADL49915	Human PKR substrat
c1612	16.4	1.7	19	1	AAQ92328	Human telocarcin	1685	16	1.6	17	1	ADL49927	Human PKR substrat
1613	16.4	1.7	19	1	AAQ92328	PCR primer 1 used	1686	16	1.6	17	1	ADL50427	Human PKR substrat
c1614	16.4	1.7	19	1	AAQ92328	Reverse primer use	1687	16	1.6	17	1	ADL49957	Human PKR substrat
1615	16.4	1.7	19	1	ABX15007	Human delta oloid	1688	16	1.6	17	1	ADP46267	Extend primer 48 u
1616	16.4	1.7	19	1	ACA88919	Selection and ampli	c1689	16	1.6	18	1	AAAT36226	Antisense oligo ta
c1617	16.4	1.7	19	1	ACA88919	Oloid receptor D1	c1690	16	1.6	18	1	AAAX90320	Oligonucleotide RT
c1618	16.4	1.7	19	1	ADH71084	Human Vbeta gene r	1692	16	1.6	18	1	AB209942	Haematopoietic cel
1619	16.4	1.7	19	1	ADH71084	Human Vbeta mltros	c1693	16	1.6	18	1	AAV57826	Human cyclin-depen
c1620	16.4	1.7	19	1	ADH70436	Human Vbeta gene r	c1694	16	1.6	19	1	ADP68319	Human chromosome 1
c1621	16.4	1.7	19	1	ADK70924	Human hepatocyte r	c1695	16	1.6	19	1	ACA88916	Human antisense Ap
c1622	16.4	1.7	19	1	ADP26951	Human P-cadherin p	c1696	16	1.6	20	1	AAH48599	Selection and ampli
c1623	16.4	1.7	20	1	AAQ95565	Primer A7 (Group 4	c1697	16	1.6	20	1	AAH48599	Human fascin assoc
1624	16.4	1.7	20	1	AAQ95565	Primer B (Group 6,	1698	16	1.6	20	1	AAH48599	Mouse Survivin ant
c1625	16.4	1.7	20	1	AAH91108	Human inflammatory	c1699	16	1.6	20	1	AAH48599	Human NOV7b gene e
c1626	16.4	1.7	20	1	ABL45527	Human chromosome 2	c1700	16	1.6	20	1	ADL71348	GFAT 1 gene inton
c1627	16.4	1.7	20	1	ACC55322	Human ADAMTS13 STS	c1701	16	1.6	20	1	ADL24993	Intestinal epithel
c1628	16.4	1.7	20	1	ABZ71060	Human HKRI phospho	c1702	16	1.6	41	1	ABV77328	Human p10n protei
c1629	16.4	1.7	20	1	ABZ74200	Chimeric antisense	c1703	16	1.6	51	1	AAI73524	Human protein 10.0
c1630	16.4	1.7	20	1	ADP15817	Human PKR exon 17	c1704	16	1.6	51	1	AAI73524	Human silent SNP c
1631	16.4	1.7	20	1	ADP29052	Human PDE4C oligon	1705	15.8	1.6	19	1	AAQ82623	Chromosome 11 (loc
c1633	16.4	1.7	20	1	ABD32083	Human PDE4C-deriva	c1706	15.8	1.6	19	1	AAQ82623	Reverse transcript
c1634	16.4	1.7	20	1	ADH56987	PCR primer used to	1707	15.8	1.6	19	1	AAQ82623	Primer B (Group 10
1635	16.4	1.7	20	1	ADJ38842	Human LIM domain k	c1708	15.8	1.6	19	1	AAQ82623	Oligonucleotide pr
c1636	16.4	1.7	20	1	ADJ38842	Human LIM domain k	c1709	15.8	1.6	19	1	AAQ82623	Primer #1 to ampli
1637	16.4	1.7	20	1	ADM15371	Human mRGS-1 chim	c1710	15.8	1.6	19	1	AAQ82623	LRPS exon primer 5
c1638	16.4	1.7	20	1	ADO46426	Human oligonucleot	c1711	15.8	1.6	19	1	AAQ82623	LRPS exon primer 5
1639	16.4	1.7	20	1	ADP45846	Extend primer 38 u	1712	15.8	1.6	19	1	AAQ82623	Aminoxy-modified

1713	15.8	1.6	19	1	AAV06820	Oligonucleotide co
1714	15.8	1.6	19	1	AAx81316	5' amino oligonucleotide
1715	15.8	1.6	19	1	AAx36671	PCR primer for mar
1716	15.8	1.6	19	1	AAx81977	Polynucleotide str
1717	15.8	1.6	19	1	AAZ01358	PCR primer for pci
1718	15.8	1.6	19	1	AAZ61390	Uniform phosphodi
1719	15.8	1.6	19	1	AAZ61404	2'-O-modified ribo
1720	15.8	1.6	19	1	AAZ62422	T19 diester for us
1721	15.8	1.6	19	1	AAZ95241	Modified oligonucleotide
1722	15.8	1.6	19	1	AAZ95240	Modified oligonucleotide
1723	15.8	1.6	19	1	AAZ06839	Modified T-contain
1724	15.8	1.6	19	1	AAZ88952	Oligonucleotide IS
1725	15.8	1.6	19	1	AAZ88965	2'-Modified chimer
1726	15.8	1.6	19	1	AAZ88949	Oligonucleotide IS
1727	15.8	1.6	19	1	AAZ88950	Oligonucleotide IS
1728	15.8	1.6	19	1	AAZ88951	Oligonucleotide IS
1729	15.8	1.6	19	1	AAZ88947	Oligonucleotide IS
1730	15.8	1.6	19	1	AAZ88948	Oligonucleotide IS
1731	15.8	1.6	19	1	AAZ16150	Phosphorothioate 2
1732	15.8	1.6	19	1	AAZ62454	Cleavage of nucleic
1733	15.8	1.6	19	1	AAZ31458	Oligonucleotide IS
1734	15.8	1.6	19	1	AAZ31564	ISIS sequence 3232
1735	15.8	1.6	19	1	AAZ6776	S. aureus groE ope
1736	15.8	1.6	19	1	AAZ8442	SNP specific lower
1737	15.8	1.6	19	1	AAZ39785	SNP specific upper
1738	15.8	1.6	19	1	AAZ40317	SNP specific upper
1739	15.8	1.6	19	1	AAZ46460	Oligonucleotide #8
1740	15.8	1.6	19	1	AAZ5737	Human type II RNAs
1741	15.8	1.6	19	1	AAZ5738	Human type II RNAs
1742	15.8	1.6	19	1	AAZ62165	PCR primer used to
1743	15.8	1.6	19	1	AAZ62165	PCR primer used to
1744	15.8	1.6	19	1	AAZ91128	Human multi drug r
1745	15.8	1.6	19	1	AAZ91127	Human multi drug r
1746	15.8	1.6	19	1	AAZ91127	Human multi drug r
1747	15.8	1.6	19	1	AAZ91127	Human multi drug r
1748	15.8	1.6	19	1	AAZ91127	Human multi drug r
1749	15.8	1.6	19	1	AAZ91127	Human multi drug r
1750	15.8	1.6	19	1	AAZ91127	Human multi drug r
1751	15.8	1.6	19	1	AAZ91127	Human multi drug r
1752	15.8	1.6	19	1	AAZ91127	Human multi drug r
1753	15.8	1.6	19	1	AAZ91127	Human multi drug r
1754	15.8	1.6	19	1	AAZ91127	Human multi drug r
1755	15.8	1.6	19	1	AAZ91127	Human multi drug r
1756	15.8	1.6	19	1	AAZ91127	Human multi drug r
1757	15.8	1.6	19	1	AAZ91127	Human multi drug r
1758	15.8	1.6	19	1	AAZ91127	Human multi drug r
1759	15.8	1.6	19	1	AAZ91127	Human multi drug r
1760	15.8	1.6	19	1	AAZ91127	Human multi drug r
1761	15.8	1.6	19	1	AAZ91127	Human multi drug r
1762	15.8	1.6	19	1	AAZ91127	Human multi drug r
1763	15.8	1.6	19	1	AAZ91127	Human multi drug r
1764	15.8	1.6	19	1	AAZ91127	Human multi drug r
1765	15.8	1.6	19	1	AAZ91127	Human multi drug r
1766	15.8	1.6	19	1	AAZ91127	Human multi drug r
1767	15.8	1.6	19	1	AAZ91127	Human multi drug r
1768	15.8	1.6	19	1	AAZ91127	Human multi drug r
1769	15.8	1.6	19	1	AAZ91127	Human multi drug r
1770	15.8	1.6	19	1	AAZ91127	Human multi drug r
1771	15.8	1.6	19	1	AAZ91127	Human multi drug r
1772	15.8	1.6	19	1	AAZ91127	Human multi drug r
1773	15.8	1.6	19	1	AAZ91127	Human multi drug r
1774	15.8	1.6	19	1	AAZ91127	Human multi drug r
1775	15.8	1.6	19	1	AAZ91127	Human multi drug r
1776	15.8	1.6	19	1	AAZ91127	Human multi drug r
1777	15.8	1.6	19	1	AAZ91127	Human multi drug r
1778	15.8	1.6	19	1	AAZ91127	Human multi drug r
1779	15.8	1.6	19	1	AAZ91127	Human multi drug r
1780	15.8	1.6	19	1	AAZ91127	Human multi drug r
1781	15.8	1.6	19	1	AAZ91127	Human multi drug r
1782	15.8	1.6	19	1	AAZ91127	Human multi drug r
1783	15.8	1.6	19	1	AAZ91127	Human multi drug r
1784	15.8	1.6	19	1	AAZ91127	Human multi drug r
1785	15.8	1.6	19	1	AAZ91127	Human multi drug r

c1859	15.4	1.6	17	1	ABT40194	Tumour suppression
1860	15.4	1.6	17	1	ABT35639	Tumour suppression
c1861	15.4	1.6	17	1	ABT40150	Tumour suppression
c1862	15.4	1.6	17	1	ABT35874	Tumour suppression
1863	15.4	1.6	17	1	ABT39264	Tumour suppression
c1864	15.4	1.6	17	1	ABT40140	Tumour suppression
1865	15.4	1.6	17	1	ADB04318	Human MD27 scanlin
1866	15.4	1.6	17	1	ADB04317	Human MD27 scanlin
1867	15.4	1.6	17	1	ADB04437	Human MD27 scanlin
1868	15.4	1.6	17	1	ADB04446	Human MD27 scanlin
1869	15.4	1.6	17	1	ADB04316	Human MD27 scanlin
1870	15.4	1.6	17	1	ADB04447	Human MD27 scanlin
1871	15.4	1.6	17	1	ADB04444	Human MD27 scanlin
1872	15.4	1.6	17	1	ADB04445	Human MD27 scanlin
1873	15.4	1.6	17	1	ABZ60575	Human K-Ras DNazym
1874	15.4	1.6	17	1	ABZ60585	Human K-Ras DNazym
1875	15.4	1.6	17	1	ABZ60574	Human K-Ras DNazym
1876	15.4	1.6	17	1	ABZ60568	Human K-Ras DNazym
1877	15.4	1.6	17	1	ABZ60586	Human K-Ras DNazym
1878	15.4	1.6	17	1	ABZ60606	Human K-Ras DNazym
1879	15.4	1.6	17	1	ABZ60566	Human K-Ras DNazym
1880	15.4	1.6	17	1	ABZ60604	Human K-Ras DNazym
1881	15.4	1.6	17	1	ABZ60597	Human K-Ras DNazym
c1882	15.4	1.6	17	1	ABZ61843	Human H-Ras DNazym
1883	15.4	1.6	17	1	ABZ60567	Human K-Ras DNazym
1884	15.4	1.6	17	1	ACC64751	Murine oligonucleo
1885	15.4	1.6	17	1	ACC68479	Tumour suppression
1886	15.4	1.6	17	1	ADB44008	Tumour suppression
c1887	15.4	1.6	17	1	ADB41143	Tumour suppression
1888	15.4	1.6	17	1	ADB43650	Tumour suppression
1889	15.4	1.6	17	1	ADB44570	Tumour suppression
1890	15.4	1.6	17	1	ADB44878	Tumour suppression
1891	15.4	1.6	17	1	ADB44306	Tumour suppression
c1892	15.4	1.6	17	1	ADB44574	Tumour suppression
c1893	15.4	1.6	17	1	ADB44518	Tumour suppression
1894	15.4	1.6	17	1	ADB14015	Optineurin promote
c1895	15.4	1.6	17	1	ADB43565	Human IDE sequenci
c1896	15.4	1.6	17	1	ADIS0915	Human tumour suppr
c1897	15.4	1.6	17	1	ADIS0915	Human tumour suppr
c1898	15.4	1.6	17	1	ADIS0723	Human tumour suppr
c1899	15.4	1.6	17	1	ADIS2180	Human tumour suppr
c1900	15.4	1.6	17	1	ADIS0051	Human tumour suppr
c1901	15.4	1.6	17	1	ADIS1643	Human tumour suppr
c1902	15.4	1.6	17	1	ACC52610	Human tumour suppr
c1903	15.4	1.6	17	1	ACC51497	Human tumour suppr
1904	15.4	1.6	17	1	ACC54006	Human tumour suppr
c1905	15.4	1.6	17	1	ACC53324	Human tumour suppr
1906	15.4	1.6	17	1	ACC54016	Human tumour suppr
c1907	15.4	1.6	17	1	ACC51566	Human tumour suppr
1908	15.4	1.6	17	1	ACC52881	Human tumour suppr
c1909	15.4	1.6	17	1	ACC53359	Human tumour suppr
1910	15.4	1.6	17	1	ACC54020	Human tumour suppr
1911	15.4	1.6	17	1	ACC49918	Human PKR substrat
1912	15.4	1.6	17	1	ADL49916	Human PKR substrat
1913	15.4	1.6	17	1	ADL49966	Human PKR substrat
1914	15.4	1.6	17	1	ADL50193	Human PKR substrat
1915	15.4	1.6	17	1	ADL50202	Human PKR substrat
1916	15.4	1.6	17	1	ADL50201	Human PKR substrat
1917	15.4	1.6	17	1	ADL49951	Human PKR substrat
1918	15.4	1.6	17	1	ADL50417	Human PKR substrat
1919	15.4	1.6	17	1	ADL49931	Human PKR substrat
1920	15.4	1.6	17	1	ADL50198	Human PKR substrat
1921	15.4	1.6	17	1	ADL50418	Human PKR substrat
1922	15.4	1.6	17	1	ADL49930	Human PKR substrat
1923	15.4	1.6	17	1	ADL50731	Human PKR substrat
1924	15.4	1.6	17	1	ADL49907	Human PKR substrat
1925	15.4	1.6	17	1	ADL50749	Human PKR substrat
1926	15.4	1.6	17	1	ADL50749	Human PKR substrat
1927	15.4	1.6	17	1	ADL49908	Human PKR substrat
1928	15.4	1.6	17	1	ADL50213	Human PKR substrat
1929	15.4	1.6	17	1	ADL50738	Human PKR substrat
1930	15.4	1.6	17	1	ADL50212	Human PKR substrat
1931	15.4	1.6	17	1	ADL49917	Human PKR substrat
1932	15.4	1.6	17	1	ADL49926	Human PKR substrat
1933	15.4	1.6	17	1	ADL49965	Human PKR substrat
1934	15.4	1.6	17	1	ADL50214	Human PKR substrat
1935	15.4	1.6	17	1	ADL50747	Human PKR substrat
1936	15.4	1.6	17	1	ADL49434	Human PKR substrat
1937	15.4	1.6	17	1	ADL50197	Human PKR substrat
1938	15.4	1.6	17	1	ADL50748	Human PKR substrat
1939	15.4	1.6	17	1	ADL50748	Human PKR substrat
1940	15.4	1.6	17	1	ADL49906	Human PKR substrat
1941	15.4	1.6	17	1	ADL49929	Human PKR substrat
1942	15.4	1.6	17	1	ADL49950	Human PKR substrat
1943	15.4	1.6	17	1	ADL49430	Human PKR substrat
c1944	15.4	1.6	17	1	ADH54043	Human neurodegener
c1945	15.4	1.6	17	1	ADK13186	Human glioma endoc
c1946	15.4	1.6	17	1	ADL82347	Human ER+ breast c
c1947	15.4	1.6	17	1	ADL82453	Human ER+ breast c
c1948	15.4	1.6	17	1	ADP08740	Extend primer 77 u
c1949	15.4	1.6	17	1	ADP09251	Extend primer 46 u
c1950	15.4	1.6	17	1	ADP09278	Extend primer 73 u
1951	15.4	1.6	17	1	ADP08765	Extend primer 102
1952	15.4	1.6	17	1	ADP08011	CENPC1 extend prim
1953	15.4	1.6	17	1	ADP079480	DIAG1 extend prim
1954	15.4	1.6	17	1	ADP08017	CENPC1 extend prim
1955	15.4	1.6	17	1	AAQ02109	Cross-linking olig
1956	15.4	1.6	17	1	AAQ30448	Oligomer TNFR943 F
c1957	15.4	1.6	18	1	AAZ21792	Exemplary oligonuc
c1958	15.4	1.6	18	1	AAF76529	Human EFEMP1 codin
1959	15.4	1.6	18	1	AAH40898	SNP specific lower
c1960	15.4	1.6	18	1	AAH38514	SNP specific lower
1961	15.4	1.6	18	1	AAH40802	SNP specific lower
c1962	15.4	1.6	18	1	ABK27429	Colon cancer assoc
1963	15.4	1.6	18	1	ABS97649	Human glutathione-
1964	15.4	1.6	18	1	ABG14613	Human IL-10 regula
c1965	15.4	1.6	18	1	ABZ10660	Haematopoietic cel
c1966	15.4	1.6	18	1	ADM47300	NOX oligonucleoti
1967	15.4	1.6	18	1	ADN02351	PCR primer 2 used
c1968	15.4	1.6	18	1	ADN06374	Human FLAP related
c1969	15.4	1.6	18	1	ADN043261	Bipolar and unipol
1970	15.4	1.6	18	1	ADN048762	Human neuropilin 1
1971	15.4	1.6	18	1	ADN048745	Human neuropilin 1
c1972	15.4	1.6	18	1	ADN056946	Human CARK/FPGT pr
1973	15.4	1.6	18	1	ADN056480	Human cyclin-depen
c1974	15.4	1.6	18	1	ADN057017	Human CARK/FPGT pr
1975	15.4	1.6	18	1	ADN087850	Extend primer 87 u
1976	15.4	1.6	18	1	ADQ78196	PCR primer used to
c1977	15.4	1.6	19	1	AAH39033	SNP specific upper
c1978	15.4	1.6	19	1	AAF91124	Human multi drug r
1979	15.4	1.6	19	1	AAF91126	Human multi drug r
c1980	15.4	1.6	19	1	ACF62694	Cancer based on Cy
1981	15.4	1.6	19	1	ACF62695	Cancer based on Cy
c1982	15.4	1.6	19	1	ADB21365	MRP1 based cancer
1983	15.4	1.6	19	1	ADB21366	MRP1 based cancer
c1984	15.4	1.6	19	1	ADB88454	Human UGT1A1 varia
1985	15.4	1.6	19	1	ADB88455	Human UGT1A1 varia
1986	15.4	1.6	19	1	ADB97438	Human MDRI variant
c1987	15.4	1.6	19	1	ADB97437	Human MDRI variant
1988	15.4	1.6	19	1	ADB92629	Human MDRI variant
c1989	15.4	1.6	19	1	ADB92628	Human MDRI variant
1990	15.4	1.6	19	1	ADN02393	PCR primer 2 used
c1991	15.4	1.6	51	1	AAI78387	Human silent SNP c
c1992	15.2	1.5	18	1	ADN056498	Human cyclin-depen
c1993	15.2	1.5	41	1	ABZ57114	Human KIAA0608 pro
c1994	15.2	1.5	51	1	AAI79765	Human nonconservat
c1995	15.2	1.5	51	1	AAI79764	Human nonconservat
1996	15.2	1.5	51	1	AAI27794	Human SNP oligonuc
c1997	15.2	1.5	51	1	AAI73760	Human silent SNP c
1998	15.2	1.5	51	1	AAI79697	Human conservative
1999	15	1.5	15	1	AAI52114	Human ICAM hammerh
2000	15	1.5	15	1	AAI30969	Tag sequence of a
2001	15	1.5	15	1	AAF98058	Human IGBA allele
c2002	15	1.5	15	1	AAF97989	Human IGBA allele
c2003	15	1.5	15	1	AAF98057	Human IGBA allele
2004	15	1.5	15	1	AAF69438	Human IL4Ra1pha ge

c2005	15	1.5	15	1	ABK31922	Human colon cancer
c2006	15	1.5	15	1	ADBI4250	Optineurin promote
c2007	15	1.5	15	1	ADBI4031	Optineurin promote
2008	15	1.5	15	1	ACC84465	NTP peptide encodi
c2009	15	1.5	16	1	AAD63090	Human tandem tag D
c2010	15	1.5	16	1	ADH59602	Non-nucleotide pro
2011	15	1.5	16	1	ADH59614	Non-nucleotide pro
c2012	15	1.5	16	1	ADQ30388	Human VRI exon 1d
c2013	15	1.5	17	1	AAA22972	Integrin subunit b
c2014	15	1.5	17	1	AAA87041	Probe to Alu2 huma
2015	15	1.5	17	1	ADB04312	Human MD27 scannin
2016	15	1.5	17	1	ADB04280	Human MD27 scannin
c2017	15	1.5	17	1	ADB04285	Human MD27 scannin
c2018	15	1.5	17	1	ABZ60369	Human K-Ras DNAzym
2019	15	1.5	17	1	ABZ60598	Human K-Ras DNAzym
c2020	15	1.5	17	1	ACC65847	Murine oligonucleo
c2021	15	1.5	17	1	ACA62876	Repeated nucleic a
2022	15	1.5	17	1	ADB43123	Tumour suppression
2023	15	1.5	17	1	AD148985	Human tumour suppl
c2024	15	1.5	17	1	AD148613	Extend primer 85 u
c2025	15	1.5	17	1	ADP45893	Tango-63 primer t6
2026	15	1.5	18	1	AAV62683	Human Her-3 mRNA 1
c2027	15	1.5	18	1	AAH47613	PCR primer 1 used
2028	15	1.5	18	1	AA813583	Human KMSL1 PCR pr
c2029	15	1.5	18	1	ADBE43701	Human Tango-63 map
2030	15	1.5	18	1	ABX11281	Tango-63 chromosom
c2031	15	1.5	18	1	ADBE74499	Human neurodegener
c2032	15	1.5	18	1	ADH54179	Human neurodegener
c2033	15	1.5	18	1	ADDA8722	Human neuropilin 1
2034	15	1.5	18	1	AA173067	Human silent SNP c
c2035	15	1.5	51	1	AA176817	Human silent SNP c
c2036	15	1.5	51	1	AA179551	Human silent SNP c
2037	15	1.5	51	1	AA174502	Human silent SNP c
2038	15	1.5	51	1	AA179093	Human silent SNP c
c2039	15	1.5	51	1	AAO22632	Antisense oligonuc
c2040	14.8	1.5	18	1	AAO20160	Cross-linking olig
c2041	14.8	1.5	18	1	AAO34110	Sequence of a micr
c2042	14.8	1.5	18	1	AAO30310	Oligomer HSV723 fo
c2043	14.8	1.5	18	1	AAO62001	Quantine quartet co
c2044	14.8	1.5	18	1	AAO44515	Antisense oligonuc
2045	14.8	1.5	18	1	AAO75025	PCR primer. Synth
c2046	14.8	1.5	18	1	AAOT01742	Peptide Nucleic ac
c2047	14.8	1.5	18	1	AAO95465	Primer A1 (Group 4
c2048	14.8	1.5	18	1	AAIT30216	Antisense oligonuc
2049	14.8	1.5	18	1	AAIT94667	Anchored poly(7) o
c2050	14.8	1.5	18	1	AAV07750	Phosphorothioate o
2051	14.8	1.5	18	1	AAV21970	Nuclease resistant
c2052	14.8	1.5	18	1	AAV19943	Primer SEQ ID NO:3
c2053	14.8	1.5	18	1	AAV19942	Primer SEQ ID NO:2
2054	14.8	1.5	18	1	AAV18372	RT-PCR primer of t
c2055	14.8	1.5	18	1	AAZ27846	PCR primer for hum
c2056	14.8	1.5	18	1	AAZ87161	Oligoarabinonucleo
2057	14.8	1.5	18	1	AAZ87162	Oligoarabinonucleo
c2058	14.8	1.5	18	1	AAZ87166	Deoxyarabinonucleo
c2059	14.8	1.5	18	1	AAZ87167	Deoxyarabinonucleo
c2060	14.8	1.5	18	1	AAZ48898	Human ICM-1 antis
c2061	14.8	1.5	18	1	AAAC60960	Group-specific com
2062	14.8	1.5	18	1	AAAD03565	Oligonucleotide #6
c2063	14.8	1.5	18	1	AAAD17014	Oligonucleotide A1
2064	14.8	1.5	18	1	AAAF9708	Immunostimulatory
c2065	14.8	1.5	18	1	AAAF9734	Immunostimulatory
2066	14.8	1.5	18	1	AAAF82472	Plasmid vector PC
2067	14.8	1.5	18	1	AAAF16625	Gastric acid produ
2068	14.8	1.5	18	1	AAAH40502	SNP specific lower
c2069	14.8	1.5	18	1	AAH38362	SNP specific lower
c2070	14.8	1.5	18	1	AAH40562	SNP specific upper
2071	14.8	1.5	18	1	AAH38461	DNA-RNA-DNA oligo
c2072	14.8	1.5	18	1	AAAB91529	Human MONO-15 locu
c2073	14.8	1.5	18	1	AAAD38323	Secretory leukopro
2074	14.8	1.5	18	1	ABK86369	Rat secreted facto
2075	14.8	1.5	18	1	AAAS94743	Angiogenesis inhib
2076	14.8	1.5	18	1	ABST78455	Angiogenesis inhib
2077	14.8	1.5	18	1	ABST78429	Angiogenesis inhib
2078	14.8	1.5	18	1	ABL39401	Immunostimulatory
2079	14.8	1.5	18	1	AAD41497	Oligonucleotide us
2080	14.8	1.5	18	1	AB142967	Human chromosome 1
2081	14.8	1.5	18	1	AB144445	Human chromosome 1
2082	14.8	1.5	18	1	AB553437	Poly d(T) primer
c2083	14.8	1.5	18	1	ABD36362	Human MONO-15 loci
2084	14.8	1.5	18	1	ABBA93339	Adaptor oligonucle
c2085	14.8	1.5	18	1	ABE10473	Haematopoietic cel
c2086	14.8	1.5	18	1	ABE10474	Haematopoietic cel
c2087	14.8	1.5	18	1	ABE10475	PCR primer used to
c2088	14.8	1.5	18	1	ABE76822	Target RNA #1 used
2089	14.8	1.5	18	1	AAE56440	Antisense oligo #1
2090	14.8	1.5	18	1	AAE56446	Antisense oligo #1
2091	14.8	1.5	18	1	ACH03247	Immunostimulatory
2092	14.8	1.5	18	1	AAE57871	Antisense DNA-RNA
2093	14.8	1.5	18	1	AAE57878	Antisense DNA-RNA
2094	14.8	1.5	18	1	AAE57879	Antisense DNA-RNA
2095	14.8	1.5	18	1	AAE57877	Antisense DNA-RNA
c2096	14.8	1.5	18	1	AAE57890	Target RNA #1 used
2097	14.8	1.5	18	1	AAE60006	Human GH-1 gene am
2098	14.8	1.5	18	1	ADB37210	Immunostimulatory
2099	14.8	1.5	18	1	ADB37236	Immunostimulatory
c2100	14.8	1.5	18	1	ADC38978	Human ICM-1 targe
c2101	14.8	1.5	18	1	ADC31139	Human microsatelli
2102	14.8	1.5	18	1	ADE14006	Optineurin promote
2103	14.8	1.5	18	1	ADE14244	Optineurin promote
c2104	14.8	1.5	18	1	ADE14203	Optineurin promote
c2105	14.8	1.5	18	1	ADE76117	Human probe NEG fo
c2106	14.8	1.5	18	1	ADBE4357	Human lymphoid cel
c2107	14.8	1.5	18	1	ADBE4358	Human lymphoid cel
c2108	14.8	1.5	18	1	ADF17789	PCR primer 1274 C3
c2109	14.8	1.5	18	1	ADG89548	Human matrilin-3 p
c2110	14.8	1.5	18	1	ACA88892	Selection and ampl
c2111	14.8	1.5	18	1	ADG31947	RNA/DNA hybrid PCR
2112	14.8	1.5	18	1	ADJ34489	Nucleotide sequenc
2113	14.8	1.5	18	1	ADH16761	MCH1 genomic sequ
c2114	14.8	1.5	18	1	ADH76763	MCH1 genomic sequ
c2115	14.8	1.5	18	1	ADH78590	Test element oligo
2116	14.8	1.5	18	1	ADH70814	Hybridisation date
c2117	14.8	1.5	18	1	ADM46455	Antisense oligonuc
c2118	14.8	1.5	18	1	ADN08321	3T3 cell transform
c2119	14.8	1.5	18	1	ADN02345	PCR primer 64 used
c2120	14.8	1.5	18	1	ADN028710	Single stranded cd
c2121	14.8	1.5	18	1	ADN028711	Single stranded cd
c2122	14.8	1.5	18	1	ADN081024	Human prion protei
c2123	14.8	1.5	18	1	ADN026682	Synthetic leader s
c2124	14.8	1.5	18	1	ADP45818	Extend primer 10 u
2125	14.8	1.5	18	1	ADP86130	CpG immunostimulat
2126	14.8	1.5	18	1	ADQ30328	Human VRI exon 1d
c2127	14.8	1.5	18	1	ADQ30328	Human VRI exon 1d
c2128	14.8	1.5	41	1	ABE245509	Human ATP-binding
c2129	14.8	1.5	41	1	ABE245915	Human ATP-binding
c2130	14.8	1.5	41	1	ABE245508	Human ATP-binding
c2131	14.8	1.5	41	1	ABE245914	Human ATP-binding
c2132	14.6	1.5	15	1	AAAD20847	Human CHRN3 gene
c2133	14.6	1.5	15	1	AAAD20847	ASO primer #5 used
c2134	14.6	1.5	15	1	AAAD20847	Human AKR1B1 gene
c2135	14.6	1.5	15	1	ABLO1115	Human AKR1B1 gene
c2136	14.6	1.5	15	1	AAAD26858	Human GPR4 gene po
c2137	14.6	1.5	15	1	ABV99766	Human PKFB2 allele
c2138	14.6	1.5	15	1	ABU51983	Human SLC18A2 alle
c2139	14.6	1.5	15	1	ABK32790	Human APPB1 gene,
c2140	14.6	1.5	15	1	ABK81776	Human APPB1 gene,
c2141	14.6	1.5	15	1	ABK81776	Human APPB1 gene,
c2142	14.6	1.5	15	1	ABK81777	Human APPB1 gene,
c2143	14.6	1.5	15	1	ABK81777	Human APPB1 gene,
c2144	14.6	1.5	15	1	ABK81777	Human APPB1 gene,
c2145	14.6	1.5	15	1	ABK81777	Human APPB1 gene,
c2146	14.6	1.5	15	1	ABK81777	Human APPB1 gene,
c2147	14.6	1.5	15	1	ABK81777	Human APPB1 gene,
c2148	14.6	1.5	15	1	ABK81777	Human APPB1 gene,
c2149	14.6	1.5	15	1	ABK81777	Human APPB1 gene,
c2150	14.6	1.5	15	1	ABK81777	Human APPB1 gene,

c2151	14.6	1.5	51	AAH89507	Human coding sequ	2224	14.4	1.5	17	1	ADB43380	Tumour suppression
2152	14.6	1.5	51	AA176153	Human silent SNP c	2225	14.4	1.5	17	1	ADB40001	Tumour suppression
2153	14.4	1.5	16	AAQ95283	Simple tandem repe	c2226	14.4	1.5	17	1	ADB42612	Tumour suppression
c2154	14.4	1.5	16	AAJ12238	Human CYP450 2C19	2227	14.4	1.5	17	1	ADB42824	Tumour suppression
c2155	14.4	1.5	16	ADD28838	Escherichia coli 0	2228	14.4	1.5	17	1	ADB42825	Tumour suppression
2156	14.4	1.5	16	ADD28839	Escherichia coli 0	c2229	14.4	1.5	17	1	ADB42928	Tumour suppression
c2157	14.4	1.5	16	ADD28836	Escherichia coli 0	c2230	14.4	1.5	17	1	ADB44164	Tumour suppression
2158	14.4	1.5	16	ADD28837	Escherichia coli 0	2231	14.4	1.5	17	1	ADB41301	Tumour suppression
2159	14.4	1.5	16	ADD14208	Optineurin promote	2232	14.4	1.5	17	1	ADB40212	Tumour suppression
c2160	14.4	1.5	16	ADB14014	Optineurin promote	2233	14.4	1.5	17	1	ADB44035	Tumour suppression
c2161	14.4	1.5	16	AAJ63061	Human NADH dehydro	c2234	14.4	1.5	17	1	ADB45601	Tumour suppression
c2162	14.4	1.5	16	AAJ63093	Human tandem tag D	c2235	14.4	1.5	17	1	ADB45590	Tumour suppression
c2163	14.4	1.5	16	AAJ63047	Human ribosomal pr	c2236	14.4	1.5	17	1	ADB45950	Tumour suppression
c2164	14.4	1.5	16	AAJ63083	Human tandem tag D	c2237	14.4	1.5	17	1	ADB30865	Cholesterol homeos
2165	14.4	1.5	16	ADH59611	Non-nucleotide pro	c2238	14.4	1.5	17	1	ADB30723	Cholesterol homeos
c2166	14.4	1.5	16	ADH59599	Non-nucleotide pro	c2239	14.4	1.5	17	1	ADH59599	Non-nucleotide pro
c2167	14.4	1.5	16	ABX14989	Human delta opioid	2240	14.4	1.5	17	1	ADH49563	Human tumour supp
c2168	14.4	1.5	16	ABT34281	Opioid receptor DI	c2241	14.4	1.5	17	1	ADH51563	Human tumour supp
c2169	14.4	1.5	16	ADH70278	Human Vbeta gene r	c2242	14.4	1.5	17	1	ADH47683	Human tumour supp
2170	14.4	1.5	16	ADQ30362	Human VKI exon 1d	c2243	14.4	1.5	17	1	ADH48354	Human tumour supp
c2171	14.4	1.5	17	AAQ95863	Primer A (Group 11	c2244	14.4	1.5	17	1	ADH52733	Human tumour supp
2172	14.4	1.5	17	AAA22692	Integrin subunit b	2245	14.4	1.5	17	1	ADH52722	Human tumour supp
c2173	14.4	1.5	17	AAA22753	Integrin subunit b	c2246	14.4	1.5	17	1	ADH52147	Human tumour supp
2174	14.4	1.5	17	AAA22754	Integrin subunit b	c2247	14.4	1.5	17	1	ADH52273	Human tumour supp
c2175	14.4	1.5	17	AAA22681	Integrin subunit b	c2248	14.4	1.5	17	1	ADH49735	Human tumour supp
c2176	14.4	1.5	17	AAA22960	Integrin subunit b	2249	14.4	1.5	17	1	ADH51656	Human tumour supp
c2177	14.4	1.5	17	AAA22965	Integrin subunit b	c2250	14.4	1.5	17	1	ADH52090	Human tumour supp
c2178	14.4	1.5	17	AAA22975	Integrin subunit b	2251	14.4	1.5	17	1	ADH49985	Human tumour supp
2179	14.4	1.5	17	AAA22835	Integrin subunit b	c2252	14.4	1.5	17	1	ADH52788	Human tumour supp
2180	14.4	1.5	17	AAA22833	Integrin subunit b	c2253	14.4	1.5	17	1	ADH47513	Human tumour supp
2181	14.4	1.5	17	AAA22735	Integrin subunit b	c2254	14.4	1.5	17	1	ADH50287	Human tumour supp
2182	14.4	1.5	17	AAA22818	Integrin subunit b	2255	14.4	1.5	17	1	ADH20628	Putative eRNA sequ
2183	14.4	1.5	17	AAA25181	Oestrogen receptor	c2256	14.4	1.5	17	1	ACC53368	Human tumour supp
2184	14.4	1.5	17	AAAF05508	Hammerhead ribozym	2257	14.4	1.5	17	1	ACC54015	Human tumour supp
2185	14.4	1.5	17	AAAF06148	Hammerhead ribozym	2258	14.4	1.5	17	1	ACC51578	Human tumour supp
2186	14.4	1.5	17	AAAF06151	Hammerhead ribozym	c2259	14.4	1.5	17	1	ACC51578	Human tumour supp
2187	14.4	1.5	17	ABA91530	DNA-RNA-DNA oligon	2260	14.4	1.5	17	1	ACC53015	Human tumour supp
c2188	14.4	1.5	17	ABN83023	Ataxia telangiecta	2261	14.4	1.5	17	1	ACC53596	Human tumour supp
2189	14.4	1.5	17	ADG14612	Human IL-10 regula	2262	14.4	1.5	17	1	ACC54007	Human tumour supp
2190	14.4	1.5	17	ABT16747	Tumour suppression	c2263	14.4	1.5	17	1	ACC52967	Human tumour supp
c2191	14.4	1.5	17	ABT19415	Tumour suppression	2264	14.4	1.5	17	1	ADL50195	Human PKR substra
c2192	14.4	1.5	17	ABT36267	Tumour suppression	2265	14.4	1.5	17	1	ADL50217	Human PKR substra
2193	14.4	1.5	17	ABT38180	Tumour suppression	2266	14.4	1.5	17	1	ADL49442	Human PKR substra
2194	14.4	1.5	17	ABT38796	Tumour suppression	2267	14.4	1.5	17	1	ADL50746	Human PKR substra
c2195	14.4	1.5	17	ABT36344	Tumour suppression	2268	14.4	1.5	17	1	ADL49424	Human PKR substra
c2196	14.4	1.5	17	ABT39345	Tumour suppression	2269	14.4	1.5	17	1	ADL49431	Human PKR substra
c2197	14.4	1.5	17	ABT37365	Tumour suppression	2270	14.4	1.5	17	1	ADL49441	Human PKR substra
2198	14.4	1.5	17	ABT38008	Tumour suppression	2271	14.4	1.5	17	1	ADL49452	Human PKR substra
2199	14.4	1.5	17	ABT35457	Tumour suppression	2272	14.4	1.5	17	1	ADL50425	Human PKR substra
c2200	14.4	1.5	17	ABT36801	Tumour suppression	2273	14.4	1.5	17	1	ADL49452	Human PKR substra
c2201	14.4	1.5	17	ABT36337	Tumour suppression	2274	14.4	1.5	17	1	ADL49425	Human PKR substra
2202	14.4	1.5	17	ABT37220	Tumour suppression	2275	14.4	1.5	17	1	ADL50192	Human PKR substra
2203	14.4	1.5	17	ABT34597	Tumour suppression	2276	14.4	1.5	17	1	ADL50735	Human PKR substra
c2204	14.4	1.5	17	ABT36198	Tumour suppression	c2277	14.4	1.5	17	1	ADH17665	Forward PCR primer
2205	14.4	1.5	17	ABT36270	Tumour suppression	c2278	14.4	1.5	17	1	ADH135123	Human FLA2618 gene
2206	14.4	1.5	17	ABT34566	Tumour suppression	2279	14.4	1.5	17	1	ADH36811	Primer of the inva
c2207	14.4	1.5	17	ABT37351	Tumour suppression	c2280	14.4	1.5	17	1	ADH13208	Human glioma endo
2208	14.4	1.5	17	ABT39059	Tumour suppression	c2281	14.4	1.5	17	1	ADJ10024	PCR primer 30 to g
2209	14.4	1.5	17	ACA06514	NFKB sub-unit modu	2282	14.4	1.5	17	1	ADN06450	Human FLAP related
2210	14.4	1.5	17	ACA06515	NFKB sub-unit modu	c2283	14.4	1.5	17	1	ADP09407	Extend primer 29 u
2211	14.4	1.5	17	ADB04319	Human MD27 scanlin	2284	14.4	1.5	17	1	ADP09403	Extend primer 25 u
2212	14.4	1.5	17	ADB04448	Human MD27 scanlin	c2285	14.4	1.5	17	1	ADP08700	Extend primer 37 u
2213	14.4	1.5	17	ADB04436	Human MD27 scanlin	c2286	14.4	1.5	17	1	AAQ95849	Primer A (Group 11
2214	14.4	1.5	17	ABZ60588	Human K-Ras DNAszm	c2287	14.4	1.5	17	1	AAH36673	PCR primer for mar
2215	14.4	1.5	17	ABZ60580	Human K-Ras DNAszm	c2288	14.4	1.5	18	1	AAH09767	Primer #17, Homo
2216	14.4	1.5	17	ABZ60579	Human K-Ras DNAszm	2289	14.4	1.5	18	1	AAH24965	PCR primer used to
2217	14.4	1.5	17	ABZ60570	Human K-Ras DNAszm	c2290	14.4	1.5	18	1	ABA82331	Zmx1 gene region
2218	14.4	1.5	17	ABZ60600	Human K-Ras DNAszm	c2291	14.4	1.5	18	1	AAH49482	Triomy 21 diagnos
2219	14.4	1.5	17	ABZ60607	Human K-Ras DNAszm	c2292	14.4	1.5	18	1	ABK23128	Human Zmx1 CDNA r
2220	14.4	1.5	17	ACG66396	Murine oligonucleo	c2293	14.4	1.5	18	1	ABT10657	Haematopoietic cel
c2221	14.4	1.5	17	ACC68207	Murine oligonucleo	c2294	14.4	1.5	18	1	ACC45711	Human HBM STS mark
c2222	14.4	1.5	17	ADB44023	Tumour suppression	c2295	14.4	1.5	18	1	ADH26921	Human PGC-1 alpha
c2223	14.4	1.5	17	ADB40222	Tumour suppression	c2296	14.4	1.5	18	1	ADH26920	Mouse PGC-1 alpha

C2297	14.4	1.5	18	1	AD598409	Sequence tagged bi	2370	13.8	1.4	17	1	AAA22730	Integrin subunit b
C2298	14.4	1.5	18	1	ACA58053	Human familial b1p	2371	13.8	1.4	17	1	AAA22842	Integrin subunit b
2299	14.4	1.5	18	1	ADM92832	SNP-containing car	2372	13.8	1.4	17	1	AAA22854	Integrin subunit b
2300	14.4	1.5	18	1	ADN06584	Human F1AP related	C2373	13.8	1.4	17	1	AAA22971	Integrin subunit b
C2301	14.4	1.5	18	1	AD056531	Human cyclin-depen	2374	13.8	1.4	17	1	AAA22687	Integrin subunit b
C2302	14.4	1.5	18	1	AD056506	Human cyclin-depen	2375	13.8	1.4	17	1	AAA22822	Integrin subunit b
2303	14.4	1.5	18	1	AD056556	Human cyclin-depen	C2376	13.8	1.4	17	1	AAA22964	Integrin subunit b
2304	14.4	1.5	18	1	ADP45830	Extend primer 22 u	C2377	13.8	1.4	17	1	AAA22974	Integrin subunit b
2305	14.2	1.5	36	1	AAH91142	Human inflammatory	2378	13.8	1.4	17	1	AAA22731	Integrin subunit b
C2306	14	1.4	14	1	AAV95956	Microsatellite ana	2379	13.8	1.4	17	1	AAA22738	Integrin subunit b
2307	14	1.4	14	1	AAA23392	Integrin subunit b	2380	13.8	1.4	17	1	AAA22753	Integrin subunit b
2308	14	1.4	14	1	AAA23382	Integrin subunit b	2381	13.8	1.4	17	1	AAA22732	Integrin subunit b
C2309	14	1.4	14	1	AAA23406	Integrin subunit b	2382	13.8	1.4	17	1	AAA22823	Integrin subunit b
2310	14	1.4	14	1	AAA23388	Integrin subunit b	2383	13.8	1.4	17	1	AAA22843	Integrin subunit b
2311	14	1.4	14	1	ACA62844	Repeated nucleic a	2384	13.8	1.4	17	1	AAA22824	Integrin subunit b
2312	14	1.4	14	1	ADH70473	Human Vbeta gene r	2385	13.8	1.4	17	1	AAV91399	Integrin subunit b
2313	14	1.4	15	1	AA752086	Human ICM hammerh	2386	13.8	1.4	17	1	AAK18370	Integrin subunit b
2314	14	1.4	15	1	AA752112	Human ICM hammerh	2387	13.8	1.4	17	1	AAK36739	Integrin subunit b
2315	14	1.4	15	1	ADH70501	Human Vbeta gene r	2388	13.8	1.4	17	1	AAA25450	Integrin subunit b
2316	14	1.4	15	1	ADQ30131	Murine VRI exon 1d	2389	13.8	1.4	17	1	AAA25600	Oestrogen receptor
2317	14	1.4	15	1	ADQ30131	Optineurin promote	2390	13.8	1.4	17	1	AAA25178	Oestrogen receptor
2318	14	1.4	16	1	ADH70756	Human Vbeta gene r	2391	13.8	1.4	17	1	AAA25603	Oestrogen receptor
2319	14	1.4	16	1	AA793352	Primer #2 for D105	2392	13.8	1.4	17	1	AAA25444	Oestrogen receptor
2320	14	1.4	17	1	AA793385	Integrin subunit b	2393	13.8	1.4	17	1	AAA25445	Human retrovirus H
2321	14	1.4	17	1	AAA22845	Integrin subunit b	2394	13.8	1.4	17	1	AAA98232	2'-methoxyethoxy-m
C2322	14	1.4	17	1	AAA22806	Integrin subunit b	2395	13.8	1.4	17	1	AA505197	Hammerhead ribozym
2323	14	1.4	17	1	AAA22967	Integrin subunit b	2396	13.8	1.4	17	1	AA505509	Hammerhead ribozym
C2324	14	1.4	17	1	AAA22846	Integrin subunit b	2397	13.8	1.4	17	1	AA705510	Hammerhead ribozym
2325	14	1.4	17	1	AA705512	Integrin subunit b	2398	13.8	1.4	17	1	AA7056381	Hammerhead ribozym
2326	14	1.4	17	1	AA705507	Hammerhead ribozym	2399	13.8	1.4	17	1	AA705469	Human NOGO inozyme
2327	14	1.4	17	1	AA705507	Hammerhead ribozym	2400	13.8	1.4	17	1	AA705469	Human NOGO inozyme
2328	14	1.4	17	1	AB736209	Tumour suppression	2401	13.8	1.4	17	1	ABK00892	Human NOGO inozyme
2329	14	1.4	17	1	ADB04202	Human MD27 scannin	2402	13.8	1.4	17	1	ABK00891	Human NOGO Hammeth
2330	14	1.4	17	1	ADB04201	Human MD27 scannin	2403	13.8	1.4	17	1	ABK00089	Human NOGO Hammeth
2331	14	1.4	17	1	ADB04204	Human MD27 scannin	C2404	13.8	1.4	17	1	ABK00237	Human GRID NCH rib
2332	14	1.4	17	1	ADB04203	Human MD27 scannin	2405	13.8	1.4	17	1	ABK46735	Zmax1 gene region
2333	14	1.4	17	1	ADB04279	Human MD27 scannin	2406	13.8	1.4	17	1	ABA82250	Zmax1 gene region
2334	14	1.4	17	1	ADB04286	Human MD27 scannin	C2407	13.8	1.4	17	1	ABA82250	Human GMLP-1 17-m
2335	14	1.4	17	1	ADB04311	Human MD27 scannin	C2408	13.8	1.4	17	1	ABNO0871	Human GMLP-1 17-m
2336	14	1.4	17	1	AC64260	Murine oligonucleo	C2409	13.8	1.4	17	1	ABNO09432	Human GMLP-1 17-m
2337	14	1.4	17	1	AC667292	Murine oligonucleo	C2410	13.8	1.4	17	1	ABNO09435	Human GMLP-1 17-m
2338	14	1.4	17	1	AC68567	Tumour suppression	C2411	13.8	1.4	17	1	ABNO6555	Human GMLP-1 17-m
2339	14	1.4	17	1	ADB40764	Tumour suppression	C2412	13.8	1.4	17	1	ABV79240	Human GMLP-1 17-m
C2340	14	1.4	17	1	ADB40441	Human tumour suppress	C2413	13.8	1.4	17	1	ABK23302	Human GMLP-1 17-m
2341	14	1.4	17	1	AD147773	Human tumour suppress	2414	13.8	1.4	17	1	ABK23027	Human GMLP-1 17-m
2342	14	1.4	17	1	AD148718	Human tumour suppress	C2415	13.8	1.4	17	1	ABK56068	Human GMLP-1 17-m
2343	14	1.4	17	1	AD149435	Human PKR substrat	C2416	13.8	1.4	17	1	ABK56068	Human GMLP-1 17-m
2344	14	1.4	17	1	AD149461	Human PKR substrat	C2417	13.8	1.4	17	1	ACN01141	Human GMLP-1 17-m
2345	14	1.4	17	1	AC685669	RNA ligand aptamer	2418	13.8	1.4	17	1	ACN14418	Human GMLP-1 17-m
2346	14	1.4	17	1	ADP08721	Extend primer 58 u	C2419	13.8	1.4	17	1	ACN08942	Human GMLP-1 17-m
C2347	14	1.4	17	1	AD080021	CENPC1 extend prim	2420	13.8	1.4	17	1	ACN08945	Human GMLP-1 17-m
C2348	14	1.4	42	1	AC684459	NTP peptide encodi	C2421	13.8	1.4	17	1	ACN04912	Human GMLP-1 17-m
C2349	14	1.4	60	1	AC684454	NTP peptide encodi	C2422	13.8	1.4	17	1	ACN01975	Human GMLP-1 17-m
C2350	13.8	1.4	17	1	AA781185	Human c-myd hammet	C2423	13.8	1.4	17	1	AB739507	Human GMLP-1 17-m
C2351	13.8	1.4	17	1	AA781185	Juvenile glaucoma	2424	13.8	1.4	17	1	AB739507	Human GMLP-1 17-m
2352	13.8	1.4	17	1	AA785611	CADASIL mutation d	C2425	13.8	1.4	17	1	AB735178	Human GMLP-1 17-m
2353	13.8	1.4	17	1	AA659800	Human fil1 VEGF re	C2426	13.8	1.4	17	1	AB738397	Human GMLP-1 17-m
2354	13.8	1.4	17	1	AA700075	Human fil1 VEGF re	C2427	13.8	1.4	17	1	AB740193	Human GMLP-1 17-m
2355	13.8	1.4	17	1	AA700073	Human fil1 VEGF re	C2428	13.8	1.4	17	1	AB735657	Human GMLP-1 17-m
2356	13.8	1.4	17	1	AA700074	Human fil1 VEGF re	2429	13.8	1.4	17	1	AB736213	Human GMLP-1 17-m
2357	13.8	1.4	17	1	AA630109	Delta-9 desaturase	2430	13.8	1.4	17	1	AB737096	Human GMLP-1 17-m
C2358	13.8	1.4	17	1	AA63010	Human c-fos target	C2431	13.8	1.4	17	1	AB738743	Human GMLP-1 17-m
C2359	13.8	1.4	17	1	AAV95380	Human EGF-R target	2432	13.8	1.4	17	1	AB735066	Human GMLP-1 17-m
C2360	13.8	1.4	17	1	AAV97762	Human EGF-R target	2433	13.8	1.4	17	1	AB736682	Human GMLP-1 17-m
C2361	13.8	1.4	17	1	AAV48871	RbB-2 gene antis	C2434	13.8	1.4	17	1	AB739288	Human GMLP-1 17-m
C2362	13.8	1.4	17	1	AAV95124	Integrin subunit b	2435	13.8	1.4	17	1	AB739318	Human GMLP-1 17-m
2363	13.8	1.4	17	1	AAV95124	Integrin subunit b	C2436	13.8	1.4	17	1	AB735464	Human GMLP-1 17-m
2364	13.8	1.4	17	1	AAA22844	Integrin subunit b	C2437	13.8	1.4	17	1	AB736625	Human GMLP-1 17-m
2365	13.8	1.4	17	1	AAA22852	Integrin subunit b	C2438	13.8	1.4	17	1	AB738938	Human GMLP-1 17-m
2366	13.8	1.4	17	1	AAA22693	Integrin subunit b	2439	13.8	1.4	17	1	AB739417	Human GMLP-1 17-m
2367	13.8	1.4	17	1	AAA22688	Integrin subunit b	C2440	13.8	1.4	17	1	AB739436	Human GMLP-1 17-m
2368	13.8	1.4	17	1	AAA22749	Integrin subunit b	2441	13.8	1.4	17	1	AB739916	Human GMLP-1 17-m
2369	13.8	1.4	17	1	AAA22825	Integrin subunit b	C2442	13.8	1.4	17	1	AB734744	Human GMLP-1 17-m



2443	13.8	1.4	17	1	ABT34859	Tumour suppression
C2444	13.8	1.4	17	1	ABT35713	Tumour suppression
C2445	13.8	1.4	17	1	ABT36965	Tumour suppression
C2446	13.8	1.4	17	1	ABT39805	Tumour suppression
C2447	13.8	1.4	17	1	ABT39426	Tumour suppression
C2448	13.8	1.4	17	1	ABT39821	Tumour suppression
C2449	13.8	1.4	17	1	ABT34652	Tumour suppression
C2450	13.8	1.4	17	1	ABT34713	Tumour suppression
C2451	13.8	1.4	17	1	ABT36681	Tumour suppression
C2452	13.8	1.4	17	1	ABT38340	Tumour suppression
C2453	13.8	1.4	17	1	ABT38870	Tumour suppression
C2454	13.8	1.4	17	1	ABT38923	Tumour suppression
C2455	13.8	1.4	17	1	ABT36025	Tumour suppression
C2456	13.8	1.4	17	1	ABT38827	Tumour suppression
C2457	13.8	1.4	17	1	ABT40033	Tumour suppression
C2458	13.8	1.4	17	1	ABT35129	Tumour suppression
C2459	13.8	1.4	17	1	ABT35655	Tumour suppression
C2460	13.8	1.4	17	1	ABT37057	Tumour suppression
C2461	13.8	1.4	17	1	ABT38389	Tumour suppression
C2462	13.8	1.4	17	1	ABT39853	Tumour suppression
C2463	13.8	1.4	17	1	ABT34445	Tumour suppression
C2464	13.8	1.4	17	1	ABT34807	Tumour suppression
C2465	13.8	1.4	17	1	ABT36651	Tumour suppression
C2466	13.8	1.4	17	1	ABT36653	Tumour suppression
C2467	13.8	1.4	17	1	ABT37037	Tumour suppression
C2468	13.8	1.4	17	1	ABT38237	Tumour suppression
C2469	13.8	1.4	17	1	ABT40087	Tumour suppression
C2470	13.8	1.4	17	1	ABT35675	Tumour suppression
C2471	13.8	1.4	17	1	ABT37579	Tumour suppression
C2472	13.8	1.4	17	1	ABT37770	Tumour suppression
C2473	13.8	1.4	17	1	ABT40151	Tumour suppression
C2474	13.8	1.4	17	1	ABT34950	Tumour suppression
C2475	13.8	1.4	17	1	ABT36577	Tumour suppression
C2476	13.8	1.4	17	1	ABT37081	Tumour suppression
C2477	13.8	1.4	17	1	ABT37662	Tumour suppression
C2478	13.8	1.4	17	1	ACA06516	NPfX sub-unit modu
C2479	13.8	1.4	17	1	ADB04310	Human MD27 scannin
C2480	13.8	1.4	17	1	ADB04414	Human MD27 scannin
C2481	13.8	1.4	17	1	ADB04387	Human MD27 scannin
C2482	13.8	1.4	17	1	ADB04390	Human MD27 scannin
C2483	13.8	1.4	17	1	ADB04420	Human MD27 scannin
C2484	13.8	1.4	17	1	ADB04486	Human MD27 scannin
C2485	13.8	1.4	17	1	ADB04376	Human MD27 scannin
C2486	13.8	1.4	17	1	ADB04320	Human MD27 scannin
C2487	13.8	1.4	17	1	ADB04388	Human MD27 scannin
C2488	13.8	1.4	17	1	ADB04413	Human MD27 scannin
C2489	13.8	1.4	17	1	ADB04421	Human MD27 scannin
C2490	13.8	1.4	17	1	ADB04271	Human MD27 scannin
C2491	13.8	1.4	17	1	ADB04205	Human MD27 scannin
C2492	13.8	1.4	17	1	ADB04377	Human MD27 scannin
C2493	13.8	1.4	17	1	ADB04386	Human MD27 scannin
C2494	13.8	1.4	17	1	ADB04435	Human MD27 scannin
C2495	13.8	1.4	17	1	ADB04466	Human MD27 scannin
C2496	13.8	1.4	17	1	ADB04378	Human MD27 scannin
C2497	13.8	1.4	17	1	ADB04481	Human MD27 scannin
C2498	13.8	1.4	17	1	ADB04275	Human MD27 scannin
C2499	13.8	1.4	17	1	ADB04467	Human MD27 scannin
C2500	13.8	1.4	17	1	ADB04277	Human MD27 scannin
C2501	13.8	1.4	17	1	ADB04321	Human MD27 scannin
C2502	13.8	1.4	17	1	ADB04385	Human MD27 scannin
C2503	13.8	1.4	17	1	ADB04395	Human MD27 scannin
C2504	13.8	1.4	17	1	ADB04482	Human MD27 scannin
C2505	13.8	1.4	17	1	ADB04485	Human MD27 scannin
C2506	13.8	1.4	17	1	ADB04278	Human MD27 scannin
C2507	13.8	1.4	17	1	ADB04449	Human MD27 scannin
C2508	13.8	1.4	17	1	ADB04480	Human MD27 scannin
C2509	13.8	1.4	17	1	ACC45610	Human HBM STS mark
C2510	13.8	1.4	17	1	ACC45885	Human HBM STS mark
C2511	13.8	1.4	17	1	ABE60820	Human K-Ras DNazym
C2512	13.8	1.4	17	1	ABE60569	Human K-Ras DNazym
C2513	13.8	1.4	17	1	ACC65127	Mutine oligonucleo
C2514	13.8	1.4	17	1	ACC68489	Mutine oligonucleo
C2515	13.8	1.4	17	1	ACC65583	Mutine oligonucleo
2516	13.8	1.4	17	1	ACC66564	Mutine oligonucleo
2517	13.8	1.4	17	1	ACC64076	Mutine oligonucleo
2518	13.8	1.4	17	1	ACC64870	Mutine oligonucleo
2519	13.8	1.4	17	1	ACA90066	Mutine oligonucleo
2520	13.8	1.4	17	1	AAD56441	Cardiovascular dis
2521	13.8	1.4	17	1	AAD56448	Cardiovascular dis
2522	13.8	1.4	17	1	AAD56449	Cardiovascular dis
2523	13.8	1.4	17	1	AAD56447	Cardiovascular dis
2524	13.8	1.4	17	1	AAD56450	Cardiovascular dis
2525	13.8	1.4	17	1	ADA50284	Human PCR primer 8
2526	13.8	1.4	17	1	ADB98583	Sequence tagged si
2527	13.8	1.4	17	1	ADB98308	Sequence tagged si
2528	13.8	1.4	17	1	ADB39800	Tumour suppression
2529	13.8	1.4	17	1	ADB40686	Tumour suppression
2530	13.8	1.4	17	1	ADB41889	Tumour suppression
2531	13.8	1.4	17	1	ADB41999	Tumour suppression
2532	13.8	1.4	17	1	ADB42848	Tumour suppression
2533	13.8	1.4	17	1	ADB42904	Tumour suppression
2534	13.8	1.4	17	1	ADB39762	Tumour suppression
2535	13.8	1.4	17	1	ADB41881	Tumour suppression
2536	13.8	1.4	17	1	ADB42307	Tumour suppression
2537	13.8	1.4	17	1	ADB42587	Tumour suppression
2538	13.8	1.4	17	1	ADB40636	Tumour suppression
2539	13.8	1.4	17	1	ADB42220	Tumour suppression
2540	13.8	1.4	17	1	ADB42668	Tumour suppression
2541	13.8	1.4	17	1	ADB42732	Tumour suppression
2542	13.8	1.4	17	1	ADB41555	Tumour suppression
2543	13.8	1.4	17	1	ADB41871	Tumour suppression
2544	13.8	1.4	17	1	ADB42115	Tumour suppression
2545	13.8	1.4	17	1	ADB43876	Tumour suppression
2546	13.8	1.4	17	1	ADB41239	Tumour suppression
2547	13.8	1.4	17	1	ADB40006	Tumour suppression
2548	13.8	1.4	17	1	ADB40041	Tumour suppression
2549	13.8	1.4	17	1	ADB40132	Tumour suppression
2550	13.8	1.4	17	1	ADB42575	Tumour suppression
2551	13.8	1.4	17	1	ADB42349	Tumour suppression
2552	13.8	1.4	17	1	ADB41338	Tumour suppression
2553	13.8	1.4	17	1	ADB41765	Tumour suppression
2554	13.8	1.4	17	1	ADB43807	Tumour suppression
2555	13.8	1.4	17	1	ADB40879	Tumour suppression
2556	13.8	1.4	17	1	ADB41273	Tumour suppression
2557	13.8	1.4	17	1	ADB43997	Tumour suppression
2558	13.8	1.4	17	1	ADB40673	Tumour suppression
2559	13.8	1.4	17	1	ADB43325	Tumour suppression
2560	13.8	1.4	17	1	ADB44153	Tumour suppression
2561	13.8	1.4	17	1	ADB40382	Tumour suppression
2562	13.8	1.4	17	1	ADB41878	Tumour suppression
2563	13.8	1.4	17	1	ADB41780	Tumour suppression
2564	13.8	1.4	17	1	ADB42420	Tumour suppression
2565	13.8	1.4	17	1	ADB41181	Tumour suppression
2566	13.8	1.4	17	1	ADB43345	Tumour suppression
2567	13.8	1.4	17	1	ADB44838	Tumour suppression
2568	13.8	1.4	17	1	ADB44927	Tumour suppression
2569	13.8	1.4	17	1	ADB44849	Tumour suppression
2570	13.8	1.4	17	1	ADB45873	Tumour suppression
2571	13.8	1.4	17	1	ADB45091	Tumour suppression
2572	13.8	1.4	17	1	ADB45070	Tumour suppression
2573	13.8	1.4	17	1	ADB45775	Tumour suppression
2574	13.8	1.4	17	1	ADB45432	Tumour suppression
2575	13.8	1.4	17	1	ADB44891	Tumour suppression
2576	13.8	1.4	17	1	ADB45471	Tumour suppression
2577	13.8	1.4	17	1	ADB45688	Tumour suppression
2578	13.8	1.4	17	1	ADB44480	Tumour suppression
2579	13.8	1.4	17	1	ADB44569	Tumour suppression
2580	13.8	1.4	17	1	ADB44573	Tumour suppression
2581	13.8	1.4	17	1	ADB45020	Tumour suppression
2582	13.8	1.4	17	1	ADB45575	Tumour suppression
2583	13.8	1.4	17	1	ADB45717	Tumour suppression
2584	13.8	1.4	17	1	ADE25242	Plant growth assoc
2585	13.8	1.4	17	1	ADE14007	Optineurin promote
2586	13.8	1.4	17	1	ADE30629	Cholesterol homeos
2587	13.8	1.4	17	1	ADE30636	Cholesterol homeos
2588	13.8	1.4	17	1	ADE30688	Cholesterol homeos



c2589	13.8	1.4	17	1	AD148550	Human tumour suppressor
c2590	13.8	1.4	17	1	AD151546	Human tumour suppressor
c2591	13.8	1.4	17	1	AD152377	Human tumour suppressor
c2592	13.8	1.4	17	1	AD151185	Human tumour suppressor
c2593	13.8	1.4	17	1	AD152079	Human tumour suppressor
c2594	13.8	1.4	17	1	AD152868	Human tumour suppressor
c2595	13.8	1.4	17	1	AD152429	Human tumour suppressor
c2596	13.8	1.4	17	1	AD152776	Human tumour suppressor
c2597	13.8	1.4	17	1	AD151234	Human tumour suppressor
c2598	13.8	1.4	17	1	AD148839	Human tumour suppressor
c2599	13.8	1.4	17	1	AD150971	Human tumour suppressor
c2600	13.8	1.4	17	1	AD151323	Human tumour suppressor
c2601	13.8	1.4	17	1	AD152101	Human tumour suppressor
c2602	13.8	1.4	17	1	AD149325	Human tumour suppressor
c2603	13.8	1.4	17	1	AD149868	Human tumour suppressor
c2604	13.8	1.4	17	1	AD148528	Human tumour suppressor
c2605	13.8	1.4	17	1	AD150607	Human tumour suppressor
c2606	13.8	1.4	17	1	AD148410	Human tumour suppressor
c2607	13.8	1.4	17	1	AD150528	Human tumour suppressor
c2608	13.8	1.4	17	1	AD151596	Human tumour suppressor
c2609	13.8	1.4	17	1	AD147945	Human tumour suppressor
c2610	13.8	1.4	17	1	AD151031	Human tumour suppressor
c2611	13.8	1.4	17	1	AD151650	Human tumour suppressor
c2612	13.8	1.4	17	1	AD152224	Human tumour suppressor
c2613	13.8	1.4	17	1	AD152687	Human tumour suppressor
c2614	13.8	1.4	17	1	AD148989	Human tumour suppressor
c2615	13.8	1.4	17	1	AD150397	Human tumour suppressor
c2616	13.8	1.4	17	1	AD150699	Human tumour suppressor
c2617	13.8	1.4	17	1	AD151116	Human tumour suppressor
c2618	13.8	1.4	17	1	AD152878	Human tumour suppressor
c2619	13.8	1.4	17	1	AD151763	Human tumour suppressor
c2620	13.8	1.4	17	1	AD152882	Human tumour suppressor
c2621	13.8	1.4	17	1	AD153358	Human tumour suppressor
c2622	13.8	1.4	17	1	AD151498	Human tumour suppressor
c2623	13.8	1.4	17	1	AD151565	Human tumour suppressor
c2624	13.8	1.4	17	1	AD152615	Human tumour suppressor
c2625	13.8	1.4	17	1	AD151477	Human tumour suppressor
c2626	13.8	1.4	17	1	AD151579	Human tumour suppressor
c2627	13.8	1.4	17	1	AD152221	Human tumour suppressor
c2628	13.8	1.4	17	1	AD153369	Human tumour suppressor
c2629	13.8	1.4	17	1	AD153326	Human tumour suppressor
c2630	13.8	1.4	17	1	AD153360	Human tumour suppressor
c2631	13.8	1.4	17	1	AD153894	Human tumour suppressor
c2632	13.8	1.4	17	1	AD154040	Human tumour suppressor
c2633	13.8	1.4	17	1	AD152644	Human tumour suppressor
c2634	13.8	1.4	17	1	AD152766	Human tumour suppressor
c2635	13.8	1.4	17	1	AD154019	Human tumour suppressor
c2636	13.8	1.4	17	1	AD151516	Human tumour suppressor
c2637	13.8	1.4	17	1	AD153325	Human tumour suppressor
c2638	13.8	1.4	17	1	AD147195	Human NOGO receptor
c2639	13.8	1.4	17	1	AD149949	Human PKR substrate
c2640	13.8	1.4	17	1	AD150742	Human PKR substrate
c2641	13.8	1.4	17	1	AD149358	Human PKR substrate
c2642	13.8	1.4	17	1	AD149905	Human PKR substrate
c2643	13.8	1.4	17	1	AD149905	Human PKR substrate
c2644	13.8	1.4	17	1	AD150737	Human PKR substrate
c2645	13.8	1.4	17	1	AD149936	Human PKR substrate
c2646	13.8	1.4	17	1	AD149964	Human PKR substrate
c2647	13.8	1.4	17	1	AD150729	Human PKR substrate
c2648	13.8	1.4	17	1	AD149414	Human PKR substrate
c2649	13.8	1.4	17	1	AD149973	Human PKR substrate
c2650	13.8	1.4	17	1	AD149413	Human PKR substrate
c2651	13.8	1.4	17	1	AD149432	Human PKR substrate
c2652	13.8	1.4	17	1	AD149961	Human PKR substrate
c2653	13.8	1.4	17	1	AD149357	Human PKR substrate
c2654	13.8	1.4	17	1	AD149412	Human PKR substrate
c2655	13.8	1.4	17	1	AD150206	Human PKR substrate
c2656	13.8	1.4	17	1	AD149420	Human PKR substrate
c2657	13.8	1.4	17	1	AD150426	Human PKR substrate
c2658	13.8	1.4	17	1	AD150428	Human PKR substrate
c2659	13.8	1.4	17	1	AD148427	Human PKR substrate
c2660	13.8	1.4	17	1	AD149962	Human PKR substrate
c2661	13.8	1.4	17	1	AD149976	Human PKR substrate

2662	13.8	1.4	17	1	AD150754	Human PKR substrate
2663	13.8	1.4	17	1	AD148820	Human IKK-gamma subunit
2664	13.8	1.4	17	1	AD149422	Human PKR substrate
2665	13.8	1.4	17	1	AD149451	Human PKR substrate
2666	13.8	1.4	17	1	AD150414	Human PKR substrate
2667	13.8	1.4	17	1	AD150736	Human PKR substrate
2668	13.8	1.4	17	1	AD150756	Human PKR substrate
2669	13.8	1.4	17	1	AD149922	Human PKR substrate
2670	13.8	1.4	17	1	AD150191	Human PKR substrate
2671	13.8	1.4	17	1	AD149403	Human PKR substrate
2672	13.8	1.4	17	1	AD149924	Human PKR substrate
2673	13.8	1.4	17	1	AD149945	Human PKR substrate
2674	13.8	1.4	17	1	AD150209	Human PKR substrate
2675	13.8	1.4	17	1	AD150222	Human PKR substrate
2676	13.8	1.4	17	1	AD150755	Human PKR substrate
2677	13.8	1.4	17	1	AD149438	Human PKR substrate
2678	13.8	1.4	17	1	AD149458	Human PKR substrate
2679	13.8	1.4	17	1	AD149462	Human PKR substrate
2680	13.8	1.4	17	1	AD150744	Human GRID mRNA subunit
2681	13.8	1.4	17	1	AD154093	Human purine-rich RNA subunit
2682	13.8	1.4	17	1	AD136228	Human Vbeta gene 1
2683	13.8	1.4	17	1	AD170367	Human Vbeta gene 1
2684	13.8	1.4	17	1	AD170550	Nucleotide sequence
2685	13.8	1.4	17	1	AD134488	Mutant human BRCA1
2686	13.8	1.4	17	1	AD132545	Human glioma endocytosis
2687	13.8	1.4	17	1	AD131775	Human glioma endocytosis
2688	13.8	1.4	17	1	AD134421	Human glioma endocytosis
2689	13.8	1.4	17	1	AD133251	Human glioma endocytosis
2690	13.8	1.4	17	1	AD182346	Human BRCA1 breast cancer
2691	13.8	1.4	17	1	AD182346	PCR primer 34 used
2692	13.8	1.4	17	1	AD182346	PCR primer 34 used
2693	13.8	1.4	17	1	AD182346	PCR primer 34 used
2694	13.8	1.4	17	1	AD182346	PCR primer 34 used
2695	13.8	1.4	17	1	AD182346	PCR primer 34 used
2696	13.8	1.4	17	1	AD182346	PCR primer 34 used
2697	13.8	1.4	17	1	AD182346	PCR primer 34 used
2698	13.8	1.4	17	1	AD182346	PCR primer 34 used
2699	13.8	1.4	17	1	AD182346	PCR primer 34 used
2700	13.8	1.4	17	1	AD182346	PCR primer 34 used
2701	13.8	1.4	17	1	AD182346	PCR primer 34 used
2702	13.8	1.4	17	1	AD182346	PCR primer 34 used
2703	13.8	1.4	17	1	AD182346	PCR primer 34 used
2704	13.8	1.4	17	1	AD182346	PCR primer 34 used
2705	13.6	1.4	15	1	AAK30951	Tag sequence of a
c2706	13.6	1.4	15	1	ABK31904	Human colon cancer
c2707	13.6	1.4	15	1	ABK31767	Human CHRM5 gene p

## ALIGNMENTS

RESULT 1  
ID ACC84455 standard; DNA; 57 BP.  
XX  
AC ACC84455;  
XX  
XX 28-AUG-2003 (first entry)  
DT  
XX  
DE NTP peptide encoding sequence #2.  
XX  
XX Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;  
KW neutral thread protein; NTP; tumour; ds.  
XX  
XX Unidentified.  
OS  
XX  
XX WO200308443-A2.  
XX  
XX 30-JAN-2003.  
XX  
XX 19-JUL-2002; 2002WO-CA001105.  
XX  
XX 19-JUL-2001; 2001US-0306150P.  
XX  
XX

PR 19-JUL-2001; 2001US-0306161P.  
PR 16-NOV-2001; 2001US-0331477P.  
XX  
PA (NYMO-) NYMOX CORP.  
XX  
PI Averbach PA;  
XX  
DR WPI; 2003-247999/24.  
DR P-PSDB; ABR63250.  
XX  
PT Novel neural thread protein peptide, referred as cell death peptide,  
PT useful for treating prostatic hyperplasia, psoriasis, eczema, dermatosis,  
PT atherosclerosis, cosmetic modification to skin, throat, mouth, muscle.  
PS Disclosure; Page 16; 77pp; English.  
XX  
XX The present invention relates to a neural thread protein (NTP) peptide  
CC referred to as cell death peptide. Thought to be cytostatic,  
CC antibacterial, immunosuppressive and antiinflammatory. It is useful for  
CC treating a condition in a patient requiring removal or destruction of  
CC cells, for treating a condition such as benign or malignant tumor,  
CC inflammatory disease, autoimmune disease and infectious disease. The  
CC peptide useful for treatment is derived from the amino acid sequence for  
CC a pancreatic thread protein. The peptide is conjugated, linked or bound  
CC to a molecule chosen from antibody or its fragment, antibody-like binding  
CC molecule, where the molecule has a higher affinity for binding to a tumor  
CC or other target than binding to other cells. Treatment using NTP peptides  
CC can remove benign tumors with less risk and fewer of the undesirable side  
CC effects of surgery. The present sequence is an NTP encoding sequence  
XX  
SQ Sequence 57 BP; 12 A; 20 C; 14 G; 11 T; 0 U; 0 Other;  
Query Match 5.8%; Score 57; DB 1; Length 57;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 354 CCTGAGCTCAAGCAGCTCCTGCTCAGCCTCCCAAGTGTGGATTACAGGCGT 410  
DB 1 CCTGAGCTCAAGCAGCTCCTGCTCAGCCTCCCAAGTGTGGATTACAGGCGT 57  
RESULT 2  
ACC84456  
ID ACC84456 standard; DNA; 57 BP.  
XX  
AC ACC84456;  
XX  
DT 28-AUG-2003 (first entry)  
XX  
DE NTP peptide encoding sequence #3.  
XX  
KM Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;  
KM neural thread protein; NTP; tumor; ds.  
XX  
OS Unidentified.  
XX  
PN WO2003008443-A2.  
XX  
PD 30-JAN-2003.  
XX  
PF 19-JUL-2002; 2002WO-CA001105.  
XX  
PR 19-JUL-2001; 2001US-0306150P.  
PR 19-JUL-2001; 2001US-0306161P.  
PR 16-NOV-2001; 2001US-0331477P.  
XX  
PA (NYMO-) NYMOX CORP.  
XX  
PI Averbach PA;  
XX  
DR WPI; 2003-247999/24.  
DR P-PSDB; ABR63251.  
XX

PT Novel neural thread protein peptide, referred as cell death peptide,  
PT useful for treating prostatic hyperplasia, psoriasis, eczema, dermatosis,  
PT atherosclerosis, cosmetic modification to skin, throat, mouth, muscle.  
PS Disclosure; Page 16; 77pp; English.  
XX  
XX The present invention relates to a neural thread protein (NTP) peptide  
CC referred to as cell death peptide. Thought to be cytostatic,  
CC antibacterial, immunosuppressive and antiinflammatory. It is useful for  
CC treating a condition in a patient requiring removal or destruction of  
CC cells, for treating a condition such as benign or malignant tumor,  
CC inflammatory disease, autoimmune disease and infectious disease. The  
CC peptide useful for treatment is derived from the amino acid sequence for  
CC a pancreatic thread protein. The peptide is conjugated, linked or bound  
CC to a molecule chosen from antibody or its fragment, antibody-like binding  
CC molecule, where the molecule has a higher affinity for binding to a tumor  
CC or other target than binding to other cells. Treatment using NTP peptides  
CC can remove benign tumors with less risk and fewer of the undesirable side  
CC effects of surgery. The present sequence is an NTP encoding sequence  
XX  
SQ Sequence 57 BP; 9 A; 21 C; 15 G; 12 T; 0 U; 0 Other;  
Query Match 5.8%; Score 57; DB 1; Length 57;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 990 CCTCCGGGCTCAAGCAGCTTCTCCTGCTCAGCCTCCCAAGTGTGGATTACGGG 1046  
DB 1 CCTCCGGGCTCAAGCAGCTTCTCCTGCTCAGCCTCCCAAGTGTGGATTACGGG 57  
RESULT 3  
AAK91064  
ID AAK91064 standard; DNA; 66 BP.  
XX  
AC AAK91064;  
XX  
DT 05-NOV-2001 (first entry)  
XX  
DE Human digestive system antigen genomic sequence SHQ ID NO: 4640.  
XX  
KM Human; digestive system antigen; gene therapy; cancer; appendicitis;  
KM ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;  
KM digestive system disorder; Meckel's diverticulum; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200155314-A2.  
XX  
PD 02-AUG-2001.  
XX  
PF 17-JAN-2001; 2001WO-US001324.  
XX  
PR 31-JAN-2000; 2000US-0179065P.  
PR 04-FEB-2000; 2000US-0180628P.  
PR 24-FEB-2000; 2000US-0184664P.  
PR 02-MAR-2000; 2000US-0186350P.  
PR 16-MAR-2000; 2000US-0189874P.  
PR 17-MAR-2000; 2000US-0190076P.  
PR 18-APR-2000; 2000US-0198123P.  
PR 19-MAY-2000; 2000US-0205515P.  
PR 07-JUN-2000; 2000US-0209467P.  
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PR 14-AUG-2000; 2000US-0226279P.  
PR 22-AUG-2000; 2000US-0226681P.  
PR 22-AUG-2000; 2000US-0226688P.  
PR 22-AUG-2000; 2000US-0227182P.  
PR 23-AUG-2000; 2000US-0227009P.  
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PR 01-SEP-2000; 2000US-0229287P.  
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PR 01-SEP-2000; 2000US-0229344P.  
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PR 05-SEP-2000; 2000US-0229509P.  
PR 05-SEP-2000; 2000US-0229513P.  
PR 06-SEP-2000; 2000US-0230437P.  
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PR 08-SEP-2000; 2000US-0231243P.  
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PR 08-SEP-2000; 2000US-0232080P.  
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PR 14-SEP-2000; 2000US-0233065P.  
PR 21-SEP-2000; 2000US-0234223P.  
PR 21-SEP-2000; 2000US-0234274P.  
PR 25-SEP-2000; 2000US-0234997P.  
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PR 20-OCT-2000; 2000US-0241221P.  
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PR 08-NOV-2000; 2000US-0246478P.

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PR 08-NOV-2000; 2000US-0246609P.  
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PR 17-NOV-2000; 2000US-0249297P.  
PR 17-NOV-2000; 2000US-0249299P.  
PR 17-NOV-2000; 2000US-0249300P.  
PR 01-DEC-2000; 2000US-0250160P.  
PR 01-DEC-2000; 2000US-0250391P.  
PR 05-DEC-2000; 2000US-0251030P.  
PR 05-DEC-2000; 2000US-0251988P.  
PR 05-DEC-2000; 2000US-0251989P.  
PR 06-DEC-2000; 2000US-0251479P.  
PR 08-DEC-2000; 2000US-0251566P.  
PR 08-DEC-2000; 2000US-0251568P.  
PR 08-DEC-2000; 2000US-0251569P.  
PR 08-DEC-2000; 2000US-0251899P.  
PR 08-DEC-2000; 2000US-0251900P.  
PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.  
  
(HUMA-) HUMAN GENOME SCI INC.  
XX PI Rosen CA, Barash SC, Ruben SM;  
XX WPI; 2001-502630/55.  
XX  
XX Polynucleotides encoding digestive system antigens, useful for  
PT diagnosing, treating, preventing and/or prognosing disorders of the  
PT digestive system, particularly cancer and cancer metastases.  
XX  
XX  
XX Disclosure; SEQ ID NO 4640; 986pp; English.  
PS  
XX  
XX The present invention provides the protein and coding sequences of a  
CC number of human digestive system antigens. These can be used in the  
CC diagnosis, treatment and prevention of digestive system disorders,  
CC including cancer, Meckel's diverticulum, bacterial or parasitic  
CC infections, appendicitis, Hirschsprung's disease, chronic colitis or  
CC ulcerative colitis. The present sequence is a genomic DNA fragment  
CC encoding a digestive system antigen of the invention  
XX  
SQ Sequence 66 BP; 14 A; 14 C; 14 G; 24 T; 0 U; 0 Other;  
  
Query Match 5.7%; Score 56.4; DB 1; Length 66;  
Best Local Similarity 90.9%; Pred. No. 44;  
Matches 60; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
  
Qy 1070 TTTTGTATTTTCATTAGAGCGGGTTTCACCATATTTGTCAGGTGTCCTCAAACTCC 1129  
Db 1 TTTTGTATTTTATGATAGACGGGTTTCACCATATTTGTCAGGTGTCCTCAAACTCC 60

Oy 1130 TGACCT 1135  
Db 61 TGACCT 66

RESULT 4  
AAS32099  
ID AAS32099 standard; DNA; 66 BP.  
XX AAS32099;  
DT 04-DEC-2001 (first entry)  
XX

Human liver associated genomic DNA #273.  
XX  
XX Liver associated protein; human; mouse; rabbit; goat; horse; cat; dog;  
KW chicken; sheep; immunosuppressive; antitachytic; vasotropic;  
KW antirheumatic; antiproliferative; cytosstatic; cardiant; neuroprotective;  
KW cerebroprotective; nootropic; antibacterial; virucide; fungicide; cancer;  
KW ophthalmological; vlnetary; gene therapy; autoimmune disease; neoplasm;  
KW hyperproliferative disorder; breast; liver; cardiovascular disorder; ds;  
KW cerebrovascular disorder; nervous system disorder; bacterial infection;  
KW fungal infection; viral infection; ocular disorder; endocrine disorder;  
KW gastrointestinal disorder; renal disorder; respiratory disorder;  
KW wound healing; skin aging; organ transplantation; tissue regeneration;  
anti-inferility.  
XX  
OS Homo sapiens.  
XX  
XX WO20015355-A1.  
XX  
XX 02-AUG-2001.  
PD  
PF 17-JAN-2001; 2001WO-US001351.  
XX  
XX 31-JAN-2000; 2000US-0179065P.  
PR 04-FEB-2000; 2000US-0180662B.  
PR 24-FEB-2000; 2000US-0184664P.  
PR 02-MAR-2000; 2000US-0186350P.  
PR 16-MAR-2000; 2000US-0189874P.  
PR 17-MAR-2000; 2000US-0190076P.  
PR 18-APR-2000; 2000US-0198123P.  
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PR 28-JUN-2000; 2000US-0214886P.  
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PR 01-SEP-2000; 2000US-0229287P.

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PR 01-NOV-2000; 2000US-0244617P.  
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 PR 05-JAN-2001; 2001US-0259678P.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX Rosen CA, Barash SC, Ruben SM;  
 PI  
 XX WPI; 2001-457728/49.  
 XX  
 PT Isolated nucleic acid molecule encoding a human liver related protein is  
 PT used in preventing, treating or ameliorating disorders of the liver  
 PT particularly cancer of the liver.  
 XX  
 PS Claim 1; SEQ ID NO 575; 526bp; English.

XX  
 CC Sequences AAS31827-AAS32182 represent genomic DNA molecules, which encode  
 CC the liver associated polypeptides of the invention. Liver associated  
 CC polypeptides and their associated polynucleotides are useful in the  
 CC diagnosis, treatment and prevention of various types of disorders in e.g.  
 CC humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A  
 CC pathological condition can be determined by detecting the presence or  
 CC absence of a mutation in a liver associated polynucleotide. The treatable  
 CC disorders include autoimmune diseases such as rheumatoid arthritis,  
 CC hyperproliferative disorders such as neoplasms of the breast or liver,  
 CC cardiovascular disorders such as cardiac arrest, cerebrovascular  
 CC disorders such as cerebral ischaemia, nervous system disorders such as  
 CC Alzheimer's disease, infections caused by bacteria, viruses and fungi,  
 CC ocular disorders such as corneal infection, endocrine disorders such as  
 CC premature labour and infertility, gastrointestinal disorders such as  
 CC Crohn's disease, renal disorders such as glomerulonephritis and  
 CC respiratory disorders such as asthma and pleurisy. The polypeptides can  
 CC also be used to aid wound healing, to prevent skin aging due to sunburn,  
 CC to maintain organs before transplantation, to regenerate tissues and in  
 CC chemotaxis. Note: The sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SO Sequence 66 BP; 14 A; 14 C; 14 G; 24 T; 0 U; 0 Other;

Query Match 5.7%; Score 56.4; DB 1; Length 66;  
 Best Local Similarity 90.9%; Pred. No. 44;  
 Matches 60; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1070 TTTTGTATTTTCATTAGAGCGGGGTTTACCATATTTGTGAGCTGGTCTCAACTCC 1129  
 DB 1 TTTTGTATTTTGTAGAGCGGGGTTTACCATATTTGTGAGCTGGTCTCAACTCC 60  
 QY 1130 TGACCT 1135  
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DB 61.TGACCT 66  
 RESULT 5  
 ABR90454  
 ID ABR90454 strand; DNA; 66 BP.  
 AC ABR90454;  
 XX  
 XX 24-JUL-2002 (first entry)  
 XX  
 DE Human liver antigen HLDV38 genomic sequence, SEQ ID NO:575.  
 XX  
 XX Human; liver antigen; liver disorder; hepatic disorder; infection;  
 XX hepatitis; viral; parasitic; bacterial; fungal; inflammatory condition;  
 XX cirrhosis; granulomatous hepatitis; toxin damage; drug damage;  
 XX autoimmune disease; Wilson's disease; primary biliary cirrhosis;  
 XX neoplastic disorder; cancer; tumour; portal hypertension;  
 XX gastrointestinal disorder; hepatitis; drug screening; gene therapy;  
 XX chromosome mapping; forensic analysis; antibody preparation;  
 XX hepatotropic; cytostatic; antiinflammatory; vitucide; antibacterial;  
 XX fungicide; parasiticicide; antidote; immunosuppressive; gene; ds.  
 OS Homo sapiens.  
 XX  
 XX US2002042096-A1.  
 XX  
 XX 11-APR-2002.  
 XX  
 PF 17-JAN-2001; 2001US-00764887.  
 XX  
 XX 31-JAN-2000; 2000US-0179065P.  
 XX 04-FEB-2000; 2000US-0180628P.  
 XX 28-JUN-2000; 2000US-0214886P.  
 XX 07-JUL-2000; 2000US-0216647P.  
 XX 11-JUL-2000; 2000US-0217487P.  
 XX 11-JUL-2000; 2000US-0217496P.  
 XX 14-JUL-2000; 2000US-0218290P.  
 XX 26-JUL-2000; 2000US-0220963P.  
 XX 14-AUG-2000; 2000US-0224518P.  
 XX 14-AUG-2000; 2000US-0224519P.  
 XX 14-AUG-2000; 2000US-0225267P.  
 XX 14-AUG-2000; 2000US-0225268P.  
 XX 14-AUG-2000; 2000US-0225270P.  
 XX 14-AUG-2000; 2000US-0225447P.  
 XX 14-AUG-2000; 2000US-0225757P.  
 XX 14-AUG-2000; 2000US-0225758P.  
 XX 22-AUG-2000; 2000US-0226868P.  
 XX 30-AUG-2000; 2000US-0228924P.  
 XX 01-SEP-2000; 2000US-0229287P.  
 XX 01-SEP-2000; 2000US-0229343P.  
 XX 01-SEP-2000; 2000US-0229344P.  
 XX 01-SEP-2000; 2000US-0229345P.  
 XX 05-SEP-2000; 2000US-0229509P.  
 XX 08-SEP-2000; 2000US-0229513P.  
 XX 21-SEP-2000; 2000US-0231423P.  
 XX 21-SEP-2000; 2000US-0234374P.  
 XX 21-SEP-2000; 2000US-0234377P.  
 XX 25-SEP-2000; 2000US-0234597P.  
 XX 27-SEP-2000; 2000US-0235834P.  
 XX 29-SEP-2000; 2000US-0236327P.  
 XX 29-SEP-2000; 2000US-0236367P.  
 XX 29-SEP-2000; 2000US-0236368P.  
 XX 29-SEP-2000; 2000US-0236369P.  
 XX 29-SEP-2000; 2000US-0236370P.  
 XX 02-OCT-2000; 2000US-0236802P.  
 XX 02-OCT-2000; 2000US-0237037P.  
 XX 02-OCT-2000; 2000US-0237038P.  
 XX 02-OCT-2000; 2000US-0237039P.  
 XX 02-OCT-2000; 2000US-0237040P.  
 XX 13-OCT-2000; 2000US-0239935P.

PR 20-OCT-2000; 2000US-0240960P.  
PR 20-OCT-2000; 2000US-0241785P.  
PR 20-OCT-2000; 2000US-0241809P.  
PR 01-NOV-2000; 2000US-0244617P.  
PR 17-NOV-2000; 2000US-0249299P.  
PR 08-DEC-2000; 2000US-0251856P.  
PR 08-DEC-2000; 2000US-0251856P.  
PR 08-DEC-2000; 2000US-0251869P.  
XX (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
XX  
PI Rosen CA, Ruben SM, Barash SC;  
DR WPI; 2002-381944/41.  
XX  
PT New nucleic acid encoding human liver antigens, useful for diagnosis,  
PT treatment and prevention of e.g. hepatitis and hepatic cancer, also  
PT related polypeptides and antibodies.  
XX  
PS Disclosure; SEQ ID NO 575; 181bp; English.  
XX  
CC The invention relates to 145 novel human liver antigens (ABP40831-  
CC ABP40975) and to cDNAs encoding them (ABN90036-ABN90180), and also  
CC encompasses polypeptides 90% identical and polynucleotides 95% identical  
CC to the sequences of the invention. The invention additionally relates to  
CC recombinant vectors and host cells comprising human liver antigen  
CC polynucleotides, antibodies against human liver antigens, and the use of  
CC liver antigen polynucleotides and polypeptides in diagnosing, treating,  
CC prognosing or preventing various disorders of the liver. Such conditions  
CC include viral infections (e.g., cytomegalovirus, Epstein-Barr virus,  
CC hepatitis A virus, hepatitis B virus and hepatitis C virus), parasitic  
CC infections (e.g., *Clonorchis sinensis*, *Echinococcus granulosus* and  
CC *Entamoeba histolytica*), and also bacterial and fungal infections. Other  
CC disorders that may be treated include inflammatory conditions (e.g.,  
CC cirrhosis and granulomatous hepatitis), damage caused by drugs or toxins,  
CC autoimmune diseases (e.g., Wilson's disease, primary biliary cirrhosis),  
CC neoplastic disorders (e.g., adenomas, haemangiomas and hepatocellular  
CC carcinoma), portal hypertension, or gastrointestinal disorders (e.g.,  
CC peptic ulcers, gastritis and peritoneal diseases). Liver antigen  
CC polypeptides and polynucleotides may also be used in screening for  
CC compounds which modulate liver antigen expression or activity. The  
CC polynucleotides may further be used for gene therapy, chromosome mapping,  
CC in the identification of individuals and in forensic analysis, and the  
CC polypeptides may be used as molecular weight markers or to prepare  
CC antibodies useful in disease diagnosis, drug targeting and phenotyping.  
CC Sequences ABN90182-ABN90537 represent human liver antigen genomic  
CC sequences. Note: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from the USPTO at seqdata.uspto.gov/sequence/  
XX  
SQ Sequence 66 BP; 14 A; 14 C; 14 G; 24 T; 0 U; 0 Other;  
Query Match 5.7%; Score 56.4; DB 1; Length 66;  
Best Local Similarity 90.9%; Pred. NO. 44;  
Matches 60; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1070 TTTTGTATTTTCATTAGAGGGGGGTTTACCATATTTTCAGGCTGCTCAACTCC 1129  
DB 1 TTTTGTATTTTACTAGAGAGGGGTTTTCACATATTTGACAGCGCTGCTCAACTCC 60  
QY 1130 TGACCT 1135  
DB 61 TGACCT 66  
RESULT 6  
ADJ15367 standard; DNA; 66 BP.  
XX  
AC ADJ15367;  
XX

DT 20-MAY-2004 (first entry)  
XX  
DE Human liver-related genomic DNA - SEQ ID 575.  
XX  
KW liver; vitruclide; fungicide; antibacterial; antiparasitic; hepatotropic;  
KW antiinflammatory; cytostatic; litholytic; antirheumatic; antidiabetic;  
KW neuroprotective; antidiabetic; anticoagulant; thrombolytic;  
KW antiarteriosclerotic; cardiant; haemostatic; antiarrhythmic;  
KW ophthalmological; antiarteriosclerotic; vasotropic; osteopathic;  
KW nootropic; antiparkinsonian; anticonvulsant; neuroleptic; vasotropic;  
KW cyrostatic; gynaecological; viral; fungal; bacterial;  
KW parasitic infection; cirrhosis; Wilson's disease;  
KW gastrointestinal disorder; pancreatic; gallbladder; immune; blood;  
KW hyperproliferative; cardiovascular; respiratory; musculoskeletal system;  
KW neurological; endocrine; reproductive system; developmental; inherited;  
KW human; de.  
XX  
OS Homo sapiens.  
XX  
PN US2003077602-A1.  
XX  
PD 24-APR-2003.  
XX  
PF 14-FEB-2002; 2002US-00073961.  
XX  
PR 31-JAN-2000; 2000US-0179065P.  
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PR 24-FEB-2000; 2000US-0184664P.  
PR 02-MAR-2000; 2000US-0186350P.  
PR 16-MAR-2000; 2000US-0189874P.  
PR 17-MAR-2000; 2000US-0190076P.  
PR 18-APR-2000; 2000US-0198123P.  
PR 19-MAY-2000; 2000US-0205515P.  
PR 07-JUN-2000; 2000US-0209467P.  
PR 28-JUN-2000; 2000US-0214886P.  
PR 30-JUN-2000; 2000US-0215153P.  
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PR 11-JUL-2000; 2000US-0216880P.  
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PR 14-JUL-2000; 2000US-0218290P.  
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PR 06-SEP-2000; 2000US-0230438P.  
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PR 29-SEP-2000; 2000US-0236369P.  
PR 29-SEP-2000; 2000US-0236370P.  
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PR 02-OCT-2000; 2000US-0237037P.  
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PR 20-OCT-2000; 2000US-0241786P.  
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PR 20-OCT-2000; 2000US-0241809P.  
PR 20-OCT-2000; 2000US-0241826P.  
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PR 08-NOV-2000; 2000US-0246474P.  
PR 08-NOV-2000; 2000US-0246475P.  
PR 08-NOV-2000; 2000US-0246476P.  
PR 08-NOV-2000; 2000US-0246477P.  
PR 08-NOV-2000; 2000US-0246478P.  
PR 08-NOV-2000; 2000US-0246523P.  
PR 08-NOV-2000; 2000US-0246524P.  
PR 08-NOV-2000; 2000US-0246525P.  
PR 08-NOV-2000; 2000US-0246526P.  
PR 08-NOV-2000; 2000US-0246527P.  
PR 08-NOV-2000; 2000US-0246528P.  
PR 08-NOV-2000; 2000US-0246532P.  
PR 08-NOV-2000; 2000US-0246609P.  
PR 08-NOV-2000; 2000US-0246610P.  
PR 08-NOV-2000; 2000US-0246611P.  
PR 08-NOV-2000; 2000US-0246613P.  
PR 17-NOV-2000; 2000US-0249207P.  
PR 17-NOV-2000; 2000US-0249208P.  
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PR 17-NOV-2000; 2000US-0249215P.  
PR 17-NOV-2000; 2000US-0249216P.  
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PR 17-NOV-2000; 2000US-0249257P.

PR 17-NOV-2000; 2000US-0249299P.  
PR 17-NOV-2000; 2000US-0249300P.  
PR 01-DEC-2000; 2000US-0250160P.  
PR 01-DEC-2000; 2000US-0250391P.  
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PR 05-DEC-2000; 2000US-0251988P.  
PR 05-DEC-2000; 2000US-0256719P.  
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PR 08-DEC-2000; 2000US-0251856P.  
PR 08-DEC-2000; 2000US-0251868P.  
PR 08-DEC-2000; 2000US-0251869P.  
PR 08-DEC-2000; 2000US-0251989P.  
PR 08-DEC-2000; 2000US-0251990P.  
PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.  
PR 17-JAN-2001; 2001US-00764887.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Ruben SM, Barash SC;  
PI  
DR WPI; 2003-765398/72.  
XX  
XX New liver related polypeptide, useful for diagnosis, treatment and/or  
PT prevention of liver, gastrointestinal, pancreatic, immune, blood related,  
PT endocrine, reproductive, hyperproliferative or reproductive disorders.  
XX  
XX Disclosure; SEQ ID NO 575; 181pp; English.  
XX  
XX The invention relates to a novel isolated, liver related polypeptide. The  
CC polypeptide of the invention demonstrates virucide, fungicide,  
CC antibacterial, antiparasitic, hepatotropic, antiinflammatory, cytosolic,  
CC litholytic, antineumatic, antiautistic, neuroprotective, antidiabetic,  
CC anticoagulant, thrombolytic, antiatherosclerotic, cardiac, haemostatic,  
CC antiarrhythmic, ophthalmological, antiaeriosclerotic, vasotropic,  
CC osteopathic, nootropic, antiparkinsonian, anticonvulsant, neuroleptic,  
CC vasotropic, cytosolic and gynaecological activities. The polypeptides  
CC and polynucleotides of the invention may be useful for diagnosis  
CC detection, treatment and/or prevention of disorders of the liver such as  
CC viral, fungal, bacterial or parasitic infections, cirrhosis, Wilson's  
CC disease, gastrointestinal disorders, pancreatic disorders, gallbladder  
CC diseases, immune disorders, blood related disorders, hyperproliferative  
CC disorders, cardiovascular disorders, neurological diseases, endocrine  
CC musculoskeletal system disorders, neurological diseases, endocrine  
CC disorders, reproductive system disorders or developmental and inherited  
CC disorders. The current sequence is that of the human liver-related  
CC genomic DNA of the invention. The current sequence is not shown within  
CC the specification per se but was obtained electronically from the USPTO  
CC web-site.  
XX  
XX  
Query Match 5.7%; Score 56.4; DB 1; Length 66;  
Best Local Similarity 90.9%; Pred. No. 44;  
Matches 60; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1070 TTTTGTATTTTCATTAGAGCGGGTTTCACCATTTTGTACGGCTGCTTAACCTCC 1129  
DB 1 TTTTGTATTTTAGTAGAGACCGGGTTTCACCATTTAGACAGCGCTGCTTAACCTCC 60  
QY 1130 TGACCT 1135  
DB 61 TGACCT 66  
RESULT 7  
ADI20573 standard; DNA; 60 BP.  
XX  
XX ADI20573;  
AC  
XX  
DT 15-APR-2004 (first entry)  
XX  
DE Oligonucleotide sequence enquiry #60.

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XX human; ds; eRNA.
KW
XX Homo sapiens.
OS
XX WO2003025229-A1.
PN
XX
XX 27-MAR-2003.
PD
XX
XX 19-SEP-2002; 2002WO-AU001286.
PE
XX
XX 19-SEP-2001; 2001US-0324127P.
PR
XX
XX (UYQU ) UNIV QUEENSLAND.
PA
XX
XX Mattick J, Gagen M, Stanley S;
PI
XX WPI; 2003-371830/35.
DR
XX
XX Identifying an eRNA or a DNA sequence comprising an eRNA-encoding
PT sequence in the nucleome of a eukaryotic cell, comprising identifying non
PT protein-encoding nucleotide sequences within an mRNA transcript or a DNA
PT sequence.
XX
XX Example 12; SEQ ID NO 63; 137bp; English.
XX
XX The present invention relates to identifying an eRNA or a DNA sequence
XX comprising an eRNA-encoding sequence in the nucleome of a eukaryotic cell
XX comprising identifying non-protein-encoding nucleotide sequences within an
XX mRNA transcript or a DNA sequence encoding same in the nucleome. The
XX methods are useful for identifying an eRNA or DNA for modifying a genetic
XX network in cell to alter the cells phenotype. The present sequence
XX represents human oligonucleotide sequence enquiry.
XX
XX Sequence 60 BP; 8 A; 22 C; 16 G; 14 T; 0 U; 0 Other;
SQ
XX
XX Query Match 5.6%; Score 55.2; DB 1; Length 60;
XX Best Local Similarity 95.0%; Pred. No. 47;
XX Matches 57; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 635 CTCTGTACCCAGGCTGAGTGCAGTGGCGCAATCTTGCTACTGCAACCTCTGCTCC 694
DB 1 CTCTGTACCCAGGCTGAGTGCAGTGGCGCAATCTTGCTACTGCAACCTCTGCTCC 60
XX
XX RESULT 8
XX ADI12552/c
XX ID ADI12552 standard; DNA; 66 BP.
XX
XX AC ADI12552;
XX
XX DT 22-APR-2004 (first entry)
XX
XX DE Mutant human BRCA1 genomic DNA resulting from deletion 5 Segid 35.
XX
XX KW ds; cancer; human; tumour suppressor;
XX breast cancer susceptibility gene 1; BRCA1; repetitive Alu;
XX ovarian cancer; recombination; mutant.
XX
XX OS Homo sapiens.
XX
XX PN WO2003104474-A2.
XX
XX PD 18-DEC-2003.
XX
XX PF 09-JUN-2003; 2003WO-US018098.
XX
XX PR 07-JUN-2002; 2002US-0387132P.
XX
XX PR 09-AUG-2002; 2002US-0402430P.
XX
XX PA (MYRI-) MYRIAD GENETICS INC.
XX
XX PI Scholl T, Hendrickson BC, Ward B, Pruss D;

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XX WPI; 2004-062369/06.
DR
XX
XX Predicting a predisposition to cancer in a patient comprising detecting a
PT deletion in the BRCA1 gene that results from the unequal crossover
PT between a pair of repetitive sequences in the BRCA1 gene.
XX
XX Disclosure; SEQ ID NO 35; 59bp; English.
XX
XX This invention relates to a novel method for predicting a predisposition
XX to cancer in a patient by detecting large deletions in the human tumour
XX suppressor gene identified as the breast cancer susceptibility gene 1
XX (BRCA1). Specifically, it refers to deletions that result from the
XX unequal crossover between a pair of repetitive Alu sequences in the BRCA1
XX gene, such that the recombined nucleotide sequence containing the
XX deletion indicates a predisposition to breast and ovarian cancer. The
XX present invention describes newly discovered deletion mutations that are
XX believed to be deleterious and cause significant alterations in the
XX structure or biochemical function of BRCA1. Accordingly, it provides
XX methods for detecting such mutants, as well as identifying and screening
XX for cytostatic compounds useful for treating or preventing cancers
XX associated with a BRCA1 genetic variant. This polynucleotide is a mutant
XX human BRCA1 genomic DNA fragment that arises as a result of a
XX recombination event (deletion 5), which causes the omission of exons 15
XX and 16, given in an exemplification of the invention.
XX
XX Sequence 66 BP; 15 A; 16 C; 24 G; 11 T; 0 U; 0 Other;
SQ
XX
XX Query Match 5.5%; Score 54.4; DB 1; Length 66;
XX Best Local Similarity 90.6%; Pred. No. 55;
XX Matches 58; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
XX
QY 687 CTGCTCCCGGAGTCAAGTATTCCTCCGCCCCAGCCTCTGAGTAGCTGGAGTACAGG 746
DB 66 CCGCTCCCGGAGTCAAGCAATTCCTGCTCAGCTCTGAGTAGCTGGAGTACAGG 7
XX
XX 747 CGCC 750
XX
XX DB 6 CACC 3
XX
XX RESULT 9
XX ADI12619/c
XX ID ADI12619 standard; DNA; 66 BP.
XX
XX AC ADI12619;
XX
XX DT 22-APR-2004 (first entry)
XX
XX DE Human BRCA1 DNA upstream from the deletion 5 recombination event.
XX
XX KW ds; cancer; human; tumour suppressor;
XX breast cancer susceptibility gene 1; BRCA1; repetitive Alu;
XX ovarian cancer; recombination.
XX
XX OS Homo sapiens.
XX
XX PN WO2003104474-A2.
XX
XX PD 18-DEC-2003.
XX
XX PF 09-JUN-2003; 2003WO-US018098.
XX
XX PR 07-JUN-2002; 2002US-0387132P.
XX
XX PR 09-AUG-2002; 2002US-0402430P.
XX
XX PA (MYRI-) MYRIAD GENETICS INC.
XX
XX PI Scholl T, Hendrickson BC, Ward B, Pruss D;
XX
XX WPI; 2004-062369/06.
XX
XX Predicting a predisposition to cancer in a patient comprising detecting a

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PT deletion in the BRCA1 gene that results from the unequal crossover  
PT between a pair of repetitive sequences in the BRCA1 gene.  
PS Disclosure; Fig 5, 59pp; English.  
XX This invention relates to a novel method for predicting a predisposition  
CC to cancer in a patient by detecting large deletions in the human tumour  
CC suppressor gene identified as the breast cancer susceptibility gene 1  
CC (BRCA1). Specifically, it refers to deletions that result from the  
CC unequal crossover between a pair of repetitive Alu sequences in the BRCA1  
CC gene, such that the recombined nucleotide sequence containing the  
CC deletion indicates a predisposition to breast and ovarian cancer. The  
CC present invention describes newly discovered deletion mutations that are  
CC believed to be deleterious and cause significant alterations in the  
CC structure or biochemical function of BRCA1. Accordingly, it provides  
CC methods for detecting such mutants, as well as identifying and screening  
CC for cytostatic compounds useful for treating or preventing cancers  
CC associated with a BRCA1 genetic variant. This polynucleotide is a human  
CC BRCA1 DNA fragment representing the region downstream of the deletion 5  
CC recombination event that causes the omission of exons 15 and 16, given in  
CC an exemplification of the invention.  
XX  
SQ Sequence 66 BP, 16 A; 15 C; 23 G; 12 T; 0 U; 0 Other;  
Query Match 5.5%; Score 54.4; DB 1; Length 66;  
Best Local Similarity 90.6%; Pred. No. 55;  
Matches 58; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 687 CTGCTCCCGGGTTCAGTATTTCTCTGCCCCAGGCTCTGTAGTACGGACTACAG 746  
DB 66 CTGCTCCCGAGTTCAAGCAATTTCTCTGCTCAGGCTCTGTAGTACGGACTACAG 7  
QY 747 CGGC 750  
DB 6 CACC 3  
Db  
RESULT 10  
AAK6585  
ID AAK6585 standard; DNA; 63 BP.  
XX  
AC AAK6585;  
XX  
DT 07-NOV-2001 (first entry)  
XX  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41397.  
XX  
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;  
KW cytoskeletal; gene therapy; vaccine; metastasis; ds.  
XX  
OS Homo sapiens.  
XX  
PN W0200157182-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 17-JAN-2001; 2001WO-US001354.  
XX  
XX 31-JAN-2000; 2000US-0179065P.  
PR 04-FEB-2000; 2000US-0180628P.  
PR 24-FEB-2000; 2000US-0184664P.  
PR 02-MAR-2000; 2000US-0186350P.  
PR 16-MAR-2000; 2000US-0189874P.  
PR 17-MAR-2000; 2000US-0190076P.  
PR 18-APR-2000; 2000US-0198123P.  
PR 19-MAY-2000; 2000US-0205515P.  
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PR 30-JUN-2000; 2000US-0215135P.  
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PR 07-JUL-2000; 2000US-0216880P.  
PR 11-JUL-2000; 2000US-0217487P.  
PR 11-JUL-2000; 2000US-0217496P.

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PR 26-JUL-2000; 2000US-0220963P.  
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PR 14-AUG-2000; 2000US-0225213P.  
PR 14-AUG-2000; 2000US-0225214P.  
PR 14-AUG-2000; 2000US-0225266P.  
PR 14-AUG-2000; 2000US-0225267P.  
PR 14-AUG-2000; 2000US-0225268P.  
PR 14-AUG-2000; 2000US-0225270P.  
PR 14-AUG-2000; 2000US-0225447P.  
PR 14-AUG-2000; 2000US-0225577P.  
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PR 14-AUG-2000; 2000US-0225759P.  
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PR 22-AUG-2000; 2000US-0226686P.  
PR 22-AUG-2000; 2000US-0227182P.  
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PR 14-SEP-2000; 2000US-0233065P.  
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PR 25-SEP-2000; 2000US-0234998P.  
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PR 26-SEP-2000; 2000US-0235344P.  
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PR 29-SEP-2000; 2000US-0236370P.  
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PR 08-NOV-2000; 2000US-0246477P.  
PR 08-NOV-2000; 2000US-0246478P.  
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PR 08-NOV-2000; 2000US-0246524P.  
PR 08-NOV-2000; 2000US-0246525P.  
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PR 17-NOV-2000; 2000US-0249212P.  
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PR 06-DEC-2000; 2000US-0251479P.  
PR 08-DEC-2000; 2000US-0251856P.  
PR 08-DEC-2000; 2000US-0251868P.  
PR 08-DEC-2000; 2000US-0251869P.  
PR 08-DEC-2000; 2000US-0251989P.  
PR 08-DEC-2000; 2000US-0251990P.  
PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Barash SC, Ruben SM,  
PI WPI; 2001-483426/52.  
XX  
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,  
PT useful for preventing, diagnosing and/or treating cancers and metastasis.  
XX  
XX Disclosure; SEQ ID NO 41397; 3071pp + Sequence Listing; English.  
XX  
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)  
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic  
CC activity, and can be used in gene therapy and vaccine production. (I)  
CC proteins and polynucleotides may be used in the prevention, diagnosis and  
CC treatment of diseases associated with inappropriate (I) expression. For  
CC example, they may be used to treat disorders associated with decreased  
CC expression by rectifying mutations or deletions in a patient's genome  
CC that affect the activity of (I) by expressing inactive proteins or to  
CC supplement the patient's own production of (I). Additionally, (I)  
CC polynucleotides may be used to produce the secreted (I), by inserting the  
CC nucleic acids into a host cell and culturing the cell to express the  
CC protein. (I) proteins and polynucleotides may be used to prevent,  
CC diagnose and treat immune/haematopoietic-related diseases, especially

CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703  
CC to AAK67694 represent human immune/haematopoietic antigen genomic  
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169  
CC represent sequences used in the exemplification of the present invention  
XX  
XX Sequence 63 BP; 11 A; 14 C; 16 G; 22 T; 0 U; 0 Other;  
SQ  
Query Match 5.5%; Score 54; DB 1; Length 63;  
Best Local Similarity 91.9%; Pred. No. 56;  
Matches 57; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
CY 172 TTTTGTAGTGAATGAGTGTTCATGTTGTCAGGCTGGTCTGGAATCCCGACT 231  
DB 2 TATTTTGTAGTGAATGAGTGTTCATGTTGTCAGGCTGGTCTGGAATCCCGACT 61  
CY 232 CA 233  
DB 62 CA 63  
RESULT 11  
AAK5681/c  
ID AAK5681 standard; DNA; 63 BP.  
XX  
XX AAK5681;  
AC  
XX 07-NOV-2001 (first entry)  
DT  
XX  
XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40493.  
DE  
XX  
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;  
KW Cytostatic; gene therapy; vaccine; metastasis; ds.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200157182-A2.  
XX  
XX 09-AUG-2001.  
XX  
XX 17-JAN-2001; 2001WO-US001354.  
XX  
XX 31-JAN-2000; 2000US-0179065P.  
XX  
XX 04-FEB-2000; 2000US-0180628P.  
XX  
XX 24-FEB-2000; 2000US-0184664P.  
XX  
XX 02-MAR-2000; 2000US-0186350P.  
XX  
XX 16-MAR-2000; 2000US-0189874P.  
XX  
XX 17-MAR-2000; 2000US-0190076P.  
XX  
XX 18-APR-2000; 2000US-0198123P.  
XX  
XX 19-MAY-2000; 2000US-0205515P.  
XX  
XX 07-JUN-2000; 2000US-0209467P.  
XX  
XX 28-JUN-2000; 2000US-0214886P.  
XX  
XX 30-JUN-2000; 2000US-0215135P.  
XX  
XX 07-JUL-2000; 2000US-0216647P.  
XX  
XX 07-JUL-2000; 2000US-0216880P.  
XX  
XX 11-JUL-2000; 2000US-0217487P.  
XX  
XX 11-JUL-2000; 2000US-0217496P.  
XX  
XX 14-JUL-2000; 2000US-0218290P.  
XX  
XX 26-JUL-2000; 2000US-0220963P.  
XX  
XX 26-JUL-2000; 2000US-0220964P.  
XX  
XX 14-AUG-2000; 2000US-0224518P.  
XX  
XX 14-AUG-2000; 2000US-0224519P.  
XX  
XX 14-AUG-2000; 2000US-0225213P.  
XX  
XX 14-AUG-2000; 2000US-0225214P.  
XX  
XX 14-AUG-2000; 2000US-0225266P.  
XX  
XX 14-AUG-2000; 2000US-0225267P.  
XX  
XX 14-AUG-2000; 2000US-0225268P.  
XX  
XX 14-AUG-2000; 2000US-0225270P.  
XX  
XX 14-AUG-2000; 2000US-0225447P.  
XX  
XX 14-AUG-2000; 2000US-0225757P.  
XX  
XX 14-AUG-2000; 2000US-0225758P.  
XX  
XX 14-AUG-2000; 2000US-0225759P.  
XX  
XX 18-AUG-2000; 2000US-0226279P.  
XX  
XX 22-AUG-2000; 2000US-0226681P.



PR 08-SEP-2000; 2000US-0231414P

[illegible]



XX (SIMP/) SIMPSON A J G.  
 PA (NETO/) NETO E D.  
 PA (BRENT/) BRENTANI R R.  
 XX Simpson AUG, Neto ED, Brentani RR;  
 PI WPI, 2003-182626/18.  
 XX  
 DR  
 XX  
 PT Determining open reading frames of genome of an organism e.g. a human  
 PT suffering from cancer involves use of single oligonucleotide primer at  
 PT low stringency for preparing single-stranded cDNA from mRNA of  
 PT individual.  
 XX  
 PS Example 9; Page 286; 959pp; English.  
 XX  
 CC The invention describes a method of determining open reading frames in  
 CC the genome of organism, comprising contacting mRNA from cell of organism  
 CC with a single oligonucleotide primer (1) at low stringency, preparing  
 CC single-stranded cDNA by reverse transcribing mRNA with (1), amplifying  
 CC cDNA, sequencing the product, and repeating the contacting, preparing  
 CC and amplifying steps with different primers and sequencing resulting  
 CC nucleic acids. The method is useful for determining that a known  
 CC nucleotide sequence from a genome of an organism corresponds to a  
 CC nucleic acid molecule from a genome of an organism; and for sequencing  
 CC all or part of a genome of an organism. mRNA is obtained from mammalian  
 CC or human cell which is associated with a pathological condition e.g. a  
 CC colon cancer or breast cancer cell. The method is useful for analyses of  
 CC populations of subjects and can be used to carry out genetic analyses of  
 CC large or small populations. Further, it can be used to study living  
 CC systems to determine if, e.g. there have been genetic shifts which render  
 CC an individual or population more or less likely to be afflicted with  
 CC diseases such as cancer, to determine antibiotic resistance or non-  
 CC tolerance, and so forth. The method can also be used in the study of  
 CC congenital diseases, and the risk of affliction to a foetus, as well as  
 CC the study of whether the conditions are likely to be passed to offspring  
 CC through ova or sperm. The analyses for pathological conditions can be  
 CC carried out in all animals, plants, birds, fish, etc. Using this method,  
 CC in the area of agriculture, for example the genomes of food crops can be  
 CC studied to determine if resistance genes are present, defects in plant  
 CC genomes can also be studied in this way. Similarly, the method permits  
 CC determination of the pathogens which integrate into the genome, such as  
 CC retroviruses and other integrating viruses such as influenza virus, have  
 CC undergone shifts or mutations, which may require different approaches to  
 CC therapy. This method is also applied to eukaryotic pathogens, such as  
 CC trypanosomes, different types of Plasmodium, etc. The method essentially  
 CC eliminates sequencing of non-coding portions. This sequence represents a  
 CC polynucleotide isolated from human colon cancer cell cDNA library  
 XX  
 SQ Sequence 65 BP; 13 A; 15 C; 27 G; 10 T; 0 U; 0 Other;  
 Query Match. 5.3%; Score 52.8; DB 1; Length 65;  
 Best Local Similarity 89.1%; Pred. No. 66;  
 Matches 57; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
 OY 690 CCTCCGGGTTCAAGTTATTCCTGCCCCAGCCTCTGAGTAGCTGGGACTACAGGCGC 749  
 DB 64 CTTCCCGGGTTATGCACTTCTCTGCTCAGCCTCCGAGTAGTGGAGCTACAGGCGC 5  
 OY 750 CCAC 753  
 DB 4 CCGC 1  
 RESULT 15  
 ID ACC84454 standard; DNA; 60 BP.  
 XX ACC84454;  
 AC  
 XX 28-AUG-2003 (first entry)  
 DT  
 XX

DE NTP peptide encoding sequence #1.  
 XX Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;  
 KW neural thread protein; NTP; tumour; ds.  
 XX Unidentified.  
 XX WO2003008443-A2.  
 XX  
 PD 30-JAN-2003.  
 XX  
 XX 19-JUL-2002; 2002WO-CA001105.  
 XX  
 PF 19-JUL-2001; 2001US-0306150P.  
 PR 19-JUL-2001; 2001US-030615P.  
 PR 16-NOV-2001; 2001US-0331477P.  
 XX  
 PA (NTMO-) NTMOX CORP.  
 XX  
 PI Averbach PA;  
 XX  
 DR WPI, 2003-247999/24.  
 DR P-FSDB; ABR63249.  
 XX  
 XX Novel neural thread protein peptide, referred as cell death peptide,  
 PT useful for treating prostatic hyperplasia, psoriasis, eczema, dermatosis,  
 PT atherosclerosis, cosmetic modification to skin, throat, mouth, muscle.  
 XX  
 PS Disclosure; Page 15; 77pp; English.  
 XX  
 CC The present invention relates to a neural thread protein (NTP) peptide  
 CC referred to as cell death peptide. Thought to be cytostatic,  
 CC antibacterial, immunosuppressive and antiinflammatory. It is useful for  
 CC treating a condition in a patient requiring removal or destruction of  
 CC cells, for treating a condition such as benign or malignant tumor,  
 CC inflammatory disease, autoimmune disease and infectious disease. The  
 CC peptide useful for treatment is derived from the amino acid sequence for  
 CC a pancreatic thread protein. The peptide is conjugated, linked or bound  
 CC to a molecule chosen from antibody or its fragment, antibody-like binding  
 CC molecule, where the molecule has a higher affinity for binding to a tumor  
 CC or other target than binding to other cells. Treatment using NTP peptides  
 CC can remove benign tumors with less risk and fewer of the undesirable side  
 CC effects of surgery. The present sequence is an NTP encoding sequence  
 XX  
 SQ Sequence 60 BP; 9 A; 21 C; 15 G; 15 T; 0 U; 0 Other;  
 Query Match. 5.2%; Score 51; DB 1; Length 60;  
 Best Local Similarity 100.0%; Pred. No. 76;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 699 TTCAAGTTATTCCTGCCCCAGCCTCTGAGTAGCTGGGACTACAGGCGC 749  
 DB 10 TTCAAGTTATTCCTGCCCCAGCCTCTGAGTAGCTGGGACTACAGGCGC 60  
 RESULT 16  
 ID AD120585 standard; DNA; 60 BP.  
 XX AD120585;  
 AC  
 XX AD120585;  
 DT 15-APR-2004 (first entry)  
 XX  
 DE Oligonucleotide sequence enquiry #72.  
 KW human; ds; eRNA.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO2003025229-A1.  
 PN  
 XX 27-MAR-2003.  
 PD  
 XX

PF 19-SEP-2002; 2002WO-AU001286.  
 XX  
 PR 19-SEP-2001; 2001US-0324127P.  
 XX  
 PA (UYOU ) UNIV QUEENSLAND.  
 XX  
 PI Mattick J, Gagen M, Stanley S;  
 XX  
 DR WPI; 2003-371830/35.  
 XX  
 PT Identifying an mRNA or a DNA sequence comprising an mRNA-encoding  
 PT sequence in the nucleome of a eukaryotic cell, comprising identifying non  
 PT protein-encoding nucleotide sequences within an mRNA transcript or a DNA  
 PT sequence.  
 XX  
 PS Example 12; SEQ ID NO 75; 137pp; English.  
 XX  
 CC The present invention relates to identifying an RNA or a DNA sequence  
 CC comprising an RNA-encoding sequence in the nucleome of a eukaryotic cell  
 CC comprising identifying non-protein-encoding nucleotide sequences within an  
 CC mRNA transcript or a DNA sequence encoding same in the nucleome. The  
 CC methods are useful for identifying an RNA or DNA for modifying a genetic  
 CC network in cell to alter the cells phenotype. The present sequence  
 CC represents human oligonucleotide sequence enquiry.  
 XX  
 SQ Sequence 60 BP; 10 A; 22 C; 16 G; 12 T; 0 U; 0 Other;  
 XX  
 Query Match 5.1%; Score 50.4; DB 1; Length 60;  
 Best Local Similarity 90.0%; Pred. No. 82;  
 Matches 54; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 637 CCGTACCCAGGCTGAGTGCAGTGGCGCAATCTTGAGCTCACTGCAACCTCTCCGCG 696  
 DB 1 CCGTACCCAGGCTGAGTGCAGTGGCGCAATCTTGAGCTCACTGCAACCTCTCCGCG 60

RESULT 17  
 ACC79017/c  
 ID ACC79017 standard; DNA; 61 BP.  
 XX  
 AC ACC79017;  
 XX  
 DT 29-JUL-2003 (first entry)  
 XX  
 DE Human genome SNP related oligonucleotide ss1000934.  
 XX  
 KW Human; regulation; single nucleotide polymorphism; SNP; gene therapy;  
 KW transcription factor binding site cluster; probe; primer; gene; db.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT variation 31  
 FT /\*tag= a  
 FT /standard\_name= "single nucleotide polymorphism"  
 XX  
 PN WO2003025198-A2.  
 XX  
 PD 27-MAR-2003.  
 XX  
 PF 11-SEP-2002; 2002WO-US028842.  
 XX  
 PR 17-SEP-2001; 2001US-0322723P.  
 PR 30-NOV-2001; 2001US-0334543P.  
 XX  
 PA (ITGE-) INT GENOMICS LLC.  
 XX  
 PI Nowotny V;  
 XX  
 DR WPI; 2003-354608/33.  
 XX  
 PT New set of regulatory single nucleotide polymorphism (SNP)  
 PT polymorphisms, useful in diagnostic assays, in testing systems for

PT finding new drugs, or for treating or preventing a disease associated  
 PT with the regulatory SNP.  
 XX  
 PS Example 2; Page 21; 37pp; English.  
 XX  
 CC The present invention describes a set of regulatory single nucleotide  
 CC polymorphism (SNP) polymorphisms or its complementary set of  
 CC polymorphisms comprising polymorphisms of at least 6 contiguous  
 CC nucleotides, where each polymorphisms of the set contains a regulatory  
 CC SNP with 5' and/or 3' genomic flanking sequence. A set of regulatory SNP  
 CC polymorphisms contains several regulatory SNPs which collectively map  
 CC to several transcription factor binding site cluster (TF) sequences so  
 CC that each SNP lies within a TFC sequence, and a genomic nucleic acid  
 CC sequence from 30 nucleotides 5' to 30 nucleotides 3' to each SNP is  
 CC identical or complementary except for the SNP, to a portion of a genomic  
 CC nucleic acid sequence from 30 nucleotides 5' to 30' nucleotides 3' to the  
 CC TFC sequence. The set of regulatory SNP polymorphisms can be used in  
 CC gene therapy. The regulatory SNP polymorphisms are useful in diagnostic  
 CC assays, in testing systems for finding new drugs, or for treating or  
 CC preventing a disease associated with the regulatory SNP. The  
 CC polymorphisms are also useful as probes or primers for detecting the  
 CC regulatory SNPs. The present sequence represents a human genome related  
 CC oligonucleotide comprising a SNP, which is used in an example from the  
 CC present invention  
 XX  
 SQ Sequence 61 BP; 11 A; 19 C; 21 G; 9 T; 0 U; 1 Other;  
 XX  
 Query Match 5.1%; Score 50; DB 1; Length 61;  
 Best Local Similarity 88.3%; Pred. No. 87;  
 Matches 53; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
 QY 643 CCCAGGCTGAGTGCAGTGGCGCAATCTTGAGCTCACTGCAACCTCTCCGCGGTCA 702  
 DB 60 CCCAGGCTGAGTGCAGTGGCGCAATCTTGAGCTCACTGCAACCTCTCCGCGGTCA 1

RESULT 18  
 AD112551/c  
 ID AD112551 standard; DNA; 56 BP.  
 XX  
 AC AD112551;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE Mutant human BRCA1 genomic DNA resulting from deletion 5 SegID 34.  
 XX  
 KW de; cancer; human; tumour suppressor;  
 KW breast cancer susceptibility gene 1; BRCA1; repetitive Alu;  
 KW ovarian cancer; recombination; mutant.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT variation 31  
 FT /\*tag= a  
 FT /standard\_name= "single nucleotide polymorphism"  
 XX  
 PN WO2003104474-A2.  
 XX  
 PD 18-DEC-2003.  
 XX  
 PF 09-JUN-2003; 2003WO-US018098.  
 XX  
 PR 07-JUN-2002; 2002US-0387132P.  
 PR 09-AUG-2002; 2002US-0402430P.  
 XX  
 PA (MYRIAD) MYRIAD GENETICS INC.  
 XX  
 PI Scholl T, Hendrickson BC, Ward B, Pruss D;  
 XX  
 DR WPI; 2004-062369/06.  
 XX  
 PT Predicting a predisposition to cancer in a patient comprising detecting a  
 PT deletion in the BRCA1 gene that results from the unequal crossover  
 PT between a pair of repetitive sequences in the BRCA1 gene.  
 XX  
 PS Disclosure; SEQ ID NO 34; 59pp; English.

CC This invention relates to a novel method for predicting a predisposition  
CC to cancer in a patient by detecting large deletions in the human tumour  
CC suppressor gene identified as the breast cancer susceptibility gene 1  
CC (BRCA1). Specifically, it refers to deletions that result from the  
CC unequal crossover between a pair of repetitive Alu sequences in the BRCA1  
CC gene, such that the recombined nucleotide sequence containing the  
CC deletion indicates a predisposition to breast and ovarian cancer. The  
CC present invention describes newly discovered deletion mutations that are  
CC believed to be deleterious and cause significant alterations in the  
CC structure or biochemical function of BRCA1. Accordingly, it provides  
CC methods for detecting such mutants, as well as identifying and screening  
CC for cytostatic compounds useful for treating or preventing cancers  
CC associated with a BRCA1 genetic variant. This polynucleotide is a mutant  
CC human BRCA1 genomic DNA fragment that arises as a result of a  
CC recombination event (deletion 5), which causes the omission of exons 15  
CC and 16, given in an exemplification of the invention.

XX  
SQ Sequence 56 BP; 13 A; 14 C; 18 G; 11 T; 0 U; 0 Other;

Query Match 4.9%; Score 48.6; DB 1; Length 56;  
Best Local Similarity 92.7%; Pred. No. 96;  
Matches 51; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 693 CCGGGTTCAAGTATTCCTGCCCCAGCCTCTGAGTACTGGAGCTACAGGC 747  
Db 56 CCGGGTTCAAGCATCTCTGCTCTGAGCTCTGAGTACTGGAGTATTAAGGC 2

RESULT 19  
AA179765  
ID AA179765 standard; DNA; 51 BP.  
XX  
AC AA179765;  
XX  
DT 09-NOV-2001 (first entry)  
XX  
DE Human nonconservative amino acid changing SNP nucleic acid SEQ:6706.  
XX  
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KW protein therapy; vaccine; probe; diagnostic assay; detection;  
KW quantitation; restorative therapy; polymorphic; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200140521-A2.  
XX  
PD 07-JUN-2001.  
XX  
PF 30-NOV-2000; 2000WO-US032758.  
XX  
PR 30-NOV-1999; 99US-0168136P.  
XX  
PR 29-NOV-2000; 2000US-00726173.  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
PI Shimkova RA, Leach M;  
XX  
DR WPI; 2001-356160/37.  
XX  
PT Polymorphic nucleic acid sequences, useful in genetic testing and  
PT therapy.  
XX  
PS Claim 1; Page 2557; 2653pp; English.

CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).  
CC AA173114 to AA175329 represent peptides related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (I) and the polypeptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides. For  
CC example, (I) may be used to treat disorders by rectifying mutations or  
CC deletions in a patient's genome that affect the activity of polypeptides

CC by expressing inactive proteins or to supplement the patients own  
CC production of polypeptide. Additionally, (I) and its complementary  
CC sequences may also be used as DNA probes in diagnostic assays to detect  
CC and quantitate the presence of similar nucleic acids in samples, and  
CC therefore which patients may be in need of restorative therapy. The  
CC polypeptides encoded by (I) may be used as antigens in the production of  
CC antibodies specific for polymorphic polypeptides. The antibodies may also  
CC be used to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples

XX  
SQ Sequence 51 BP; 8 A; 17 C; 15 G; 11 T; 0 U; 0 Other;

Query Match 4.9%; Score 48.4; DB 1; Length 51;  
Best Local Similarity 98.0%; Pred. No. 91;  
Matches 49; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 638 TGTGACCCAGGCTGAGTGCAGTGGCCCAATCTTGCTCACTGCACCTC 687  
Db 1 TGTGACCCAGGCTGAGTGCAGTGGCCCAATCTTGCTCACTGCACCTC 50

RESULT 20  
AD120575  
ID AD120575 standard; DNA; 60 BP.  
XX  
AC AD120575;  
XX  
DT 15-APR-2004 (first entry)  
XX  
DE Oligonucleotide sequence enquiry #62.  
XX  
KW human; ds; eRNA.  
XX  
OS Homo sapiens.  
XX  
PN WO2003025229-A1.  
XX  
PD 27-MAR-2003.  
XX  
PF 19-SEP-2002; 2002WO-AU001286.  
XX  
PR 19-SEP-2001; 2001US-0324127P.  
XX  
PA (UNYU) UNIV QUEENSLAND.  
XX  
PI Mattick J, Gagen M, Stanley S;  
XX  
DR WPI; 2003-371830/35.  
XX  
PT Identifying an eRNA or a DNA sequence comprising an eRNA-encoding  
PT sequence in the nucleome of a eukaryotic cell, comprising identifying non  
PT protein-encoding nucleotide sequences within an mRNA transcript or a DNA  
PT sequence.  
XX  
PS Example 12; SEQ ID NO 65; 137pp; English.

CC The present invention relates to identifying an eRNA or a DNA sequence  
CC comprising an eRNA-encoding sequence in the nucleome of a eukaryotic cell  
CC comprising identifying non-protein-encoding nucleotide sequences within an  
CC mRNA transcript or a DNA sequence encoding same in the nucleome. The  
CC methods are useful for identifying an eRNA or DNA for modifying a genetic  
CC network in cell to alter the cells phenotype. The present sequence  
CC represents human oligonucleotide sequence enquiry.

XX  
SQ Sequence 60 BP; 9 A; 18 C; 18 G; 15 T; 0 U; 0 Other;

Query Match 4.9%; Score 48.2; DB 1; Length 60;  
Best Local Similarity 94.3%; Pred. No. 1.1e+02;  
Matches 50; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 696 GGGTTCAAGTATTCCTGCCCCAGCCTCTGAGTACTGGAGCTACAGGC 748  
|||||



Db 2 GGTTCAAGTATCTCTGCTCAGCCTCCGAGTAGCTGGAGCTACAGCG 54

## RESULT 21

AAA77228  
ID AAA77228 standard, cDNA; 51 BP.

AC AAA77228;

DT 16-NOV-2000 (first entry)

DE Human clone c943971764 polymorphic site, SEQ ID NO:911.

KW Human; single nucleotide polymorphism; SNP; chromosome 15; detection;  
KW identification; gene therapy; ss.

OS Homo sapiens.

XX Key Location/Qualifiers  
XX Variation replace(26,C)  
XX FT /\*tag= a

PN MO200029623-A2.

PD 25-MAY-2000.

PF 17-NOV-1999; 99WO-US027293.

PR 17-NOV-1998; 98US-0109024P.

PR 16-NOV-1999; 99US-00443199.

XX (CURA-) CURAGEN CORP.

PI Shinkets RA, Leach MD;

DR WPI; 2000-387826/33.

PT Human nucleic acids containing single nucleotide polymorphisms, useful  
PT for treating a subject suffering, or at risk from a pathology due to the  
PT presence of a sequence polymorphism.

PS Claim 1; Page 433; 543pp; English.

XX Sequences AAA7318-A77509 represent 1192 human nucleic acid sequences  
CC which contain single nucleotide polymorphisms (SNPs). Sequences 1 to 1112  
CC (AAA76338-A77429) are consecutive pairs of nucleotides which contain  
CC silent SNPs. Sequences 1113 to 1192 (AAA77430-A77509) are consecutive  
CC pairs of nucleotides containing SNPs which result in changes in the  
CC corresponding amino acid sequences (AAB11749-B11828). The SNPs in  
CC sequences 1113 to 1128 (AAA77430-A77445) lead to conservative amino acid  
CC changes, while those in sequences 1129 to 1186 (AAA77446-A77503) result  
CC in non-conservative changes. The SNPs in sequences 1187 to 1192  
CC (AAA77504-A77509) generate frameshift mutations. The invention also  
CC relates to a method of detecting a polymorphic site in a nucleic acid and  
CC a method of determining the relatedness of two nucleic acids. It also  
CC encompasses peptides containing polymorphic sites, antibodies raised  
CC against such peptides, and a method of detecting polymorphic  
CC proteins/peptides using the antibodies. The nucleic acids are useful for  
CC gene therapy of an individual having, suspected of having, or at risk of  
CC developing a pathological condition due to the presence of a sequence  
CC polymorphism. Such treatment would comprise administration of the wild-  
CC type nucleic acid sequence. Antibodies raised against polymorphic  
CC peptides can also be used in the treatment of such individuals

XX Sequence 51 BP; 11 A; 20 C; 13 G; 7 T; 0 U; 0 Other;

SO Query Match 4.8%; Score 47.8; DB 1; Length 51;

Best Local Similarity 96.1%; Pred. No. 97;

Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 847 CTTGCGCTCCCAAGTGGGATTAACGCGGAGCCACGCGCCGCG 897  
DB 1 CTTGAGCTCCCAAGTGGGATTAACGCGGAGCCACGCGCCGCG 51

## RESULT 22

AAI76251/C  
ID AAI76251 standard; DNA; 51 BP.

AC AAI76251;

DT 09-NOV-2001 (first entry)

DE Human silent SNP containing nucleic acid SEQ:3192.

KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KW protein therapy; vaccine; probe; diagnostic assay; detection;  
KW quantitation; restorative therapy; polymorphic; ds.

OS Homo sapiens.

XX WO200140521-A2.

PD 07-JUN-2001.

PF 30-NOV-2000; 2000WO-US032758.

PR 30-NOV-1999; 99US-0168138P.

PR 29-NOV-2000; 2000US-00726173.

XX (CURA-) CURAGEN CORP.

PI Shinkets RA, Leach M;

DR WPI; 2001-356160/37.

PT Polymorphic nucleic acid sequences, useful in genetic testing and  
PT therapy.

PS Claim 1; Page 1027; 2653pp; English.

XX AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide  
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).  
CC AAM53114 to AAM53329 represent peptides related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (I) and the polypeptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides. For  
CC example, (I) may be used to treat disorders by rectifying mutations or  
CC deletions in a patient's genome that affect the activity of polypeptides  
CC by expressing inactive proteins or to supplement the patient's own  
CC production of polypeptide. Additionally, (I) and its complementary  
CC sequences may also be used as DNA probes in diagnostic assays to detect  
CC and quantitate the presence of similar nucleic acids in samples, and  
CC therefore which patients may be in need of restorative therapy. The  
CC polypeptides encoded by (I) may be used as antigens in the production of  
CC antibodies specific for polymorphic polypeptides. The antibodies may also  
CC be used to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples

XX Sequence 51 BP; 12 A; 16 C; 15 G; 8 T; 0 U; 0 Other;

SO Query Match 4.8%; Score 47.8; DB 1; Length 51;

Best Local Similarity 96.1%; Pred. No. 97;

Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 639 GTACCCAGGCTGAGTGCAGTGCCTGCTGCTGCTGCTGCTGCTG 689  
DB 51 GTACCCAGGCTGAGTGCAGTGCCTGCTGCTGCTGCTGCTGCTG 1

## RESULT 23

AAI78079  
ID AAI78079 standard; DNA; 51 BP.

XX

AC AA178079;  
XX 09-NOV-2001 (first entry)  
XX Human silent SNP containing nucleic acid SEQ:5020.  
DE  
XX  
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KW protein therapy; vaccine; probe; diagnostic assay; detection;  
KW quantitation; restorative therapy; polymorphic; ds.  
XX  
OS Homo sapiens.  
XX WO200140521-A2.  
XX  
XX 07-JUN-2001.  
XX  
XX 30-NOV-2000; 2000WO-US032758.  
XX  
XX 30-NOV-1999; 99US-0168138P.  
XX 29-NOV-2000; 2000US-00726173.  
XX  
XX (CURA-) CURAGEN CORP.  
XX  
XX Shimkets RA, Leach M;  
XX WPI, 2001-356160/37.  
XX  
XX Polymorphic nucleic acid sequences, useful in genetic testing and  
PT therapy.  
XX  
XX Claim 1; Page 2046; 2653bp; English.  
XX  
XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).  
CC AAWS3114 to AAWS3329 represent peptides related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (I) and the polypeptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides. For  
CC example, (I) may be used to treat disorders by rectifying mutations or  
CC deletions in a patient's genome that affect the activity of polypeptides  
CC by expressing inactive proteins or to supplement the patients own  
CC production of polypeptide. Additionally, (I) and its complementary  
CC sequences may also be used as DNA probes in diagnostic assays to detect  
CC and quantitate the presence of similar nucleic acids in samples, and  
CC therefore which patients may be in need of restorative therapy. The  
CC polypeptides encoded by (I) may be used as antigens in the production of  
CC antibodies specific for polymorphic polypeptides. The antibodies may also  
CC be used to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples  
XX  
SQ Sequence 51 BP; 9 A; 20 C; 14 G; 8 T; 0 U; 0 Other;  
XX  
Query Match 4.8%; Score 47.8; DB 1; Length 51;  
Best Local Similarity 96.1%; Pred. No. 97;  
Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 641 CACCCAGGCTGAGTGCAGTGGCGCAATCTTGGCTCACTGCAACCTCTGCC 691  
DB 1 CACCCAGGCTGAGTGCAGTGGCGCAATCTTGGCTCACTGCAACCTCTGCC 51  
RESULT 24  
AA173248/C  
ID AA173248 standard; DNA; 51 BP.  
XX  
XX AA173248;  
AC  
XX 09-NOV-2001 (first entry)  
XX  
XX Human silent SNP containing nucleic acid SEQ:189.  
XX

KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KW protein therapy; vaccine; probe; diagnostic assay; detection;  
KW quantitation; restorative therapy; polymorphic; ds.  
XX  
XX Homo sapiens.  
XX WO200140521-A2.  
XX  
XX 07-JUN-2001.  
XX  
XX 30-NOV-2000; 2000WO-US032758.  
XX  
XX 30-NOV-1999; 99US-0168138P.  
XX 29-NOV-2000; 2000US-00726173.  
XX  
XX (CURA-) CURAGEN CORP.  
XX  
XX Shimkets RA, Leach M;  
XX WPI, 2001-356160/37.  
XX  
XX Polymorphic nucleic acid sequences, useful in genetic testing and  
PT therapy.  
XX  
XX Claim 1; Page 113; 2653bp; English.  
XX  
XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).  
CC AAWS3114 to AAWS3329 represent peptides related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (I) and the polypeptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides. For  
CC example, (I) may be used to treat disorders by rectifying mutations or  
CC deletions in a patient's genome that affect the activity of polypeptides  
CC by expressing inactive proteins or to supplement the patients own  
CC production of polypeptide. Additionally, (I) and its complementary  
CC sequences may also be used as DNA probes in diagnostic assays to detect  
CC and quantitate the presence of similar nucleic acids in samples, and  
CC therefore which patients may be in need of restorative therapy. The  
CC polypeptides encoded by (I) may be used as antigens in the production of  
CC antibodies specific for polymorphic polypeptides. The antibodies may also  
CC be used to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples  
XX  
SQ Sequence 51 BP; 12 A; 8 C; 23 G; 8 T; 0 U; 0 Other;  
XX  
Query Match 4.8%; Score 47.8; DB 1; Length 51;  
Best Local Similarity 96.1%; Pred. No. 97;  
Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 974 CTCACGACCTCTGCTCCCGGCTCAACGATTCCTCTGTCAGCCT 1024  
DB 51 CTCACGACCTCTGCTCCCGGCTCAACGATTCCTCTGTCAGCCT 1  
RESULT 25  
AD112542/C  
ID AD112542 standard; DNA; 49 BP.  
XX  
XX AD112542;  
AC  
XX 22-APR-2004 (first entry)  
XX  
XX Mutant human BRCA1 genomic DNA resulting from deletion 3 Segid 25.  
XX  
XX ds; cancer; human; tumour suppressor;  
KW breast cancer susceptibility gene 1; BRCA1; repetitive Alu;  
KW ovarian cancer; recombination; mutant.  
XX  
XX Homo sapiens.  
XX



XX Polymorphic nucleic acid sequences, useful in genetic testing and  
PT therapy.  
PS Claim 1; Page 56; 2653pp; English.  
XX  
CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).  
CC AA173114 to AA175329 represent peptides related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (I) and the polypeptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides. For  
CC example, (I) may be used to treat disorders by rectifying mutations or  
CC deletions in a patient's genome that affect the activity of polypeptides  
CC by expressing inactive proteins or to supplement the patient's own  
CC production of polypeptide. Additionally, (I) and its complementary  
CC sequences may also be used as DNA probes in diagnostic assays to detect  
CC and quantitate the presence of similar nucleic acids in samples, and  
CC therefore which patients may be in need of restorative therapy. The  
CC polypeptides encoded by (I) may be used as antigens in the production of  
CC antibodies specific for polymorphic polypeptides. The antibodies may also  
CC be used to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples  
SQ Sequence 51 BP; 10 A; 15 C; 18 G; 8 T; 0 U; 0 Other;  
XX  
Query Match 4.7%; Score 46.8; DB 1; Length 51;  
Best Local Similarity 96.0%; Pred. No. 1.1e+02;  
Matches 48; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 638 TGTCAACCCAGCTGGAGTGCAGTGGCGCAATCTGGCTCACTGCAACCTC 687  
DB 51 TGTCCGCCAGCTGGAGTGCAGTGGCGCAATCTGGCTCACTGCAACCTC 2  
RESULT 28  
AA177229  
ID AA177229 standard; cDNA; 51 BP.  
XX  
AC AA177229;  
XX  
DT 16-NOV-2000 (first entry)  
XX  
DE Human clone CG43971764 polymorphic site, SEQ ID NO:912.  
XX  
KW Human; single nucleotide polymorphism; SNP; chromosome 15; detection;  
KM identification; gene therapy; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT variation replace(26,T)  
FT /\*tag= a  
XX  
PN WO200029623-A2.  
XX  
PD 25-MAY-2000.  
XX  
PF 17-NOV-1999; 99WO-US027293.  
XX  
PR 17-NOV-1999; 98US-0109024P.  
XX  
PR 16-NOV-1999; 99US-00443199.  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
PI Shimkels RA, Leach MD;  
XX  
DR WPI; 2000-387626/33.  
XX  
PT Human nucleic acids containing single nucleotide polymorphisms, useful  
PT for treating a subject suffering, or at risk from a pathology due to the

PT presence of a sequence polymorphism.  
XX  
PS Claim 1; Page 433; 543pp; English.  
XX  
CC Sequences AA176318-A77509 represent 1192 human nucleic acid sequences  
CC which contain single nucleotide polymorphisms (SNPs). Sequences 1 to 1112  
CC (AA176318-A77429) are consecutive pairs of nucleotides which contain  
CC silent SNPs. Sequences 1113 to 1192 (AA177430-A77509) are consecutive  
CC pairs of nucleotides containing SNPs which result in changes in the  
CC corresponding amino acid sequences (AA11749-11828). The SNPs in  
CC sequences 1113 to 1128 (AA177430-A77445) lead to conservative amino acid  
CC changes, while those in sequences 1129 to 1186 (AA177446-A77509) result  
CC in non-conservative changes. The SNPs in sequences 1187 to 1192  
CC (AA177504-A77509) generate frameshift mutations. The invention also  
CC relates to a method of detecting a polymorphic site in a nucleic acid  
CC a method of determining the relatedness of two nucleic acids. It also  
CC encompasses peptides containing polymorphic sites, antibodies raised  
CC against such peptides, and a method of detecting polymorphic  
CC proteins/peptides using the antibodies. The nucleic acids are useful for  
CC gene therapy of an individual having, suspected of having, or at risk of  
CC developing a pathological condition due to the presence of a sequence  
CC polymorphism. Such treatment would comprise administration of the wild-  
CC type nucleic acid sequence. Antibodies raised against polymorphic  
CC peptides can also be used in the treatment of such individuals  
SQ Sequence 51 BP; 11 A; 21 C; 13 G; 6 T; 0 U; 0 Other;  
XX  
Query Match 4.7%; Score 46.2; DB 1; Length 51;  
Best Local Similarity 94.1%; Pred. No. 1.2e+02;  
Matches 48; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 847 CCTGGGCTCCCAAGAGTGTGGATTACAGGCGTGAAGCCACCGCCGGC 897  
DB 1 CCTAGGCTCCCAAGAGTGTGGATTACAGGCGTGAAGCCACCGCCGGC 51  
RESULT 29  
AA173249/C  
ID AA173249 standard; DNA; 51 BP.  
XX  
AC AA173249;  
XX  
DT 09-NOV-2001 (first entry)  
XX  
DE Human silent SNP containing nucleic acid SEQ:190.  
XX  
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KM protein therapy; vaccine; probe; diagnostic assay; detection;  
XX  
OS Homo sapiens.  
XX  
FH WO200140521-A2.  
FT 07-JUN-2001.  
XX  
PN 30-NOV-2000; 2000WO-US032758.  
XX  
PD 30-NOV-1999; 98US-0168138P.  
XX  
PF 29-NOV-2000; 2000US-00726173.  
XX  
PR (CURA-) CURAGEN CORP.  
XX  
PI Shimkels RA, Leach M;  
XX  
DR WPI; 2001-356160/37.  
XX  
PT Polymorphic nucleic acid sequences, useful in genetic testing and  
PT therapy.  
PS Claim 1; Page 113; 2653pp; English.  
XX  
CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide

CC sequences (1), which contain single nucleotide polymorphisms (SNPs).  
CC AAM5314 to AAM5329 represent peptides related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (1) and the polypeptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides. For  
CC example, (1) may be used to treat disorders by rectifying mutations or  
CC deletions in a patient's genome that affect the activity of polypeptides  
CC by expressing inactive proteins or to supplement the patients own  
CC production of polypeptide. Additionally, (1) and its complementary  
CC sequences may also be used as DNA probes in diagnostic assays to detect  
CC and quantitate the presence of similar nucleic acids in samples, and  
CC therefore which patients may be in need of restorative therapy. The  
CC polypeptides encoded by (1) may be used as antigens in the production of  
CC antibodies specific for polymorphic polypeptides. The antibodies may also  
CC be used to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples  
XX  
SQ Sequence 51 BP; 13 A; 8 C; 22 G; 8 T; 0 U; 0 Other;  
XX  
Query Match 4.7%; Score 46.2; DB 1; Length 51;  
Best Local Similarity 94.1%; Pred. No. 1.2e+02;  
Matches 48; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
XX  
QY 974 CTCACCTGCAACCTCTGCTCCGCGGCTCAAGCGATTCTCTCTCAGCCT 1024  
DB 51 CTCACCTGCAACCTCTGCTCCGCGGCTCAAGCGATTCTCTCTCAGCCT 1  
XX  
RESULT 30  
AA178078  
ID AA178078 standard; DNA; 51 BP.  
XX  
AC AA178078;  
XX  
DT 09-NOV-2001 (first entry)  
XX  
DE Human silent SNP containing nucleic acid SEQ:5019.  
XX  
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KW protein therapy; vaccine; probe; diagnostic assay; detection;  
KW quantitation; restorative therapy; polymorphic; ds.  
XX  
OS Homo sapiens.  
XX  
PN MO200140521-A2.  
XX  
PD 07-JUN-2001.  
XX  
PF 30-NOV-2000; 2000MO-US032758.  
XX  
PR 30-NOV-1999; 99US-0168138P.  
PR 29-NOV-2000; 2000US-00726173.  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
PI Shimkets RA, Leach M;  
XX  
DR WPI, 2001-356160/37.  
XX  
PT Polymorphic nucleic acid sequences, useful in genetic testing and  
PT therapy.  
XX  
PS Claim 1; Page 2046; 2653pp; English.  
XX  
CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).  
CC AAM5314 to AAM5329 represent peptides related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (1) and the polypeptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides. For

CC example, (1) may be used to treat disorders by rectifying mutations or  
CC deletions in a patient's genome that affect the activity of polypeptides  
CC by expressing inactive proteins or to supplement the patients own  
CC production of polypeptide. Additionally, (1) and its complementary  
CC sequences may also be used as DNA probes in diagnostic assays to detect  
CC and quantitate the presence of similar nucleic acids in samples, and  
CC therefore which patients may be in need of restorative therapy. The  
CC polypeptides encoded by (1) may be used as antigens in the production of  
CC antibodies specific for polymorphic polypeptides. The antibodies may also  
CC be used to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples  
XX  
SQ Sequence 51 BP; 8 A; 20 C; 15 G; 8 T; 0 U; 0 Other;  
XX  
Query Match 4.7%; Score 46.2; DB 1; Length 51;  
Best Local Similarity 94.1%; Pred. No. 1.2e+02;  
Matches 48; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
XX  
QY 641 CACCCAGGCTGAGTCGACATGCGGCAATCTGCGTCACTGCAACCTCGCC 691  
DB 1 CACCCAGGCTGAGTCGACATGCGGCAATCTGCGTCACTGCAACCTCGCC 51  
XX  
RESULT 31  
AA179818  
ID AA179818 standard; DNA; 51 BP.  
XX  
AC AA179818;  
XX  
DT 09-NOV-2001 (first entry)  
XX  
DE Human nonconservative amino acid changing SNP nucleic acid SEQ:6759.  
XX  
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KW protein therapy; vaccine; probe; diagnostic assay; detection;  
KW quantitation; restorative therapy; polymorphic; ds.  
XX  
OS Homo sapiens.  
XX  
PN MO200140521-A2.  
XX  
PD 07-JUN-2001.  
XX  
PF 30-NOV-2000; 2000MO-US032758.  
XX  
PR 30-NOV-1999; 99US-0168138P.  
PR 29-NOV-2000; 2000US-00726173.  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
PI Shimkets RA, Leach M;  
XX  
DR WPI, 2001-356160/37.  
XX  
PT Polymorphic nucleic acid sequences, useful in genetic testing and  
PT therapy.  
XX  
PS Claim 1; Page 2573; 2653pp; English.  
XX  
CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).  
CC AAM5314 to AAM5329 represent peptides related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (1) and the polypeptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides. For  
CC example, (1) may be used to treat disorders by rectifying mutations or  
CC deletions in a patient's genome that affect the activity of polypeptides  
CC by expressing inactive proteins or to supplement the patients own  
CC production of polypeptide. Additionally, (1) and its complementary  
CC sequences may also be used as DNA probes in diagnostic assays to detect  
CC and quantitate the presence of similar nucleic acids in samples, and

CC therefore which patients may be in need of restorative therapy. The  
CC polypeptides encoded by (I) may be used as antigens in the production of  
CC antibodies specific for polymorphic polypeptides. The antibodies may also  
CC be used to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples

XX  
SQ Sequence 51 BP; 9 A; 16 C; 14 G; 12 T; 0 U; 0 Other;

Query Match 4.7%; Score 46.2; DB 1; Length 51;  
Best Local Similarity 94.1%; Pred. No. 1.2e+02;  
Matches 48; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 695 CGGGTTCAAGTATTCTCTCCGCCAGCCTCTGAGTAGTGGAGTACAG 745  
DB 1 CGGGTTCAAGCATCTCTCTGCTCAGCCTCTGAGTAGTGGAGTACAG 51

RESULT 32  
AA176250/c  
ID AA176250 standard; DNA; 51 BP.

XX  
AC AA176250;  
DT 09-NOV-2001 (first entry)

XX  
DE Human silent SNP containing nucleic acid SEQ:3191.

XX  
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KW protein therapy; vaccine; probe; diagnostic assay; detection;  
KW quantitation; restorative therapy; polymorphic; ds.

XX  
OS Homo sapiens.

XX  
PN WO200140521-A2.

XX  
PD 07-JUN-2001.

XX  
PF 30-NOV-2000; 2000WO-US032758.

XX  
PR 30-NOV-1999; 99US-0168138P.

XX  
PR 29-NOV-2000; 2000US-00726173.

XX  
PA (CURA-) CURAGEN CORP.

XX  
PI Shimkets RA, Leach M;

XX  
DR WPI; 2001-356160/37.

XX  
PT polymorphic nucleic acid sequences, useful in genetic testing and  
PT therapy.

XX  
PS Claim 1; Page 1026; 2653pp; English.

CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).  
CC AA173114 to AA173329 represent peptides related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (I) and the polypeptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides. For  
CC example, (I) may be used to treat disorders by rectifying mutations or  
CC deletions in a patient's genome that affect the activity of polypeptides  
CC by expressing inactive proteins or to supplement the patients own  
CC production of polypeptide. Additionally, (I) and its complementary  
CC sequences may also be used as DNA probes in diagnostic assays to detect  
CC and quantitate the presence of similar nucleic acids in samples, and  
CC therefore which patients may be in need of restorative therapy. The  
CC polypeptides encoded by (I) may be used as antigens in the production of  
CC antibodies specific for polymorphic polypeptides. The antibodies may also  
CC be used to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples

XX  
SQ Sequence 51 BP; 12 A; 15 C; 15 G; 9 T; 0 U; 0 Other;

Query Match 4.7%; Score 46.2; DB 1; Length 51;  
Best Local Similarity 94.1%; Pred. No. 1.2e+02;  
Matches 48; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 639 GTCAACCAGGCTGAGTGCAGTGGCGCATCTTGGCTCACTGCAACTCTG 689  
DB 51 GTCAACCAGGCTGAGTGCAGTGGCGCATCTTGGCTCACTGCAACTCTG 1

RESULT 33  
AA177676/c  
ID AA177676 standard; DNA; 51 BP.

XX  
AC AA177676;  
DT 09-NOV-2001 (first entry)

XX  
DE Human silent SNP containing nucleic acid SEQ:4617.

XX  
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KW protein therapy; vaccine; probe; diagnostic assay; detection;  
KW quantitation; restorative therapy; polymorphic; ds.

XX  
OS Homo sapiens.

XX  
PN WO200140521-A2.

XX  
PD 07-JUN-2001.

XX  
PF 30-NOV-2000; 2000WO-US032758.

XX  
PR 30-NOV-1999; 99US-0168138P.

XX  
PR 29-NOV-2000; 2000US-00726173.

XX  
PA (CURA-) CURAGEN CORP.

XX  
PI Shimkets RA, Leach M;

XX  
DR WPI; 2001-356160/37.

XX  
PT polymorphic nucleic acid sequences, useful in genetic testing and  
PT therapy.

XX  
PS Claim 1; Page 1923; 2653pp; English.

CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).  
CC AA173114 to AA173329 represent peptides related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (I) and the polypeptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides. For  
CC example, (I) may be used to treat disorders by rectifying mutations or  
CC deletions in a patient's genome that affect the activity of polypeptides  
CC by expressing inactive proteins or to supplement the patients own  
CC production of polypeptide. Additionally, (I) and its complementary  
CC sequences may also be used as DNA probes in diagnostic assays to detect  
CC and quantitate the presence of similar nucleic acids in samples, and  
CC therefore which patients may be in need of restorative therapy. The  
CC polypeptides encoded by (I) may be used as antigens in the production of  
CC antibodies specific for polymorphic polypeptides. The antibodies may also  
CC be used to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples

XX  
SQ Sequence 51 BP; 12 A; 10 C; 21 G; 8 T; 0 U; 0 Other;

Query Match 4.7%; Score 46.2; DB 1; Length 51;  
Best Local Similarity 94.1%; Pred. No. 1.2e+02;  
Matches 48; Conservative 0; Mismatches 3; Indels 0; Gaps 0;





the invention may also be useful for gene therapy. The genes and proteins of the invention are useful for modulating the maturation of an immune system cell, kidney cell, pancreas cell, retinal cell, spleen cell or reticuloendothelial cell, modulating interactions between lymphoid and non-lymphoid immune system cells, as molecular markers, as drug targets, assessing kidney, pancreas or spleen function and for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating diseases and conditions associated with genes of the bone marrow, kidney, spleen, pancreas, retina, spleen or lymphoid disease (for example neuropenia, leucopenia, cancer, multiple myeloma, renal failure, glomerular disease, diabetes, retinal degeneration, optic neuritis, glaucoma or anaemia. The present sequence is that of a human tissue-specific gene promoter DNA sequence which is related to the invention.

Query Match	4.6%	Score 45.2;	DB 1;	length 50;
Best Local Similarity	94.0%;	Pred. No. 1.3e+02;		
Matches 47; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

```

Oy      836  TGA TCTG CCGCTCG GCGCTCC CAAAGTGC TGGGATTAC AGGCGTGAGCC 885
         |||||
Db      50  TGA TCCACCTG CCGCTCG GCGCTCC CAAAGTGC TGGGATTAT AGGCGTGAGCC 1

```

KM Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KM protein therapy; vaccine; probe; diagnostic assay; detection;  
KM quantitation; restorative therapy; polymorphic; ds.

PN WO200140521-A2

PD 07-JUN-2001.

PF 30-NOV-2000; 2000WO-US032758.

PR 30-NOV-1999; 99US-0168138P.

PR 29-NOV-2000; 2000US-00726173.

PA (CURA-) CURAGEN CORP.

PI Shimkets RA, Leach M;

DR WPI; 2001-356160/37.

**PT** Polymorphic nucleic acid sequences, useful in genetic testing and therapy.

PS Claim 1; Page 56; 2653pp; English.

CC AAI73066to AAI79867 represent isolated human polymorphic polynucleotide  
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).  
CC AAM53114 to AAM53329 represent peptides related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC technology, and in vaccine production. (I) and the polypeptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides. For  
CC example, (I) may be used to treat disorders by rectifying mutations or  
CC deletions in a patient's genome that affect the activity of polypeptides  
CC by expressing inactive proteins or to supplement the patients own  
CC production of polypeptide. Additionally, (I) and its complementary  
CC sequences may also be used as DNA probes in diagnostic assays to detect

CC and quantitate the presence of similar nucleic acids in samples, and  
CC therefore which patients may be in need of restorative therapy. The  
CC polypeptides encoded by (1) may be used as antigens in the production of  
CC antibodies specific for polymorphic polypeptides. The antibodies may also  
CC be used to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples

Query Match 4.6%; Score 45.2; DB 1; Length 51;  
SQ Sequence 51 BP; 11 A; 15 C; 17 G; 8 T; 0 U; 0 Other;

QY	638	TGTCACCCAGGCTGGAGTGCAGTGCGCAATCTTGGCTCATTGCAACTC	68
Db	51	TGTGCCCAAGCTGGAGTGCAGTGCGCAATCTTGGCTCATTGCAACTC	2

DT	09-NOV-2001 (First entry)
XX	
DE	Human silent SNP containing nucleic acid SEQ:1495.

PN WO200140521-A2.

PD 07-JUN-2001.

PF 30-NOV-2000; 2000WO-US032758.

PR 30-NOV-1999; 99US-0168138P.

29-NOV-2000; 2000US-00726173.

PA (CURA-) CURAGEN CORP.

PI Shimkets RA, Leach M;

DR WPI; 2001-356160/37.

**PT** Polymorphic nucleic acid sequences, useful in genetic testing and therapy.

PS Claim 1; Page 511; 2653pp; English

AA173060 COAA179867 represent: isolated human polymorphic polynucleotide sequences (1), which contain single nucleotide polymorphisms (SNPs). AAM53114 to AAM53129 represent peptides related to human polymorphic polynucleotide sequences. The sequences can be used in gene and protein therapy, and in vaccine production. (1) and the polypeptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of polymorphic polypeptides. For example, (1) may be used to treat disorders by rectifying mutations or deletions in a patient's genome that affect the activity of polypeptides by expressing inactive proteins or to supplement the patients own production of polypeptide. Additionally, (1) and its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The polypeptides encoded by (1) may be used as antigens in the production of antibodies specific for polymorphic polypeptides. The antibodies may also be used to down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of polymorphic



CC polypeptides in samples  
XX Sequence 51 BP; 10 A; 15 C; 17 G; 9 T; 0 U; 0 Other;

Query Match 4.6%; Score 45.2; DB 1; Length 51;  
Best Local Similarity 94.0%; Pred. No. 1.3e+02;  
Matches 47; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 635 CTCTGTCACCCGAGGCGAGTGCAGTGCAGTCTTGGCTCACTGCAAC 684  
DB 50 CTCTGTCACCCGAGGCGAGTGCAGTGCAGTCTTGGCTCACTGCAAC 1

RESULT 38  
AA173064/C  
ID AA173064 standard; DNA; 51 BP.

XX AA173064;  
AC  
XX  
XX  
DT 09-NOV-2001 (first entry)

XX Human silent SNP containing nucleic acid SEQ.5.

XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KW protein therapy; vaccine; probe; diagnostic assay; detection;  
KW quantitation; restorative therapy; polymorphic; ds.

XX Homo sapiens.

XX WO200140521-A2.

XX 07-JUN-2001.

XX 30-NOV-2000; 2000MO-US032758.

XX 30-NOV-1999; 99US-0168138P.

XX 29-NOV-2000; 2000US-00726173.

XX (CURA-) CURAGEN CORP.

XX Shimkete RA, Leach M;

XX WPI; 2001-356160/37.

PT Polymorphic nucleic acid sequences, useful in genetic testing and  
XX therapy.

XX Claim 1; Page 55; 2653pp; English.

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX Sequence 51 BP; 14 A; 10 C; 19 G; 8 T; 0 U; 0 Other;

Query Match 4.5%; Score 44.8; DB 1; Length 51;  
Best Local Similarity 95.8%; Pred. No. 1.4e+02;

Matches 46; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 966 AATCTGGCTCACTGCAACCTTCTGCTCCCGGCTCAAGCATTTCTCC 1013  
DB 48 AATCTGGCTCACTGCAACCTTCTGCTCCCGGCTCAAGCATTTCTCC 1

RESULT 39  
AA177324  
ID AA177324 standard; DNA; 51 BP.

XX AA177324;

XX 09-NOV-2001 (first entry)

XX Human silent SNP containing nucleic acid SEQ.4265.

XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KW protein therapy; vaccine; probe; diagnostic assay; detection;  
KW quantitation; restorative therapy; polymorphic; ds.

XX Homo sapiens.

XX WO200140521-A2.

XX 07-JUN-2001.

XX 30-NOV-2000; 2000MO-US032758.

XX 30-NOV-1999; 99US-0168138P.

XX 29-NOV-2000; 2000US-00726173.

XX (CURA-) CURAGEN CORP.

XX Shimkete RA, Leach M;

XX WPI; 2001-356160/37.

PT Polymorphic nucleic acid sequences, useful in genetic testing and  
XX therapy.

XX Claim 1; Page 1815; 2653pp; English.

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

QY 843 CTGCTGCTGCTCCCAAGTCTGGGATTACAGGCTGACCAAC 890  
DB 4 CCGCTGCTGCTCCCAAGTCTGGGATTACAGGCTGACCAAC 51

Query Match 4.5%; Score 44.8; DB 1; Length 51;  
Best Local Similarity 95.8%; Pred. No. 1.4e+02;  
Matches 46; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
RESULT 40
AAA77498
ID AAA77498 standard; cDNA; 51 BP.
XX
AC AAA77498;
XX
DT 16-NOV-2000 (first entry)
XX
DE Human Alu subfamily S9 gene polymorphic site, SEQ ID NO:1181.
XX
KM Human, single nucleotide polymorphism; SNP; detection; identification;
KW gene therapy; ss.
XX
OS Homo sapiens.
XX
FH Key location/Qualifiers
FT variation replace(26,T)
FT /*tag= a
XX
PN WO200029623-A2.
XX
PD 25-MAY-2000.
XX
PF 17-NOV-1999; 99WO-US027293.
XX
PR 17-NOV-1998; 98US-0109024P.
PR 16-NOV-1999; 99US-00443199.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shinkets RA, Leach MD;
XX
DR WPI; 2000-387826/33.
XX
DR P-PSDB; AAB11817.
XX
PT Human nucleic acids containing single nucleotide polymorphisms, useful
PT for treating a subject suffering, or at risk from a pathology due to the
PT presence of a sequence polymorphism.
XX
PS Claim 1; Page 515; 543pp; English.
XX
CC Sequences AAA76318-A77509 represent 1192 human nucleic acid sequences
CC which contain single nucleotide polymorphisms (SNPs). Sequences 1 to 1112
CC (AAA76318-A77429) are consecutive pairs of nucleotides which contain
CC silent SNPs. Sequences 1113 to 1192 (AAA77430-A77509) are consecutive
CC pairs of nucleotides containing SNPs which result in changes in the
CC corresponding amino acid sequences (AAB11749-B11828). The SNPs in
CC sequences 1113 to 1128 (AAA77430-A77445) lead to conservative amino acid
CC changes, while those in sequences 1129 to 1186 (AAA77446-A77503) result
CC in non-conservative changes. The SNPs in sequences 1187 to 1192
CC (AAA77504-A77509) generate frameshift mutations. The invention also
CC relates to a method of detecting a polymorphic site in a nucleic acid and
CC a method of determining the relatedness of two nucleic acids. It also
CC encompasses peptides containing polymorphic sites, antibodies raised
CC against such peptides, and a method of detecting polymorphic
CC proteins/peptides using the antibodies. The nucleic acids are useful for
CC gene therapy of an individual having, suspected of having, or at risk of
CC developing a pathological condition due to the presence of a sequence
CC polymorphism. Such treatment would comprise administration of the wild-
CC type nucleic acid sequence. Antibodies raised against polymorphic
CC peptides can also be used in the treatment of such individuals
XX
SQ Sequence 51 BP; 12 A; 18 C; 10 G; 11 T; 0 U; 0 Other;
Query Match 4.5%; Score 44.6; DB 1; Length 51;
Best Local Similarity 92.2%; Pred. No. 1.4e+02;
Matches 47; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
RESULT 41
AAA77230
ID AAA77230 standard; cDNA; 51 BP.
XX
AC AAA77230;
XX
DT 16-NOV-2000 (first entry)
XX
DE Human clone CG43972482 polymorphic site, SEQ ID NO:913.
XX
KM Human, single nucleotide polymorphism; SNP; chromosome 8; detection;
KW identification; gene therapy; ss.
XX
OS Homo sapiens.
XX
FH Key location/Qualifiers
FT variation replace(26,C)
FT /*tag= a
XX
PN WO200029623-A2.
XX
PD 25-MAY-2000.
XX
PF 17-NOV-1999; 99WO-US027293.
XX
PR 17-NOV-1998; 98US-0109024P.
PR 16-NOV-1999; 99US-00443199.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shinkets RA, Leach MD;
XX
DR WPI; 2000-387826/33.
XX
DR P-PSDB; AAB11817.
XX
PT Human nucleic acids containing single nucleotide polymorphisms, useful
PT for treating a subject suffering, or at risk from a pathology due to the
PT presence of a sequence polymorphism.
XX
PS Claim 1; Page 433; 543pp; English.
XX
CC Sequences AAA76318-A77509 represent 1192 human nucleic acid sequences
CC which contain single nucleotide polymorphisms (SNPs). Sequences 1 to 1112
CC (AAA76318-A77429) are consecutive pairs of nucleotides which contain
CC silent SNPs. Sequences 1113 to 1192 (AAA77430-A77509) are consecutive
CC pairs of nucleotides containing SNPs which result in changes in the
CC corresponding amino acid sequences (AAB11749-B11828). The SNPs in
CC sequences 1113 to 1128 (AAA77430-A77445) lead to conservative amino acid
CC changes, while those in sequences 1129 to 1186 (AAA77446-A77503) result
CC in non-conservative changes. The SNPs in sequences 1187 to 1192
CC (AAA77504-A77509) generate frameshift mutations. The invention also
CC relates to a method of detecting a polymorphic site in a nucleic acid and
CC a method of determining the relatedness of two nucleic acids. It also
CC encompasses peptides containing polymorphic sites, antibodies raised
CC against such peptides, and a method of detecting polymorphic
CC proteins/peptides using the antibodies. The nucleic acids are useful for
CC gene therapy of an individual having, suspected of having, or at risk of
CC developing a pathological condition due to the presence of a sequence
CC polymorphism. Such treatment would comprise administration of the wild-
CC type nucleic acid sequence. Antibodies raised against polymorphic
CC peptides can also be used in the treatment of such individuals
XX
SQ Sequence 51 BP; 9 A; 11 C; 16 G; 15 T; 0 U; 0 Other;
Query Match 4.5%; Score 44.6; DB 1; Length 51;
Best Local Similarity 92.2%; Pred. No. 1.4e+02;
Matches 47; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
RESULT 42
AAL31459
ID AAL31459 standard; DNA; 51 BP.
XX
AC AAL31459;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #4667.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US035498.
XX
PR 28-DEC-1999; 99US-0173419P.
XX
PR 27-DEC-2000; 2000US-00173419.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shinketsu RA, Leach M;
XX
DR WPI; 2001-465210/50.
XX
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
XX oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
XX autoimmune diseases and infections.
XX
PS Claim 1; Page 2729; 4143pp; English.
XX
CC The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiotensin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-
CC protein coupled receptors and thioesterases. The present sequence is one
CC such oligonucleotide. The oligonucleotides and the peptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of the proteins listed above.
CC Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukemia), diseases of the nervous system and an infection of pathogenic
CC organisms
XX
SQ Sequence 51 BP; 11 A; 20 C; 12 G; 8 T; 0 U; 0 Other;
XX
Query Match 4.5%; Score 44.6; DB 1; Length 51;
Best Local Similarity 92.2%; Pred. No. 1.4e+02;
Matches 47; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 843 CTTGCTCTGGCTCCCAAGTCTGAGTACAGGCGTGAAGCCACCGCC 893
DB 1 CCGCGCTTGGCTCCCAAGTCTGAGTACAGGCGTGAAGCCACCGCC 51
RESULT 43
AAL29843
ID AAL29843 standard; DNA; 51 BP.
```

```
XX
AC AAL29843;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #3051.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US035498.
XX
PR 28-DEC-1999; 99US-0173419P.
XX
PR 27-DEC-2000; 2000US-00173419.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shinketsu RA, Leach M;
XX
DR WPI; 2001-465210/50.
XX
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
XX oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
XX autoimmune diseases and infections.
XX
PS Claim 1; Page 2260; 4143pp; English.
XX
CC The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiotensin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-
CC protein coupled receptors and thioesterases. The present sequence is one
CC such oligonucleotide. The oligonucleotides and the peptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of the proteins listed above.
CC Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukemia), diseases of the nervous system and an infection of pathogenic
CC organisms
XX
SQ Sequence 51 BP; 7 A; 24 C; 9 G; 11 T; 0 U; 0 Other;
XX
Query Match 4.5%; Score 44.6; DB 1; Length 51;
Best Local Similarity 92.2%; Pred. No. 1.4e+02;
Matches 47; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 974 CTCATGCAACCTCTGCTCCGCGGCTCAAGCATTTCTGTCAGCCT 1024
DB 1 CTCATGCAAGCTCTGCACTCCGCGGCTCAAGCATTTCTGTCAGCCT 51
RESULT 44
AAL173062/c
ID AAL173062 standard; DNA; 51 BP.
XX
AC AAL173062;
XX
```

DT 09-NOV-2001 (first entry)  
XX Human silent SNP containing nucleic acid SEQ:3.  
DE  
XX  
XX Human, single nucleotide polymorphism; SNP; genome; gene therapy;  
KW protein therapy; vaccine; probe; diagnostic assay; detection;  
KW quantitation; restorative therapy; polymorphic; ds.  
XX  
OS Homo sapiens.  
XX  
XX WO200140521-A2.  
XX  
XX 07-JUN-2001.  
XX  
XX 30-NOV-2000; 2000WO-US032758.  
XX  
XX 30-NOV-1999; 99US-0168138P.  
XX  
XX 29-NOV-2000; 2000US-00726173.  
XX  
XX (CURA-) CURAGEN CORP.  
XX  
XX Shimkets RA, Leach M;  
XX  
XX WPI; 2001-356160/37.  
XX  
XX Polymorphic nucleic acid sequences, useful in genetic testing and  
PT therapy.  
XX  
XX Claim 1; Page 55; 2653pp; English.  
XX  
XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).  
CC AA173114 to AA175329 represent peptides related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (I) and the polypeptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides. For  
CC example, (I) may be used to treat disorders by rectifying mutations or  
CC deletions in a patient's genome that affect the activity of polypeptides  
CC by expressing inactive proteins or to supplement the patient's own  
CC production of polypeptide. Additionally, (I) and its complementary  
CC sequences may also be used as DNA probes in diagnostic assays to detect  
CC and quantitate the presence of similar nucleic acids in samples, and  
CC therefore which patients may be in need of restorative therapy. The  
CC polypeptides encoded by (I) may be used as antigens in the production of  
CC antibodies specific for polymorphic polypeptides. The antibodies may also  
CC be used to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples  
XX  
XX Sequence 51 BP; 12 A; 11 C; 21 G; 7 T; 0 U; 0 Other;  
SQ  
Query Match 4.5%; Score 44.6; DB 1; Length 51;  
Best Local Similarity 92.2%; Pred. No. 1.4e+02;  
Matches 47; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 971 CGGCTCAGTCAACCTGCTCCGCGGCTCAAGGATCTCTGCTCAG 1021  
DB 51 CGGCTCAGTCAACCTGCTCCGCGGCTCAAGGATCTCTGCTCAG 1

RESULT 45  
AA177522/C  
ID AA177522 standard; DNA; 51 BP.  
XX  
XX AA177522;  
XX  
XX 09-NOV-2001 (first entry)  
XX  
XX Human silent SNP containing nucleic acid SEQ:4463.  
XX  
XX Human, single nucleotide polymorphism; SNP; genome; gene therapy;  
KW protein therapy; vaccine; probe; diagnostic assay; detection;  
KW

KW quantitation; restorative therapy; polymorphic; ds.  
XX  
XX Homo sapiens.  
XX  
XX WO200140521-A2.  
XX  
XX 07-JUN-2001.  
XX  
XX 30-NOV-2000; 2000WO-US032758.  
XX  
XX 30-NOV-1999; 99US-0168138P.  
XX  
XX 29-NOV-2000; 2000US-00726173.  
XX  
XX (CURA-) CURAGEN CORP.  
XX  
XX Shimkets RA, Leach M;  
XX  
XX WPI; 2001-356160/37.  
XX  
XX Polymorphic nucleic acid sequences, useful in genetic testing and  
PT therapy.  
XX  
XX Claim 1; Page 1876; 2653pp; English.  
XX  
XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).  
CC AA173114 to AA175329 represent peptides related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (I) and the polypeptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides. For  
CC example, (I) may be used to treat disorders by rectifying mutations or  
CC deletions in a patient's genome that affect the activity of polypeptides  
CC by expressing inactive proteins or to supplement the patient's own  
CC production of polypeptide. Additionally, (I) and its complementary  
CC sequences may also be used as DNA probes in diagnostic assays to detect  
CC and quantitate the presence of similar nucleic acids in samples, and  
CC therefore which patients may be in need of restorative therapy. The  
CC polypeptides encoded by (I) may be used as antigens in the production of  
CC antibodies specific for polymorphic polypeptides. The antibodies may also  
CC be used to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples  
XX  
XX Sequence 51 BP; 18 A; 14 C; 10 G; 9 T; 0 U; 0 Other;  
SQ  
Query Match 4.5%; Score 44.6; DB 1; Length 51;  
Best Local Similarity 92.2%; Pred. No. 1.4e+02;  
Matches 47; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 175 TTTTAGTAGATGAGATTTCTCCATGTTGGTCAAGGCTGCTCAACTCC 225  
DB 51 TTTTAGTAGATGAGATGAGGTTTCAACATGTTGGTCAAGGCTGCTCAACTCC 1

RESULT 46  
AA178388  
ID AA178388 standard; DNA; 51 BP.  
XX  
XX AA178388;  
XX  
XX 09-NOV-2001 (first entry)  
XX  
XX Human silent SNP containing nucleic acid SEQ:5329.  
XX  
XX Human, single nucleotide polymorphism; SNP; genome; gene therapy;  
KW protein therapy; vaccine; probe; diagnostic assay; detection;  
KW quantitation; restorative therapy; polymorphic; ds.  
XX  
XX Homo sapiens.  
XX  
XX WO200140521-A2.  
XX  
XX

PD 07-JUN-2001.  
XX  
PD 30-NOV-2000; 2000WO-US032758.  
XX  
PF 30-NOV-1999; 99US-0168138P.  
XX  
PR 29-NOV-2000; 2000US-00726173.  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
XX Shinkets RA, Leach M;  
PI WPI; 2001-356160/37.  
XX  
PT Polymorphic nucleic acid sequences, useful in genetic testing and  
therapy.  
PS Claim 1; Page 2141; 2653pp; English.  
XX  
XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).  
CC AA173114 to AA1753329 represent peptides related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (I) and the polypeptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides. For  
CC example, (I) may be used to treat disorders by rectifying mutations or  
CC deletions in a patient's genome that affect the activity of polypeptides  
CC by expressing inactive proteins or to supplement the patients own  
CC production of polypeptide. Additionally, (I) and its complementary  
CC sequences may also be used as DNA probes in diagnostic assays to detect  
CC and quantitate the presence of similar nucleic acids in samples, and  
CC therefore which patients may be in need of restorative therapy. The  
CC polypeptides encoded by (I) may be used as antigens in the production of  
CC antibodies specific for polymorphic polypeptides. The antibodies may also  
CC be used to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples  
XX  
SQ Sequence 51 BP; 10 A; 19 C; 13 G; 9 T; 0 U; 0 Other;  
XX  
Query Match 4.5%; Score 44.6; DB 1; Length 51;  
Best Local Similarity 92.2%; Pred. No. 1.4e+02;  
Matches 47; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 847 CCTCGGCTCCCAAGTGTGATTACAGCGCTGAGCCACACGCCCCG 897  
DB 1 CCTCGGCTCCCAAGTGTGATTACAGCGCTGAGCCACACGCCCCG 51  
XX  
RESULT 47  
AA179819  
ID AA179819 standard; DNA; 51 BP.  
XX  
XX AA179819;  
AC  
XX  
DT 09-NOV-2001 (first entry)  
XX  
XX Human nonconservative amino acid changing SNP nucleic acid SEQ:6760.  
DE  
XX  
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KW protein therapy; vaccine; probe; diagnostic assay; detection;  
KW quantitation; restorative therapy; polymorphic; ds.  
XX  
XX Homo sapiens.  
OS  
XX  
XX MO200140521-A2.  
PN  
XX  
XX 07-JUN-2001.  
PD  
XX  
XX 30-NOV-2000; 2000WO-US032758.  
PF  
XX  
XX 30-NOV-1999; 99US-0168138P.  
PR  
XX  
XX 29-NOV-2000; 2000US-00726173.  
PR

XX  
PA (CURA-) CURAGEN CORP.  
XX  
XX Shinkets RA, Leach M;  
PI WPI; 2001-356160/37.  
XX  
PT Polymorphic nucleic acid sequences, useful in genetic testing and  
therapy.  
PS Claim 1; Page 2573; 2653pp; English.  
XX  
XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).  
CC AA173114 to AA1753329 represent peptides related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (I) and the polypeptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides. For  
CC example, (I) may be used to treat disorders by rectifying mutations or  
CC deletions in a patient's genome that affect the activity of polypeptides  
CC by expressing inactive proteins or to supplement the patients own  
CC production of polypeptide. Additionally, (I) and its complementary  
CC sequences may also be used as DNA probes in diagnostic assays to detect  
CC and quantitate the presence of similar nucleic acids in samples, and  
CC therefore which patients may be in need of restorative therapy. The  
CC polypeptides encoded by (I) may be used as antigens in the production of  
CC antibodies specific for polymorphic polypeptides. The antibodies may also  
CC be used to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples  
XX  
SQ Sequence 51 BP; 8 A; 16 C; 15 G; 12 T; 0 U; 0 Other;  
XX  
Query Match 4.5%; Score 44.6; DB 1; Length 51;  
Best Local Similarity 92.2%; Pred. No. 1.4e+02;  
Matches 47; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 695 CGGGTCAAGTATTTCTCTGCCCCAGCTCTGTAGTACGCTGAGCTACG 745  
DB 1 CGGGTCAAGCATTTCTCTGCGCTGCGCTCTGTAGTACGCTGAGCTACG 51  
XX  
RESULT 48  
AA177677/C  
ID AA177677 standard; DNA; 51 BP.  
XX  
XX AA177677;  
AC  
XX  
DT 09-NOV-2001 (first entry)  
XX  
XX Human silent SNP containing nucleic acid SEQ:4618.  
DE  
XX  
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KW protein therapy; vaccine; probe; diagnostic assay; detection;  
KW quantitation; restorative therapy; polymorphic; ds.  
XX  
XX Homo sapiens.  
OS  
XX  
XX MO200140521-A2.  
PN  
XX  
XX 07-JUN-2001.  
PD  
XX  
XX 30-NOV-2000; 2000WO-US032758.  
PF  
XX  
XX 30-NOV-1999; 99US-0168138P.  
PR  
XX  
XX 29-NOV-2000; 2000US-00726173.  
PR  
XX  
XX (CURA-) CURAGEN CORP.  
PA  
XX  
XX Shinkets RA, Leach M;  
PI WPI; 2001-356160/37.  
DR

XX polymorphic nucleic acid sequences, useful in genetic testing and  
PT therapy.  
XX  
PS Claim 1; Page 1924; 2653pp; English.  
XX  
CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).  
CC AA153114 to AA153129 represent peptides related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (I) and the polypeptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides. For  
CC example, (I) may be used to treat disorders by rectifying mutations or  
CC deletions in a patient's genome that affect the activity of polypeptides  
CC by expressing inactive proteins or to supplement the patients own  
CC production of polypeptide. Additionally, (I) and its complementary  
CC sequences may also be used as DNA probes in diagnostic assays to detect  
CC and quantitate the presence of similar nucleic acids in samples, and  
CC therefore which patients may be in need of restorative therapy. The  
CC polypeptides encoded by (I) may be used as antigens in the production of  
CC antibodies specific for polymorphic polypeptides. The antibodies may also  
CC be used to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples  
XX  
SQ Sequence 51 BP; 12 A; 9 C; 21 G; 9 T; 0 U; 0 Other;  
Query Match 4.5%; Score 44.6; DB 1; Length 51;  
Best Local Similarity 92.2%; Pred. No. 1.4e+02;  
Matches 47; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Oy 971 CGGCTCACTGCACCTCTGCTCCCGGCTCAAGGATTCTCTCTCAG 1021  
Db 51 CGGCTCACTGCACCTCTGCTCCCGGCTCAAGGATTCTCTCTCAG 1  
RESULT 49  
AAH89407  
ID AAH89407 standard; DNA; 51 BP.  
AC AAH89407;  
XX  
DT 01-OCT-2001 (first entry)  
XX  
DE Human coding sequence polymorphic site SEQ ID NO: 188.  
XX  
XX Human; single nucleotide polymorphism; SNP; paternity test;  
KW forensic test; aberrant protein expression; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200151670-A2.  
XX  
XX 19-JUL-2001.  
PD  
XX 05-JAN-2001; 2001WO-US000322.  
PE  
XX 07-JAN-2000; 2000US-0174962P.  
PR  
XX (CURA-) CURAGEN CORP.  
PA  
XX Shimketa RA, Leach MD;  
PI  
XX WPI; 2001-451871/48.  
DR  
XX P-PSDB; AAM00294.  
PT Isolated human polynucleotides containing single nucleotide  
PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,  
PT infection and diabetes.  
XX  
PS Claim 1; Page 160; 475pp; English.

CC The present invention relates to human nucleic acids containing single  
CC nucleotide polymorphisms (SNPs). These can be used in forensic and  
CC paternity tests, and to aid in the treatment of diseases associated with  
CC aberrant protein expression, including cancer, amyloidosis, diabetes,  
CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,  
CC glomerulonephritis, haemolytic anaemia, thrombocytopenia, arthritis,  
CC meningitis, muscular disorders, dementia, neurological diseases, tubercous  
CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,  
CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or  
CC autoimmunity. The present sequence is a polymorphism-containing  
CC oligonucleotide fragment of the invention  
XX  
SQ Sequence 51 BP; 8 A; 23 C; 8 G; 12 T; 0 U; 0 Other;  
Query Match 4.5%; Score 44.6; DB 1; Length 51;  
Best Local Similarity 92.2%; Pred. No. 1.4e+02;  
Matches 47; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Oy 974 CTCACCTGCACCTCTGCTCCCGGCTCAAGGATTCTCTCTCAGCCT 1024  
Db 1 CTCACCTGCACCTCTGCTCCCGGCTCAAGGATTCTCTCTCAGCCT 51  
RESULT 50  
AAH89406  
ID AAH89406 standard; DNA; 51 BP.  
AC AAH89406;  
XX  
DT 01-OCT-2001 (first entry)  
XX  
DE Human coding sequence polymorphic site SEQ ID NO: 187.  
XX  
XX Human; single nucleotide polymorphism; SNP; paternity test;  
KW forensic test; aberrant protein expression; de.  
XX  
OS Homo sapiens.  
XX  
PN WO200151670-A2.  
XX  
XX 19-JUL-2001.  
PD  
XX 05-JAN-2001; 2001WO-US000322.  
PE  
XX 07-JAN-2000; 2000US-0174962P.  
PR  
XX (CURA-) CURAGEN CORP.  
PA  
XX Shimketa RA, Leach MD;  
PI  
XX WPI; 2001-451871/48.  
DR  
XX P-PSDB; AAM00293.  
PT Isolated human polynucleotides containing single nucleotide  
PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,  
PT infection and diabetes.  
XX  
PS Claim 1; Page 159; 475pp; English.  
XX  
CC The present invention relates to human nucleic acids containing single  
CC nucleotide polymorphisms (SNPs). These can be used in forensic and  
CC paternity tests, and to aid in the treatment of diseases associated with  
CC aberrant protein expression, including cancer, amyloidosis, diabetes,  
CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,  
CC glomerulonephritis, haemolytic anaemia, thrombocytopenia, arthritis,  
CC meningitis, muscular disorders, dementia, neurological diseases, tubercous  
CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,  
CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or  
CC autoimmunity. The present sequence is a polymorphism-containing  
CC oligonucleotide fragment of the invention  
XX  
SQ Sequence 51 BP; 8 A; 22 C; 8 G; 13 T; 0 U; 0 Other;

Query Match 4.5%; Score 44.6; DB 1; Length 51;  
Best Local Similarity 92.2%; Pred. No. 1.4e+02;  
Matches 47; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 674 CTCACGCAACCTGCTCCGCGGTCAAGTATTCCTGCGCCAGGCT 724  
DB 1 CTCACGCAACCTGCTCCGCGGTCAAGTATTCCTGCGCCAGGCT 51

## RESULT 51

ABL00260  
ID ABL00260 standard; DNA; 51 BP.

AC ABL00260;

XX 05-MAR-2002 (first entry)

XX Human silent noncoding SNP oligonucleotide SEQ ID NO:251.

XX Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic;

KW immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;

KW autoimmune disease; inflammation; cancer; nervous system disease;

KW infection; polymorphic protein; ds.

XX Homo sapiens.

XX MO200138586-A2.

XX 31-MAY-2001.

XX 22-NOV-2000; 2000WO-US032311.

XX 24-NOV-1999; 99US-0167383P.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach M;

XX WPI; 2001-355949/37.

XX Isolated human nucleic acids comprising one or more single nucleotide

XX polymorphisms, useful for treating a subject suffering from a pathology,

XX e.g. autoimmune diseases, ascribed to the presence of a sequence

XX polymorphism.

XX Claim 1; Page 323; 674pp; English.

XX ABL00010 to ABL01104 represent human nucleic acid oligonucleotides

XX comprising one or more single nucleotide polymorphisms (SNPs). ABB56531

XX to ABB56903 represent human peptides encoded by some of the SNP

XX oligonucleotides. The sequences from the present invention can have

XX immunosuppressive, cytostatic, antiinflammatory, neuroprotective and

XX antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides

XX and antibodies from the present invention can be used for treating a

XX subject suffering from, at risk for, or suspected of, suffering from a

XX pathology ascribed to the presence of a sequence polymorphism. The

XX the nervous system, and infection by pathogenic microorganisms. The SNPs

XX are also useful for determining which forms of a characterised

XX polymorphism are present in individuals. The antibodies may be used in

XX the detection, quantitation and/or cellular or tissue localisation of a

XX polymorphic protein (e.g., for use in measuring levels of the polymorphic

XX protein within appropriate physiological samples)

XX Sequence 51 BP; 9 A; 17 C; 13 G; 12 T; 0 U; 0 Other;

XX Query Match 4.5%; Score 44.6; DB 1; Length 51;

XX Best Local Similarity 92.2%; Pred. No. 1.4e+02;

XX Matches 47; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 954 GTGCAATGGCAATCTGGCTCACTGCAACCTGCTCCGCGGTCAAG 1004

DB 1 GTGCAATGGCAATCTGGCTCACTGCAACCTGCTCCGCGGTCAAG 51

## RESULT 52

AAH89761  
ID AAH89761 standard; DNA; 50 BP.

AC AAH89761;

XX 01-OCT-2001 (first entry)

XX Human coding sequence polymorphic site SEQ ID NO: 542.

KW Human; single nucleotide polymorphism; SNP; paternity test;

KW forensic test; aberrant protein expression; ds.

XX Homo sapiens.

XX MO200151670-A2.

XX 19-JUL-2001.

XX 05-JAN-2001; 2001WO-US000322.

XX 07-JAN-2000; 2000US-0174962P.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach MD;

XX WPI; 2001-451871/48.

XX P-P-SDB; AAM00644.

XX Isolated human polynucleotides containing single nucleotide

XX polymorphisms, useful for the treatment and diagnosis of e.g. cancer,

XX infection and diabetes.

XX Claim 1; Page 260; 475pp; English.

XX The present invention relates to human nucleic acids containing single

XX nucleotide polymorphisms (SNPs). These can be used in forensic and

XX paternity tests, and to aid in the treatment of diseases associated with

XX aberrant protein expression, including cancer, amyloidosis, diabetes,

XX Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,

XX glomerulonephritis, haemolytic anaemia, thrombocytopenia, arthritis,

XX meningitis, muscular disorders, dementia, neurological diseases, tubercu-

XX sclerosis, male infertility, hypercalcaemia, blood pressure disorders,

XX osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or

XX autoimmunity. The present sequence is a polymorphism-containing

XX oligonucleotide fragment of the invention

XX Sequence 50 BP; 10 A; 10 C; 11 G; 19 T; 0 U; 0 Other;

XX Query Match 4.4%; Score 43.8; DB 1; Length 50;

XX Best Local Similarity 95.7%; Pred. No. 1.5e+02;

XX Matches 45; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 750 CCACCAAGCCTAGCTAATTTTGTATTTTGTATTTAGTAGAGATGCGGTT 796

DB 3 CCACCAAGCCTAGCTAATTTTGTATTTTGTATTTAGTAGAGATGCGGTT 49

RESULT 53

AAH89763

ID AAH89763 standard; DNA; 50 BP.

AC AAH89763;

XX 01-OCT-2001 (first entry)

XX Human coding sequence polymorphic site SEQ ID NO: 544.

XX Human; single nucleotide polymorphism; SNP; paternity test;

XX forensic test; aberrant protein expression; ds.

```
XX OS Homo sapiens.
XX PN WO200151670-A2.
XX PD 19-JUL-2001.
XX PF 05-JAN-2001; 2001WO-US000322.
XX PR 07-JAN-2000; 2000US-0174962P.
XX PA (CURA-) CURAGEN CORP.
XX PI Shimkets RA, Leach MD;
XX DR WPI; 2001-451871/48.
XX P-PSDB; AAM00646.
XX PT Isolated human polynucleotides containing single nucleotide
XX PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
XX PT infection and diabetes.
XX PS Claim 1; Page 260; 475pp; English.
XX CC The present invention relates to human nucleic acids containing single
XX CC nucleotide polymorphisms (SNPs). These can be used in forensic and
XX CC paternity tests, and to aid in the treatment of diseases associated with
XX CC aberrant protein expression, including cancer, amyloidosis, diabetes,
XX CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
XX CC glomerulonephritis, haemolytic anaemia, thrombocytopenia, arthritis,
XX CC meningitis, muscular disorders, dementia, neurological diseases, tubercu
XX CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,
XX CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or
XX CC autoimmunity. The present sequence is a polymorphism-containing
XX CC oligonucleotide fragment of the invention
XX SQ Sequence 50 BP; 10 A; 10 C; 11 G; 19 T; 0 U; 0 Other;
XX
Query Match 4.4%; Score 43.8; DB 1; Length 50;
Best Local Similarity 95.7%; Pred.No.1.5e+02;
Matches 45; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 750 CCACGACGCGCTAATTTTGTATTTTGTATTTAGTAGAGATGGGCTT 796
Db 2 CCACGACGCGCTAATTTTGTATTTTGTATTTAGTAGAGATGGGCTT 48
RESULT 54
AAH89759
ID AAH89759 standard; DNA; 50 BP.
XX AC AAH89759;
XX DT 01-OCT-2001 (first entry)
XX DE Human coding sequence polymorphic site SEQ ID NO: 540.
XX DE Human; single nucleotide polymorphism; SNP; paternity test;
XX KM forensic test; aberrant protein expression; ds.
XX KM Homo sapiens.
XX OS Homo sapiens.
XX PN WO200151670-A2.
XX PD 19-JUL-2001.
XX PF 05-JAN-2001; 2001WO-US000322.
XX PR 07-JAN-2000; 2000US-0174962P.
XX PA (CURA-) CURAGEN CORP.
XX PI Shimkets RA, Leach MD;
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XX XX WPI; 2001-451871/48.
XX DR P-PSDB; AAM00642.
XX XX Isolated human polynucleotides containing single nucleotide
XX PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
XX PT infection and diabetes.
XX PS Claim 1; Page 259; 475pp; English.
XX CC The present invention relates to human nucleic acids containing single
XX CC nucleotide polymorphisms (SNPs). These can be used in forensic and
XX CC paternity tests, and to aid in the treatment of diseases associated with
XX CC aberrant protein expression, including cancer, amyloidosis, diabetes,
XX CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
XX CC glomerulonephritis, haemolytic anaemia, thrombocytopenia, arthritis,
XX CC meningitis, muscular disorders, dementia, neurological diseases, tubercu
XX CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,
XX CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or
XX CC autoimmunity. The present sequence is a polymorphism-containing
XX CC oligonucleotide fragment of the invention
XX SQ Sequence 50 BP; 10 A; 11 C; 11 G; 18 T; 0 U; 0 Other;
XX
Query Match 4.4%; Score 43.8; DB 1; Length 50;
Best Local Similarity 95.7%; Pred.No.1.5e+02;
Matches 45; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 750 CCACGACGCGCTAATTTTGTATTTTGTATTTAGTAGAGATGGGCTT 796
Db 4 CCACGACGCGCTAATTTTGTATTTTGTATTTAGTAGAGATGGGCTT 50
RESULT 55
AAI75600/C
ID AAI75600 standard; DNA; 51 BP.
XX AC AAI75600;
XX DT 09-NOV-2001 (first entry)
XX DE Human silent SNP containing nucleic acid SEQ:2541.
XX DE Human; single nucleotide polymorphism; SNP; genome; gene therapy;
XX KM protein therapy; vaccine; probe; diagnostic assay; detection;
XX KM quantitation; restorative therapy; polymorphic; ds.
XX OS Homo sapiens.
XX PN WO200140521-A2.
XX PD 07-JUN-2001.
XX PF 30-NOV-2000; 2000WO-US032758.
XX PR 30-NOV-1999; 99US-0168138P.
XX PR 29-NOV-2000; 2000US-00726173.
XX PA (CURA-) CURAGEN CORP.
XX PI Shimkets RA, Leach M;
XX DR WPI; 2001-356160/37.
XX PT Polymorphic nucleic acid sequences, useful in genetic testing and
XX PT therapy.
XX PS Claim 1; Page 829; 2653pp; English.
XX CC AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide
XX CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
XX CC AAM53114 to AAM53129 represent peptides related to human polymorphic
XX CC polynucleotide sequences. The sequences can be used in gene and protein
```



therapy, and in vaccine production. (1) and the polypeptides encoded by CC them may be used in the prevention, diagnosis and treatment of diseases CC associated with inappropriate expression of polymorphic polypeptides. For CC example, (1) may be used to treat disorders by rectifying mutations or CC deletions in a patient's genome that affect the activity of polypeptides CC by expressing inactive proteins or to supplement the patients own CC production of polypeptide. Additionally, (1) and its complementary CC sequences may also be used as DNA probes in diagnostic assays to detect CC and quantitate the presence of similar nucleic acids in samples, and CC therefore which patients may be in need of restorative therapy. The CC polypeptides encoded by (1) may be used as antigens in the production of CC antibodies specific for polymorphic polypeptides. The antibodies may also CC be used to down regulate expression and activity. The antibodies may also CC be used as diagnostic agents for detecting the presence of polymorphic CC polypeptides in samples

SQ Sequence 51 BP; 13 A; 14 C; 16 G; 8 T; 0 U; 0 Other;

Query Match 4.4%; Score 43.8; DB 1; Length 51;  
Best Local Similarity 95.7%; Pred. No. 1.5e+02;  
Matches 45; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 634 ACTGTGTACCCGAGTGCAGTGGCGCAATCTTGCTGACTG 680  
|||||  
DB 48 ACTGTGTCCGCGAGGCTGGAGTGCAGTGCACAACTCTGCTCAGT 2

RESULT 56  
AD12550/C  
ID AD12550 standard; DNA; 50 BP.  
XX  
AC AD12550;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE Mutant human BRCA1 genomic DNA resulting from deletion 5 SeqID 33.  
XX  
KM ds; cancer; human; tumour suppressor;  
KM breast cancer susceptibility gene 1; BRCA1; repetitive Alu;  
KM ovarian cancer; recombination; mutant.  
XX  
OS Homo sapiens.  
XX  
PN MO2003104474-A2.  
XX  
PD 18-DEC-2003.  
XX  
PF 09-JUN-2003; 2003MO-US018098.  
XX  
PR 07-JUN-2002; 2002US-0387132P.  
PR 09-AUG-2002; 2002US-0402430P.  
XX  
PA (MYRI-) MYRIAD GENETICS INC.  
XX  
PI Scholl T, Hendrickson BC, Ward B, Pruss D;  
XX WPI; 2004-062369/06.  
XX  
DR  
XX  
PT Predicting a predisposition to cancer in a patient comprising detecting a  
PT deletion in the BRCA1 gene that results from the unequal crossover  
PT between a pair of repetitive sequences in the BRCA1 gene.  
XX  
PS Disclosure; SEQ ID NO 33; 59pp; English.  
XX  
XX This invention relates to a novel method for predicting a predisposition  
CC to cancer in a patient by detecting large deletions in the human tumour  
CC suppressor gene identified as the breast cancer susceptibility gene 1  
CC (BRCA1). Specifically, it refers to deletions that result from the  
CC unequal crossover between a pair of repetitive Alu sequences in the BRCA1  
CC gene, such that the recombined nucleotide sequence containing the  
CC deletion indicates a predisposition to breast and ovarian cancer. The  
CC present invention describes newly discovered deletion mutations that are  
CC believed to be deleterious and cause significant alterations in the

structure or biochemical function of BRCA1. Accordingly, it provides  
CC methods for detecting such mutants, as well as identifying and screening  
CC for cytostatic compounds useful for treating or preventing cancers  
CC associated with a BRCA1 genetic variant. This polynucleotide is a mutant  
CC human BRCA1 genomic DNA fragment that arises as a result of a  
CC recombination event (deletion 5), which causes the omission of exons 15  
CC and 16, given in an exemplification of the invention.

SQ Sequence 50 BP; 13 A; 12 C; 15 G; 10 T; 0 U; 0 Other;

Query Match 4.4%; Score 43.6; DB 1; Length 50;  
Best Local Similarity 92.0%; Pred. No. 1.6e+02;  
Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 695 CCGGTTCAAGTTATTTCTCTGCCCCAGCCTCTGTAGTACGCTGACTACA 744  
|||||  
DB 50 CCGGTTCAAGCAATTTCTCTGCTGAGCTCTGAGTACGCTGACTACA 1

RESULT 57  
AAL29844  
ID AAL29844 standard; DNA; 51 BP.  
XX  
AC AAL29844;  
XX  
DT 24-JAN-2002 (first entry)  
XX  
DE Human SNP oligonucleotide #3052.  
XX  
KM Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
KM neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;  
KM amyloid protein; angiotensin; apoptosis related protein; cadherin;  
KM cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
KM complement related protein; cytochrome; kinesin; cytokine; interferon;  
KM interleukin; G-protein coupled receptor; thioesterase; inflammation;  
KM multifactorial disease; autoimmune disease; infection;  
KM nervous system disease; ss.  
XX  
OS Homo sapiens.  
XX  
PN MO200147944-A2.  
XX  
PD 05-JUL-2001.  
XX  
PF 28-DEC-2000; 2000MO-US035498.  
XX  
PR 28-DEC-1999; 99US-0173419P.  
PR 27-DEC-2000; 2000US-00173419.  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
PI Shinkete RA, Leach M;  
XX WPI; 2001-465210/50.  
XX  
DR  
XX  
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,  
PT autoimmune diseases and infections.  
XX  
PS Claim 1; Page 2260; 4143pp; English.  
XX  
XX The present invention relates to oligonucleotides encoding polymorphic  
CC variants of proteins related to amylases, amyloid proteins, angiotensin,  
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
CC histones, kinases, colony stimulating factors, complement related  
CC proteins, cytochromes, kinesins, cytokines, interferon, interleukins, G-  
CC protein coupled receptors and thioesterases. The present sequence is one  
CC such oligonucleotide. The oligonucleotides and the peptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of the proteins listed above.  
CC Disorders that may be prevented, diagnosed and/or treated include  
CC multifactorial diseases with a genetic component, such as autoimmune  
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,

CC systemic lupus erythromatous and Grave's disease), inflammation, cancer  
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
CC leukaemia), diseases of the nervous system and an infection of pathogenic  
CC organisms

XX Sequence 51 BP; 9 A; 20 C; 12 G; 10 T; 0 U; 0 Other;

Query Match 4.4%; Score 43.6; DB 1; Length 51;  
Best Local Similarity 92.0%; Pred. No. 1.6e+02;  
Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 990 CCTCCGGGCTACAGATTCTCTGCTCAGCTTCCCAAGAGCTGGGA 1039  
DB 2 CCTCCGGGCTTCCAGGATTCTCCGCTCAGCTTCCCAAGAGCTGGGA 51

RESULT 58  
AA173532/c  
ID AA173532 standard; DNA; 51 BP.

XX AA173532;

DT 09-NOV-2001 (first entry)

DE Human silent SNP containing nucleic acid SEQ:473.

XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KM protein therapy; vaccine; probe; diagnostic assay; detection;  
KW quantitation; restorative therapy; polymorphic; ds.

XX Homo sapiens.

XX WO200140521-A2.

PD 07-JUN-2001.

PF 30-NOV-2000; 2000WO-US032758.

PR 30-NOV-1999; 99US-0168138P.

PR 29-NOV-2000; 2000US-00726173.

XX (CURA-) CURAGEN CORP.

PI Shimkets RA, Leach M;

DR WPI; 2001-356160/37.

PT Polymorphic nucleic acid sequences, useful in genetic testing and  
therapy.

PS Claim 1; Page 199; 2653pp; English.

CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
sequences (I), which contain single nucleotide polymorphisms (SNPs).

CC AA173114 to AA175329 represent peptides related to human polymorphic  
polynucleotide sequences. The sequences can be used in gene and protein  
therapy, and in vaccine production. (I) and the polypeptides encoded by  
them may be used in the prevention, diagnosis and treatment of diseases  
associated with inappropriate expression of polymorphic polypeptides. For  
example, (I) may be used to treat disorders by rectifying mutations or  
deletions in a patient's genome that affect the activity of polypeptides  
by expressing inactive proteins or to supplement the patients own  
production of polypeptide. Additionally, (I) and its complementary  
sequences may also be used as DNA probes in diagnostic assays to detect  
and quantitate the presence of similar nucleic acids in samples, and  
therefore which patients may be in need of restorative therapy. The  
polypeptides encoded by (I) may be used as antigens in the production of  
antibodies specific for polymorphic polypeptides. The antibodies may also  
be used to down regulate expression and activity. The antibodies may also  
be used as diagnostic agents for detecting the presence of polymorphic  
polypeptides in samples

XX Sequence 51 BP; 10 A; 14 C; 18 G; 9 T; 0 U; 0 Other;

Query Match 4.4%; Score 43.6; DB 1; Length 51;  
Best Local Similarity 92.0%; Pred. No. 1.6e+02;  
Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 842 GCTTCGCTCGGCTTCCCAAGAGTCTGGAGTTACAGGCTGACACAG 891  
DB 50 GCTTCGCTCGGCTTCCCAAGAGTCTGGAGTTACAGGCTGACACAGT 1

RESULT 59  
AA179585/c  
ID AA179585 standard; DNA; 51 BP.

XX AA179585;

DT 09-NOV-2001 (first entry)

DE Human silent SNP containing nucleic acid SEQ:6526.

XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KM protein therapy; vaccine; probe; diagnostic assay; detection;  
KW quantitation; restorative therapy; polymorphic; ds.

XX Homo sapiens.

XX WO200140521-A2.

PD 07-JUN-2001.

PF 30-NOV-2000; 2000WO-US032758.

PR 30-NOV-1999; 99US-0168138P.

PR 29-NOV-2000; 2000US-00726173.

XX (CURA-) CURAGEN CORP.

PI Shimkets RA, Leach M;

DR WPI; 2001-356160/37.

PT Polymorphic nucleic acid sequences, useful in genetic testing and  
therapy.

PS Claim 1; Page 2504; 2653pp; English.

CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
sequences (I), which contain single nucleotide polymorphisms (SNPs).

CC AA173114 to AA175329 represent peptides related to human polymorphic  
polynucleotide sequences. The sequences can be used in gene and protein  
therapy, and in vaccine production. (I) and the polypeptides encoded by  
them may be used in the prevention, diagnosis and treatment of diseases  
associated with inappropriate expression of polymorphic polypeptides. For  
example, (I) may be used to treat disorders by rectifying mutations or  
deletions in a patient's genome that affect the activity of polypeptides  
by expressing inactive proteins or to supplement the patients own  
production of polypeptide. Additionally, (I) and its complementary  
sequences may also be used as DNA probes in diagnostic assays to detect  
and quantitate the presence of similar nucleic acids in samples, and  
therefore which patients may be in need of restorative therapy. The  
polypeptides encoded by (I) may be used as antigens in the production of  
antibodies specific for polymorphic polypeptides. The antibodies may also  
be used to down regulate expression and activity. The antibodies may also  
be used as diagnostic agents for detecting the presence of polymorphic  
polypeptides in samples

XX Sequence 51 BP; 11 A; 14 C; 17 G; 9 T; 0 U; 0 Other;

Query Match 4.4%; Score 43.6; DB 1; Length 51;  
Best Local Similarity 92.0%; Pred. No. 1.6e+02;  
Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 646 AGCTGAGTGCAGTGGCGCAATCTTGCTCATGCAACTCTGCTCC 695





XX 26-APR-2001.  
PD 13-OCT-2000; 2000MO-US028436.  
XX 15-OCT-1999; 99US-0160096P.  
XX (ORCH-) ORCHID BIOSCIENCES INC.  
XX Picoult-Newburg L, Pohl M;  
XX WPI; 2001-290930/30.  
XX New genotyping oligonucleotide, useful for detecting the presence,  
PT absence or identity of single polynucleotide polymorphism in a nucleic  
PT acid sample.  
XX  
XX Claim 1; Page 56; 83pp; English.  
XX  
XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
CC primer extension (SNPE) primers, and the sequences of regions flanking  
CC sites of single nucleotide polymorphisms SNPs. The present invention  
CC includes kits for determining the presence or absence of a SNP, using the  
CC oligonucleotides of the invention. The PCR primers are used to amplify a  
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.  
CC The oligonucleotides are useful for genotyping a nucleic acid sample by  
CC performing a single-nucleotide primer extension reaction. The  
CC oligonucleotides are useful for determining the presence, absence or  
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
CC assess by association analysis the genotype of an individual or group of  
CC individuals, having a pathological phenotypic trait suspected of being  
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular  
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,  
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
CC traits also include symptoms of or susceptibility to multifactorial  
CC disease of which a component is or may be genetic such as autoimmune  
CC diseases, including rheumatoid arthritis, multiple sclerosis,  
CC inflammation, cancer, nervous system diseases and infection by pathogenic  
CC microorganism. The method is also useful in forensic investigations and  
CC paternity analysis. The present sequence represents a fragment of human  
CC DNA flanking the site of a single nucleotide polymorphism  
XX  
XX  
XX Sequence 51 BP; 9 A; 16 C; 13 G; 13 T; 0 U; 0 Other;  
SQ  
XX  
XX Query Match 4.4%; Score 43.6; DB 1; Length 51;  
XX Best Local Similarity 92.0%; Pred. No. 1.6e+02;  
XX Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
OY 645 CAGGCTGAGTGCAGTGGCGCAATCTTGCTCACTGCACCTTGCTCC 694  
DB 1 CAGGCTGAGTGCAGTGGCGCAATCTTGCTCACTGCACCTTGCTCC 50

RESULT 65  
AA173065/c  
ID AA173065 standard; DNA; 51 BP.  
XX  
XX AA173065;  
XX  
XX 09-NOV-2001 (first entry)  
XX  
XX Human silent SNP containing nucleic acid SEQ.6.  
XX  
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KW protein therapy; vaccine; probe; diagnostic assay; detection;  
KM quantitation; restorative therapy; polymorphic; ds.  
XX  
XX Homo sapiens.  
XX  
XX W0200140521-A2.  
XX  
XX 07-JUN-2001.

XX 30-NOV-2000; 2000MO-US032758.  
XX 30-NOV-1999; 99US-0168138P.  
XX 29-NOV-2000; 2000US-00726173.  
XX (CURA-) CURAGEN CORP.  
XX Shinkets RA, Leach M;  
XX WPI; 2001-356160/37.  
XX  
XX Polymorphic nucleic acid sequences, useful in genetic testing and  
PT therapy.  
XX  
XX Claim 1; Page 56; 2653pp; English.  
XX  
XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).  
CC AA173114 to AA175329 represent peptides related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (I) and the polypeptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides. For  
CC example, (I) may be used to treat disorders by rectifying mutations or  
CC deletions in a patient's genome that affect the activity of polypeptides  
CC by expressing inactive proteins or to supplement the patients own  
CC production of polypeptide. Additionally, (I) and its complementary  
CC sequences may also be used as DNA probes in diagnostic assays to detect  
CC and quantitate the presence of similar nucleic acids in samples, and  
CC therefore which patients may be in need of restorative therapy. The  
CC polypeptides encoded by (I) may be used as antigens in the production of  
CC antibodies specific for polymorphic polypeptides. The antibodies may also  
CC be used to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples  
XX  
XX  
XX Sequence 51 BP; 13 A; 10 C; 20 G; 8 T; 0 U; 0 Other;  
SQ  
XX  
XX Query Match 4.4%; Score 43.2; DB 1; Length 51;  
XX Best Local Similarity 93.8%; Pred. No. 1.7e+02;  
XX Matches 45; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 966 AATCTGGCTCACTGCACCTTGCTCCCGGCTCAACGATTCTCC 1013  
DB 48 AATCTGGCTCACTGCACCTTGCTCCCGGCTCAACGATTCTCC 1

RESULT 66  
AA177325  
ID AA177325 standard; DNA; 51 BP.  
XX  
XX AA177325;  
XX  
XX 09-NOV-2001 (first entry)  
XX  
XX Human silent SNP containing nucleic acid SEQ.4266.  
XX  
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KW protein therapy; vaccine; probe; diagnostic assay; detection;  
KM quantitation; restorative therapy; polymorphic; ds.  
XX  
XX Homo sapiens.  
XX  
XX W0200140521-A2.  
XX  
XX 07-JUN-2001.  
XX  
XX 30-NOV-2000; 2000MO-US032758.  
XX  
XX 30-NOV-1999; 99US-0168138P.  
XX  
XX 29-NOV-2000; 2000US-00726173.  
XX

PA	(CURA-) CURAGEN CORP.
XX	
P1	Shimkets RA, Leach M;
XX	
DR	WPI; 2001-356160/37.
XX	
PT	Polymorphic nucleic acid sequences, useful in genetic testing and therapy.
PS	Claim 1; Page 1815; 2653pp; English.
CC	AAT73060 to AAT79867 represent isolated human polymorphic polynucleotide sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC	AAM53114 to AAM53129 represent peptides related to human polymorphic polynucleotide sequences. The sequences can be used in gene and protein therapy, and in vaccine production. (I) and the polypeptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of polymorphic polypeptides. For example, (I) may be used to treat disorders by rectifying mutations or deletions in a patient's genome that affect the activity of polypeptides by expressing inactive proteins or to supplement the patients own sequences of polypeptide. Additionally, (I) and its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The polypeptides encoded by (I) may be used as antigens in the production of antibodies specific for polymorphic polypeptides. The antibodies may also be used to down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of polymorphic polypeptides in samples
SQ	Sequence 51 BP; 8 A; 20 C; 14 G; 9 T; 0 U; 0 Other;
	Query Match            4.4%; Score 43.2; DB 1; Length 51; Best Local Similarity 93.8%; Pred. No. 1.7e+02; Matches 45; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY	843 CCTGCCTGGGCTCCCAAGTGTGGATTACAGCGTGAGCCACC 890           4 CCCGCCCTGGCCTCCCAAGTGTGGATTACAGCGTGAGCCACC 51
D6	
RESULT 67	
ID	AAA77231 standard; cDNA; 51 BP.
AA	AAA77231
AC	AAA77231;
XX	
DT	16-NOV-2000 (first entry)
XX	
DE	Human clone cg43972482 polymorphic site, SEQ ID NO:914.
XX	
KW	Human; single nucleotide polymorphism; SNP; chromosome 8; detection; identification; gene therapy; ss.
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	variation replace(26,T) /*tag= a
FN	WO200029623-A2.
PD	25-MAY-2000.
XX	
PF	17-NOV-1999; 99MO-US0277293.
XX	
PR	17-NOV-1998; 98US-0109024P.
XX	
PR	16-NOV-1999; 99US-00443199.
XX	
PA	(CURA-) CURAGEN CORP.
XX	
P1	Shimkets RA, Leach MD;

XX	WPI, 2000-387826/33.
DR	
XX	
PT	Human nucleic acids containing single nucleotide polymorphisms, useful
PT	for treating a subject suffering, or at risk from a pathology due to the
PT	presence of a sequence polymorphism.
XX	
XX	
PS	Claim 1; Page 433; 543pp; English.
XX	
CC	Sequences AAA76318-A77509 represent 1192 human nucleic acid sequences
CC	which contain single nucleotide polymorphisms (SNPs). Sequences 1 to 1112
CC	(AAA76318-A77429) are consecutive pairs of nucleotides which contain
CC	silent SNPs. Sequences 1113 to 1192 (AAA77430-A77509) are consecutive
CC	pairs of nucleotides containing SNPs which result in changes in the
CC	corresponding amino acid sequences (AAB11749-B11828). The SNPs in
CC	sequences 1113 to 1128 (AAA77430-A77445) lead to conservative amino acid
CC	changes, while those in sequences 1129 to 1186 (AAA77446-A77503) result
CC	in non-conservative changes. The SNPs in sequences 1187 to 1192
CC	(AAA77504-A77509) generate frameshift mutations. The invention also
CC	relates to a method of detecting a polymorphic site in a nucleic acid and
CC	a method of determining the relatedness of two nucleic acids. It also
CC	encompasses peptides containing polymorphic sites, antibodies raised
CC	against such peptides, and a method of detecting polymorphic
CC	proteins/peptides using the antibodies. The nucleic acids are useful for
CC	gene therapy of an individual having, suspected of having, or at risk of
CC	developing a pathological condition due to the presence of a sequence
CC	polymorphism. Such treatment would comprise administration of the wild-
CC	type nucleic acid sequence. Antibodies raised against polymorphic
CC	peptides can also be used in the treatment of such individuals
XX	
SQ	Sequence 51 BP; 9 A; 12 C; 16 G; 14 T; 0 U; 0 Other;
XX	
Query Match	4.3%; Score 43; DB 1; Length 51;
Best Local Similarity	90.2%; Pred. No. 1.7e+02;
Matches	46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX	
QY	177 TTAGTAGAGAGAGAGCTTCTCCAGCTGTCAGGCTGCTCGAATCCCG 227
DB	1 TTAGTAGAGAGAGGGGTTTCACCATGCTGTCAGGCTGCTCGAATCTCG 51
XX	
RESULT 68	
AAA77499	
ID	AAA77499 standard; cDNA; 51 BP.
XX	
AC	AAA77499;
XX	
DT	16-NOV-2000 (first entry)
XX	
DE	Human ALU subfamily SQ gene polymorphic site, SEQ ID NO:1182.
XX	
KM	Human; single nucleotide polymorphism; SNP; detection; identification;
XX	gene therapy; ss.
OS	Homo sapiens.
XX	
FH	Key
FT	variation
XX	
PN	WO200029623-A2.
XX	
PD	25-MAY-2000.
XX	
PF	17-NOV-1999; 99WO-US027293.
XX	
PR	17-NOV-1998; 98US-0109024P.
XX	
PA	16-NOV-1999; 99US-00443199.
XX	
XX	(CURA-) CURAGEN CORP.
XX	
PT	Shimkets RA, Leach MD;
XX	



XX polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,  
XX autoimmune diseases and infections.  
PS Claim 1; Page 2728; 4143pp; English.  
XX  
XX The present invention relates to oligonucleotides encoding polymorphic  
CC variants of proteins related to amylases, amyloid proteins, angiotensin,  
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
CC histones, kinases, colony stimulating factors, complement related  
CC proteins, cytochromes, kinases, cytokines, interferons, interleukins, G-  
CC protein coupled receptors and thioesterases. The present sequence is one  
CC such oligonucleotide. The oligonucleotides and the peptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of the proteins listed above.  
CC Disorders that may be prevented, diagnosed and/or treated include  
CC multifactorial diseases with a genetic component, such as autoimmune  
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer  
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
CC leukaemia), diseases of the nervous system and an infection of pathogenic  
CC organisms  
SQ Sequence 51 BP; 11 A; 19 C; 10 G; 11 T; 0 U; 0 Other;  
XX  
XX  
Query Match 4.3%; Score 43; DB 1; Length 51;  
Best Local Similarity 90.2%; Pred. No. 1.7e+02;  
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 1008 TTCTCTGCTCTGAGCTTCCAGACAGCTGGATTACGGGACCTGCCACCA 1058  
DB 1 TTCTCTGCTCTGAGCTTCCAGACAGCTGGATTACGGGACCTGCCACCA 51  
RESULT 71  
AAL31460  
ID AAL31460 standard; DNA; 51 BP.  
XX  
XX AAL31460;  
AC  
XX  
XX 24-JAN-2002 (first entry)  
DT  
XX  
XX Human SNP oligonucleotide #4668.  
DE  
XX  
XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;  
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
KW complement related protein; cytochrome; kinase; cytokine; interferon;  
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
KW multifactorial disease; autoimmune disease; infection;  
KW nervous system disease; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200147944-A2.  
PN  
XX  
XX 05-JUL-2001.  
PD  
XX  
XX 28-DEC-2000; 2000WO-US035498.  
PF  
XX  
XX 28-DEC-1999; 99US-0173419P.  
PR  
XX  
XX 27-DEC-2000; 2000US-00173419.  
PR  
XX  
XX (CURA-) CURAGEN CORP.  
PA  
XX  
XX Shimkets RA, Leach M;  
PI  
XX  
XX MPI; 2001-465210/50.  
DR  
XX  
XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer.

PT autoimmune diseases and infections.  
XX  
XX  
PS Claim 1; Page 2729; 4143pp; English.  
XX  
XX The present invention relates to oligonucleotides encoding polymorphic  
CC variants of proteins related to amylases, amyloid proteins, angiotensin,  
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
CC histones, kinases, colony stimulating factors, complement related  
CC proteins, cytochromes, kinases, cytokines, interferons, interleukins, G-  
CC protein coupled receptors and thioesterases. The present sequence is one  
CC such oligonucleotide. The oligonucleotides and the peptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of the proteins listed above.  
CC Disorders that may be prevented, diagnosed and/or treated include  
CC multifactorial diseases with a genetic component, such as autoimmune  
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer  
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
CC leukaemia), diseases of the nervous system and an infection of pathogenic  
CC organisms  
SQ Sequence 51 BP; 10 A; 16 C; 14 G; 11 T; 0 U; 0 Other;  
XX  
XX  
Query Match 4.3%; Score 43; DB 1; Length 51;  
Best Local Similarity 90.2%; Pred. No. 1.7e+02;  
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 849 TCGGCTTCCCAAGTGTGCTGATTACAGCGTGGACCAAGCCGCGGCTT 899  
DB 1 TTGGCTTCCCAAGTGTGCTGATTACAGCGTGGACCAAGCCGCGGCTT 51  
RESULT 72  
AA177523/C  
ID AA177523 standard; DNA; 51 BP.  
XX  
XX AA177523;  
AC  
XX  
XX 09-NOV-2001 (first entry)  
DT  
XX  
XX Human silent SNP containing nucleic acid SEQ:4464.  
DE  
XX  
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KW protein therapy; vaccine; probe; diagnostic assay; detection;  
KW quantitation; restorative therapy; polymorphic; ds.  
XX  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200140521-A2.  
PN  
XX  
XX 07-JUN-2001.  
PD  
XX  
XX 30-NOV-2000; 2000WO-US032758.  
PF  
XX  
XX 30-NOV-1999; 99US-0168138P.  
PR  
XX  
XX 29-NOV-2000; 2000US-00726173.  
PR  
XX  
XX (CURA-) CURAGEN CORP.  
PA  
XX  
XX Shimkets RA, Leach M;  
PI  
XX  
XX MPI; 2001-356160/37.  
DR  
XX  
XX Polymorphic nucleic acid sequences, useful in genetic testing and  
PT therapy.  
PT  
XX  
XX Claim 1; Page 1877; 2653pp; English.  
PS  
XX  
XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).  
CC AA453114 to AA453329 represent peptide sequences related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (I) and the polypeptides encoded by



CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides. For  
CC example, (I) may be used to treat disorders by rectifying mutations or  
CC deletions in a patient's genome that affect the activity of polypeptides  
CC by expressing inactive proteins or to supplement the patient's own  
CC production of polypeptide. Additionally, (I) and its complementary  
CC sequences may also be used as DNA probes in diagnostic assays to detect  
CC and quantitate the presence of similar nucleic acids in samples, and  
CC therefore which patients may be in need of restorative therapy. The  
CC polypeptides encoded by (I) may be used as antigens in the production of  
CC antibodies specific for polymorphic polypeptides. The antibodies may also  
CC be used to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples

SO Sequence 51 BP; 17 A; 14 C; 11 G; 9 T; 0 U; 0 Other;

Query Match 4.3%; Score 43; DB 1; Length 51;  
Best Local Similarity 90.2%; Pred. No. 1.7e+02;  
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 175 TTTTGTAGAGATGAGTTTCCATGTTGTGACGGCTGTCGAATCC 225  
DB 51 TTTTGTAGACATGGGGTTTACACGCTGTGTCAGCTGTTGAATCC 1

## RESULT 73

AA178387  
ID AA178387 standard; DNA; 51 BP.

XX AA178387;

DT 09-NOV-2001 (first entry)

DE Human silent SNP containing nucleic acid SEQ:5328.

XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;

KW protein therapy; vaccine; probe; diagnostic assay; detection;

XX quantitation; restorative therapy; polymorphic; ds.

OS Homo sapiens.

XX MO200140521-A2.

PD 07-JUN-2001.

PF 30-NOV-2000; 2000MO-US032758.

XX 30-NOV-1999; 99US-0168138P.

PR 29-NOV-2000; 2000US-00726173.

XX (CURA-) CURAGEN CORP.

PA Shimkets RA, Leach M;

PI WPI; 2001-356160/37.

PT Polymorphic nucleic acid sequences, useful in genetic testing and

XX therapy.

PS Claim 1; Page 2140; 2653bp; English.

CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide

CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

CC AA173114 to AA175329 represent peptides related to human polymorphic

CC polynucleotide sequences. The sequences can be used in gene and protein

CC therapy, and in vaccine production. (I) and the polypeptides encoded by

CC them may be used in the prevention, diagnosis and treatment of diseases

CC associated with inappropriate expression of polymorphic polypeptides. For

CC example, (I) may be used to treat disorders by rectifying mutations or

CC deletions in a patient's genome that affect the activity of polypeptides

CC by expressing inactive proteins or to supplement the patient's own

CC production of polypeptide. Additionally, (I) and its complementary

CC sequences may also be used as DNA probes in diagnostic assays to detect  
CC and quantitate the presence of similar nucleic acids in samples, and  
CC therefore which patients may be in need of restorative therapy. The  
CC polypeptides encoded by (I) may be used as antigens in the production of  
CC antibodies specific for polymorphic polypeptides. The antibodies may also  
CC be used to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples

SO Sequence 51 BP; 9 A; 16 C; 16 G; 10 T; 0 U; 0 Other;

Query Match 4.3%; Score 43; DB 1; Length 51;  
Best Local Similarity 90.2%; Pred. No. 1.7e+02;  
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 646 AGGCTGAGTGAAGTGGCGCATCTTGGCTCACTGCAACCTGCTCCCG 696  
DB 1 AGGCTGAGTGAAGTGGCGCATCTTGGCTCACTGCAACCTGCTCCCG 51

## RESULT 74

AA176192/c  
ID AA176192 standard; DNA; 51 BP.

XX AA176192;

DT 09-NOV-2001 (first entry)

DE Human silent SNP containing nucleic acid SEQ:3133.

XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;

KW protein therapy; vaccine; probe; diagnostic assay; detection;

XX quantitation; restorative therapy; polymorphic; ds.

OS Homo sapiens.

XX MO200140521-A2.

PD 07-JUN-2001.

PF 30-NOV-2000; 2000MO-US032758.

XX 30-NOV-1999; 99US-0168138P.

PR 29-NOV-2000; 2000US-00726173.

XX (CURA-) CURAGEN CORP.

PA Shimkets RA, Leach M;

PI WPI; 2001-356160/37.

PT Polymorphic nucleic acid sequences, useful in genetic testing and

XX therapy.

PS Claim 1; Page 1009; 2653bp; English.

CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide

CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

CC AA173114 to AA175329 represent peptides related to human polymorphic

CC polynucleotide sequences. The sequences can be used in gene and protein

CC therapy, and in vaccine production. (I) and the polypeptides encoded by

CC them may be used in the prevention, diagnosis and treatment of diseases

CC associated with inappropriate expression of polymorphic polypeptides. For

CC example, (I) may be used to treat disorders by rectifying mutations or

CC deletions in a patient's genome that affect the activity of polypeptides

CC by expressing inactive proteins or to supplement the patient's own

CC production of polypeptide. Additionally, (I) and its complementary

CC sequences may also be used as DNA probes in diagnostic assays to detect

CC and quantitate the presence of similar nucleic acids in samples, and

CC therefore which patients may be in need of restorative therapy. The

CC polypeptides encoded by (I) may be used as antigens in the production of

CC antibodies specific for polymorphic polypeptides. The antibodies may also

CC be used to down regulate expression and activity. The antibodies may also

CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples

XX Sequence 51 BP; 14 A; 16 C; 12 G; 9 T; 0 U; 0 Other;

Query Match 4.3%; Score 43; DB 1; Length 51;  
Best Local Similarity 90.2%; Pred. No. 1.7e+02;  
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 177 TTAGTAGAGATGAGTTCCTCATGTTGTCAGGCTGCTCGAATCCCG 227  
ID |||||  
Db 51 TTAGTAGAGAGCGGGTTTCACCATGTG3CCAGCGTGGTCTCGAATCCTCG 1

RESULT 75  
AA177583/C  
ID AA177583 standard; DNA; 51 BP.

XX AA177583;

XX 09-NOV-2001 (first entry)

XX Human silent SNP containing nucleic acid SEQ:4524.

XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KW protein therapy; vaccine; probe; diagnostic assay; detection;  
KW quantitation; restorative therapy; polymorphic; ds.

XX Homo sapiens.

XX WO200140521-A2.

XX 07-JUN-2001.

XX 30-NOV-2000; 2000WO-US032758.

XX 30-NOV-1999; 99US-0168138P.

XX 29-NOV-2000; 2000US-00726173.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach M;

XX WPI; 2001-356160/37.

XX Polymorphic nucleic acid sequences, useful in genetic testing and  
PT therapy.

XX Claim 1; Page 1895; 2653bp; English.

CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).  
CC AA173114 to AA175329 represent peptides related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (I) and the polypeptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides. For  
CC example, (I) may be used to treat disorders by rectifying mutations or  
CC deletions in a patient's genome that affect the activity of polypeptides  
CC by expressing inactive proteins or to supplement the patients own  
CC production of polypeptide. Additionally, (I) and its complementary  
CC sequences may also be used as DNA probes in diagnostic assays to detect  
CC and quantitate the presence of similar nucleic acids in samples, and  
CC therefore which patients may be in need of restorative therapy. The  
CC polypeptides encoded by (I) may be used as antigens in the production of  
CC antibodies specific for polymorphic polypeptides. The antibodies may also  
CC be used to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples

XX Sequence 51 BP; 15 A; 7 C; 20 G; 9 T; 0 U; 0 Other;

Query Match 4.3%; Score 43; DB 1; Length 51;

Best Local Similarity 90.2%; Pred. No. 1.7e+02;  
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 681 CAACCTGCTCCCGGGTTCAGTTATTCCTCCGCCCCAGCCCTCCGAGT 731  
Db 51 CAACCTGCTCCCGAGGTTCAAGTAATCTCTCACTCAAGCCCTTAGT 1

RESULT 76  
AA173060/C  
ID AA173060 standard; DNA; 51 BP.

XX AA173060;

XX 09-NOV-2001 (first entry)

XX Human silent SNP containing nucleic acid SEQ:1.

XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KW protein therapy; vaccine; probe; diagnostic assay; detection;  
KW quantitation; restorative therapy; polymorphic; ds.

XX Homo sapiens.

XX WO200140521-A2.

XX 07-JUN-2001.

XX 30-NOV-2000; 2000WO-US032758.

XX 30-NOV-1999; 99US-0168138P.

XX 29-NOV-2000; 2000US-00726173.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach M;

XX WPI; 2001-356160/37.

XX Polymorphic nucleic acid sequences, useful in genetic testing and  
PT therapy.

XX Claim 1; Page 54; 2653bp; English.

CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).  
CC AA173114 to AA175329 represent peptides related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (I) and the polypeptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides. For  
CC example, (I) may be used to treat disorders by rectifying mutations or  
CC deletions in a patient's genome that affect the activity of polypeptides  
CC by expressing inactive proteins or to supplement the patients own  
CC production of polypeptide. Additionally, (I) and its complementary  
CC sequences may also be used as DNA probes in diagnostic assays to detect  
CC and quantitate the presence of similar nucleic acids in samples, and  
CC therefore which patients may be in need of restorative therapy. The  
CC polypeptides encoded by (I) may be used as antigens in the production of  
CC antibodies specific for polymorphic polypeptides. The antibodies may also  
CC be used to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples

XX Sequence 51 BP; 13 A; 11 C; 21 G; 6 T; 0 U; 0 Other;

Query Match 4.3%; Score 43; DB 1; Length 51;  
Best Local Similarity 90.2%; Pred. No. 1.7e+02;  
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 684 CCTGCTCCCGGGTTCAGTTATTCCTCCGCCCCAGCCCTCCGAGTAC 734  
Db 51 CCTGCTCCCGGGTTCAGGATTCCTGCTCCCTCCAGCCCTCCGAGTAC 1

```
RESULT 77
AA179782/c
ID AA179782 standard; DNA; 51 BP.
XX
XX
XX AA179782;
XX
XX 09-NOV-2001 (first entry)
XX
XX Human nonconservative amino acid changing SNP nucleic acid SEQ:6723.
DE
XX
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200140521-A2.
XX
XX 07-JUN-2001.
XX
XX 30-NOV-2000; 2000WO-US032758.
XX
XX 30-NOV-1999; 99US-0168138P.
XX
XX 29-NOV-2000; 2000US-00726173.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shinketsu RA, Leach M;
XX
XX WPI; 2001-356160/37.
XX
XX Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.
XX
XX Claim 1; Page 2562; 2653pp; English.
XX
XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AA173060 to AA179867 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patient's own
CC production of polypeptide. Additionally, (I) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples
XX
XX
XX Sequence 51 BP; 12 A; 12 C; 18 G; 9 T; 0 U; 0 Other;
SQ
XX
XX Query Match 4.3%; Score 43; DB 1; Length 51;
XX Best Local Similarity 90.2%; Pred. No. 1.7e+02;
XX Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
XX
XX 989 GCCTCCGGGCTCAGGAGTCTCTCTCTCAGGCTCCCAAGCAGCTGGGA 1039
DB 51 GCCTCTGGGCTTCAAGCAATCTCTCTCAGGCTCCCAAGTGTGGGA 1
XX
XX
XX RESULT 78
XX AA173863
XX ID AA173863 standard; DNA; 51 BP.
XX
```

```
AC AA173863;
XX
XX 09-NOV-2001 (first entry)
XX
XX Human silent SNP containing nucleic acid SEQ:804.
DE
XX
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200140521-A2.
XX
XX 07-JUN-2001.
XX
XX 30-NOV-2000; 2000WO-US032758.
XX
XX 30-NOV-1999; 99US-0168138P.
XX
XX 29-NOV-2000; 2000US-00726173.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shinketsu RA, Leach M;
XX
XX WPI; 2001-356160/37.
XX
XX Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy.
XX
XX Claim 1; Page 300; 2653pp; English.
XX
XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AA173060 to AA179867 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patient's own
CC production of polypeptide. Additionally, (I) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples
XX
XX
XX Sequence 51 BP; 9 A; 21 C; 9 G; 12 T; 0 U; 0 Other;
SQ
XX
XX Query Match 4.3%; Score 43; DB 1; Length 51;
XX Best Local Similarity 90.2%; Pred. No. 1.7e+02;
XX Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
XX
XX 671 TGGCTCAGTCCAGCACTTCTGCTCCGGGTTCAAGTATTCTCTGCCCCAG 721
DB 1 TGGCTCAGTCCAGCACTTCTGCTCCGGGTTCAAGCAATCTCTGCTCTAG 51
XX
XX
XX RESULT 79
XX AA17582/c
XX ID AA17582 standard; DNA; 51 BP.
XX
XX AA17582;
XX
XX 09-NOV-2001 (first entry)
XX
XX Human silent SNP containing nucleic acid SEQ:4523.
DE
```

KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KW protein therapy; vaccine; probe; diagnostic assay; detection;  
KW quantitation; restorative therapy; polymorphic; ds.  
XX Homo sapiens.  
OS  
XX WO200140521-A2.  
XX  
XX PD 07-JUN-2001.  
XX  
XX PD 30-NOV-2000; 2000WO-US032758.  
XX  
XX PR 30-NOV-1999; 99US-0168138P.  
XX PR 29-NOV-2000; 2000US-00726173.  
XX  
XX PA (CURA-) CURAGEN CORP.  
XX PI Shimkets RA, Leach M;  
XX DR WPI; 2001-356160/37.  
XX  
XX PT Polymorphic nucleic acid sequences, useful in genetic testing and  
XX therapy.  
XX  
XX PS Claim 1; Page 1895; 2653pp; English.  
XX  
XX CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
XX sequences (I), which contain single nucleotide polymorphisms (SNPs).  
XX CC AA173114 to AA175329 represent peptides related to human polymorphic  
XX CC polynucleotide sequences. The sequences can be used in gene and protein  
XX CC therapy, and in vaccine production. (I) and the polypeptides encoded by  
XX CC them may be used in the prevention, diagnosis and treatment of diseases  
XX CC associated with inappropriate expression of polymorphic polypeptides. For  
XX CC example, (I) may be used to treat disorders by rectifying mutations or  
XX CC deletions in a patient's genome that affect the activity of polypeptides  
XX CC by expressing inactive proteins or to supplement the patients own  
XX CC production of polypeptide. Additionally, (I) and its complementary  
XX CC sequences may also be used as DNA probes in diagnostic assays to detect  
XX CC and quantitate the presence of similar nucleic acids in samples, and  
XX CC therefore which patients may be in need of restorative therapy. The  
XX CC polypeptides encoded by (I) may be used as antigens in the production of  
XX CC antibodies specific for polymorphic polypeptides. The antibodies may also  
XX CC be used to down regulate expression and activity. The antibodies may also  
XX CC be used as diagnostic agents for detecting the presence of polymorphic  
XX CC polypeptides in samples  
XX  
XX SQ Sequence 51 BP; 15 A; 6 C; 21 G; 9 T; 0 U; 0 Other;  
  
Query Match 4.3%; Score 43; DB 1; Length 51;  
Best Local Similarity 90.2%; Pred. No. 1.7e+02;  
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
  
QY 681 CAACCTGCTGCTCCGGGTTCAAGTATTCTCTGCCCAAGCTCTGAGT 731  
DB 51 CAACCTGCTGCTCCAGGTTCAAGTATTCTCTGAGCTCTGAGT 1  
  
RESULT 80  
AA173063/C  
ID AA173063 standard; DNA; 51 BP.  
XX  
XX AC AA173063;  
XX  
XX DT 09-NOV-2001 (first entry)  
XX  
XX DE Human silent SNP containing nucleic acid SEQ:4.  
XX  
XX KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
XX KW protein therapy; vaccine; probe; diagnostic assay; detection;  
XX KW quantitation; restorative therapy; polymorphic; ds.  
XX  
XX OS Homo sapiens.  
XX

PN WO200140521-A2.  
XX  
XX PD 07-JUN-2001.  
XX  
XX PR 30-NOV-2000; 2000WO-US032758.  
XX  
XX PR 30-NOV-1999; 99US-0168138P.  
XX PR 29-NOV-2000; 2000US-00726173.  
XX  
XX PA (CURA-) CURAGEN CORP.  
XX PI Shimkets RA, Leach M;  
XX DR WPI; 2001-356160/37.  
XX  
XX PT Polymorphic nucleic acid sequences, useful in genetic testing and  
XX therapy.  
XX  
XX PS Claim 1; Page 55; 2653pp; English.  
XX  
XX CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
XX sequences (I), which contain single nucleotide polymorphisms (SNPs).  
XX CC AA173114 to AA175329 represent peptides related to human polymorphic  
XX CC polynucleotide sequences. The sequences can be used in gene and protein  
XX CC therapy, and in vaccine production. (I) and the polypeptides encoded by  
XX CC them may be used in the prevention, diagnosis and treatment of diseases  
XX CC associated with inappropriate expression of polymorphic polypeptides. For  
XX CC example, (I) may be used to treat disorders by rectifying mutations or  
XX CC deletions in a patient's genome that affect the activity of polypeptides  
XX CC by expressing inactive proteins or to supplement the patients own  
XX CC production of polypeptide. Additionally, (I) and its complementary  
XX CC sequences may also be used as DNA probes in diagnostic assays to detect  
XX CC and quantitate the presence of similar nucleic acids in samples, and  
XX CC therefore which patients may be in need of restorative therapy. The  
XX CC polypeptides encoded by (I) may be used as antigens in the production of  
XX CC antibodies specific for polymorphic polypeptides. The antibodies may also  
XX CC be used to down regulate expression and activity. The antibodies may also  
XX CC be used as diagnostic agents for detecting the presence of polymorphic  
XX CC polypeptides in samples  
XX  
XX SQ Sequence 51 BP; 12 A; 10 C; 21 G; 8 T; 0 U; 0 Other;  
  
Query Match 4.3%; Score 43; DB 1; Length 51;  
Best Local Similarity 90.2%; Pred. No. 1.7e+02;  
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
  
QY 971 CGGCTCACTGCAACCTGCTCCCGGCTCAAGCATTTCTGCTCAG 1021  
DB 51 CGGCTCACTGCAACCTCGCTCTAGTTCAAGCATTTCTGCTCAG 1  
  
RESULT 81  
AA176093/C  
ID AA176093 standard; DNA; 51 BP.  
XX  
XX AC AA176093;  
XX  
XX DT 09-NOV-2001 (first entry)  
XX  
XX DE Human silent SNP containing nucleic acid SEQ:3034.  
XX  
XX KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
XX KW protein therapy; vaccine; probe; diagnostic assay; detection;  
XX KW quantitation; restorative therapy; polymorphic; ds.  
XX  
XX OS Homo sapiens.  
XX  
XX PN WO200140521-A2.  
XX  
XX PD 07-JUN-2001.  
XX  
XX PR 30-NOV-2000; 2000WO-US032758.  
XX

PR 30-NOV-1999; 99US-0168138P.  
PR 29-NOV-2000; 2000US-00726173.  
XX (CURA-) CURAGEN CORP.  
XX  
XX Shimkets RA, Leach M;  
XX  
XX WPI, 2001-356160/37.  
DR  
XX Polymorphic nucleic acid sequences, useful in genetic testing and  
PT therapy.  
PS Claim 1; Page 979; 2653pp; English.  
XX  
XX AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide  
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).  
CC AAM53114 to AAM53329 represent peptides related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (I) and the polypeptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides. For  
CC example, (I) may be used to treat disorders by rectifying mutations or  
CC deletions in a patient's genome that affect the activity of polypeptides  
CC by expressing inactive proteins or to supplement the patients own  
CC production of polypeptide. Additionally, (I) and its complementary  
CC sequences may also be used as DNA probes in diagnostic assays to detect  
CC and quantitate the presence of similar nucleic acids in samples, and  
CC therefore which patients may be in need of restorative therapy. The  
CC polypeptides encoded by (I) may be used as antigens in the production of  
CC antibodies specific for polymorphic polypeptides. The antibodies may also  
CC be used to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples  
XX  
SQ Sequence 51 BP; 11 A; 8 C; 24 G; 8 T; 0 U; 0 Other;  
XX  
Query Match 4.3%; Score 43; DB 1; Length 51;  
Best Local Similarity 90.2%; Pred. No. 1.7e+02;  
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
XX  
QY 974 CTCACGTGCAACCTCTGCTCCGCGGCTCAAGCGATTCTCTGCTCAGCCT 1024  
DB 51 CTCACGTGCAACCTCTGCTCCGCGGCTCAAGCGATTCTCTGCTCAGCCT 1  
XX  
RESULT 82  
AAI76247/C  
ID AAI76247 standard; DNA; 51 BP.  
XX  
XX AAI76247;  
AC  
XX  
XX 09-NOV-2001 (first entry)  
DT  
XX  
XX Human silent SNP containing nucleic acid SEQ:3188.  
DE  
XX  
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KW protein therapy; vaccine; probe; diagnostic assay; detection;  
KW quantitation; restorative therapy; polymorphic; ds.  
XX  
XX Homo sapiens.  
OS  
XX  
XX W0200140521-A2.  
PN  
XX  
XX 07-JUN-2001.  
PD  
XX  
XX 30-NOV-2000; 2000WO-US032758.  
PF  
XX  
XX 30-NOV-1999; 99US-0168138P.  
PR  
XX 29-NOV-2000; 2000US-00726173.  
XX  
XX (CURA-) CURAGEN CORP.  
PA  
XX Shimkets RA, Leach M;  
PI

XX  
DR WPI, 2001-356160/37.  
XX  
XX Polymorphic nucleic acid sequences, useful in genetic testing and  
PT therapy.  
PS Claim 1; Page 1026; 2653pp; English.  
XX  
XX AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide  
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).  
CC AAM53114 to AAM53329 represent peptides related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (I) and the polypeptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides. For  
CC example, (I) may be used to treat disorders by rectifying mutations or  
CC deletions in a patient's genome that affect the activity of polypeptides  
CC by expressing inactive proteins or to supplement the patients own  
CC production of polypeptide. Additionally, (I) and its complementary  
CC sequences may also be used as DNA probes in diagnostic assays to detect  
CC and quantitate the presence of similar nucleic acids in samples, and  
CC therefore which patients may be in need of restorative therapy. The  
CC polypeptides encoded by (I) may be used as antigens in the production of  
CC antibodies specific for polymorphic polypeptides. The antibodies may also  
CC be used to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples  
XX  
SQ Sequence 51 BP; 10 A; 14 C; 18 G; 9 T; 0 U; 0 Other;  
XX  
Query Match 4.3%; Score 43; DB 1; Length 51;  
Best Local Similarity 90.2%; Pred. No. 1.7e+02;  
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
XX  
QY 697 GGTTCAGATTATTCTCCGCGGCTCAAGCGATTCTCTGCTCAGCCT 747  
DB 51 GGTTCAGATTATTCTCCGCGGCTCAAGCGATTCTCTGCTCAGCCT 1  
XX  
RESULT 83  
AAI78389  
ID AAI78389 standard; DNA; 51 BP.  
XX  
XX AAI78389;  
AC  
XX  
XX 09-NOV-2001 (first entry)  
DT  
XX  
XX Human silent SNP containing nucleic acid SEQ:5330.  
DE  
XX  
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KW protein therapy; vaccine; probe; diagnostic assay; detection;  
KW quantitation; restorative therapy; polymorphic; ds.  
XX  
XX Homo sapiens.  
OS  
XX  
XX W0200140521-A2.  
PN  
XX  
XX 07-JUN-2001.  
PD  
XX  
XX 30-NOV-2000; 2000WO-US032758.  
PF  
XX  
XX 30-NOV-1999; 99US-0168138P.  
PR  
XX 29-NOV-2000; 2000US-00726173.  
XX  
XX (CURA-) CURAGEN CORP.  
PA  
XX Shimkets RA, Leach M;  
PI  
XX WPI, 2001-356160/37.  
XX  
XX Polymorphic nucleic acid sequences, useful in genetic testing and  
PT therapy.  
XX

PS Claim 1; Page 2141; 2653bp; English.  
XX  
CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).  
CC AA153114 to AA153329 represent peptides related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (I) and the polypeptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides. For  
CC example, (I) may be used to treat disorders by rectifying mutations or  
CC deletions in a patient's genome that affect the activity of polypeptides  
CC by expressing inactive proteins or to supplement the patient's own  
CC production of polypeptide. Additionally, (I) and its complementary  
CC sequences may also be used as DNA probes in diagnostic assays to detect  
CC and quantitate the presence of similar nucleic acids in samples, and  
CC therefore which patients may be in need of restorative therapy. The  
CC polypeptides encoded by (I) may be used as antigens in the production of  
CC antibodies specific for polymorphic polypeptides. The antibodies may also  
CC be used to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples  
XX  
SQ Sequence 51 BP; 10 A; 20 C; 13 G; 8 T; 0 U; 0 Other;  
  
Query Match 4.3%; Score 43; DB 1; Length 51;  
Best Local Similarity 90.2%; Pred. No. 1.7e+02;  
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
  
CY 847 CCTGGCCTCCCAAGTCTGGATTACAGCGCTGAGCCACCGCCCGCC 897  
DB 1 CCTGGCCTCCCAAGTCTGACATCACAGCGGTGAGCCACCATGCTCGGC 51  
  
RESULT 84  
AAH89507  
ID AAH89507 standard; DNA; 51 BP.  
XX  
XX AAH89507;  
XX  
XX 01-OCT-2001 (first entry)  
XX  
DE Human coding sequence polymorphic site SEQ ID NO: 288.  
XX  
XX Human; single nucleotide polymorphism; SNP; paternity test;  
XX forensic test; aberrant protein expression; ds.  
XX  
OS Homo sapiens.  
XX  
XX WO200151670-A2.  
XX  
XX 19-JUL-2001.  
XX  
XX 05-JAN-2001; 2001WO-US000322.  
XX  
XX 07-JAN-2000; 2000US-0174962P.  
XX  
XX (CURA-) CURAGEN CORP.  
XX  
XX Shimkets RA, Leach MD;  
XX  
XX WPI; 2001-451871/48.  
XX  
XX P-PSDB; AAM00390.  
XX  
XX Isolated human polynucleotides containing single nucleotide  
XX polymorphisms, useful for the treatment and diagnosis of e.g. cancer,  
XX infection and diabetes.  
XX  
XX Claim 1; Page 186; 475bp; English.  
XX  
XX The present invention relates to human nucleic acids containing single  
XX nucleotide polymorphisms (SNPs). These can be used in forensic and  
XX paternity tests, and to aid in the treatment of diseases associated with  
XX aberrant protein expression, including cancer, amyloidosis, diabetes,

CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,  
CC glomerulonephritis, haemolytic anaemia, thrombocytopenia, arthritis,  
CC meningitis, muscular disorders, dementia, neurological diseases, tubercous  
CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,  
CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or  
CC autoimmunity. The present sequence is a polymorphism-containing  
CC oligonucleotide fragment of the invention  
XX  
SQ Sequence 51 BP; 11 A; 13 C; 15 G; 12 T; 0 U; 0 Other;  
  
Query Match 4.3%; Score 43; DB 1; Length 51;  
Best Local Similarity 90.2%; Pred. No. 1.7e+02;  
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
  
CY 1083 ATTAGAGCGGGGTTTCCACCATTTGTGACGCTGATCTCAACTCTGAC 1133  
DB 1 AGTAGAGAGCGGGGTTTCCACCATTTGTGACGCTGATCTCAACTCTGAC 51  
  
RESULT 85  
AAH89506  
ID AAH89506 standard; DNA; 51 BP.  
XX  
XX AAH89506;  
XX  
XX 01-OCT-2001 (first entry)  
XX  
XX Human coding sequence polymorphic site SEQ ID NO: 287.  
XX  
XX Human; single nucleotide polymorphism; SNP; paternity test;  
XX forensic test; aberrant protein expression; ds.  
XX  
XX Homo sapiens.  
XX  
XX WO200151670-A2.  
XX  
XX 19-JUL-2001.  
XX  
XX 05-JAN-2001; 2001WO-US000322.  
XX  
XX 07-JAN-2000; 2000US-0174962P.  
XX  
XX (CURA-) CURAGEN CORP.  
XX  
XX Shimkets RA, Leach MD;  
XX  
XX WPI; 2001-451871/48.  
XX  
XX P-PSDB; AAM00389.  
XX  
XX Isolated human polynucleotides containing single nucleotide  
XX polymorphisms, useful for the treatment and diagnosis of e.g. cancer,  
XX infection and diabetes.  
XX  
XX Claim 1; Page 186; 475bp; English.  
XX  
XX The present invention relates to human nucleic acids containing single  
XX nucleotide polymorphisms (SNPs). These can be used in forensic and  
XX paternity tests, and to aid in the treatment of diseases associated with  
XX aberrant protein expression, including cancer, amyloidosis, diabetes,  
XX Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,  
XX glomerulonephritis, haemolytic anaemia, thrombocytopenia, arthritis,  
XX meningitis, muscular disorders, dementia, neurological diseases, tubercous  
XX sclerosis, male infertility, hypercalcaemia, blood pressure disorders,  
XX osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or  
XX autoimmunity. The present sequence is a polymorphism-containing  
XX oligonucleotide fragment of the invention  
XX  
SQ Sequence 51 BP; 12 A; 13 C; 14 G; 12 T; 0 U; 0 Other;  
  
Query Match 4.3%; Score 43; DB 1; Length 51;  
Best Local Similarity 90.2%; Pred. No. 1.7e+02;  
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;







DR WPI; 2001-355949/37.  
XX Isolated human nucleic acids comprising one or more single nucleotide  
PT polymorphisms, useful for treating a subject suffering from a pathology,  
PT e.g. autoimmune diseases, ascribed to the presence of a sequence  
PT polymorphism.  
XX  
XX Claim 1; Page 248; 674pp; English.  
XX  
XX ABL00010 to ABL01104 represent human nucleic acid oligonucleotides  
CC comprising one or more single nucleotide polymorphisms (SNPs). ABB56531  
CC to ABB59903 represent human peptides encoded by some of the SNP  
CC oligonucleotides. The sequences from the present invention can have  
CC immunosuppressive, cytostatic, antiinflammatory, neuroprotective and  
CC antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides  
CC and antibodies from the present invention can be used for treating a  
CC subject suffering from, at risk for, or suspected of, suffering from a  
CC pathology ascribed to the presence of a sequence polymorphism. The  
CC the nervous system, and infection by pathogenic microorganisms. The SNPs  
CC are also useful for determining which forms of a characterised  
CC polymorphism are present in individuals. The antibodies may be used in  
CC the detection, quantitation and/or cellular or tissue localisation of a  
CC polymorphic protein (e.g., for use in measuring levels of the polymorphic  
CC protein within appropriate physiological samples)  
XX  
XX Sequence 51 BP; 7 A; 20 C; 13 G; 11 T; 0 U; 0 Other;  
SQ  
XX  
XX Query Match 4.3%; Score 43; DB 1; Length 51;  
XX Best Local Similarity 90.2%; Pred. No. 1.7e+02;  
XX Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 987 CTGGCTCCCGGGGCTCAAGGATTCCTCTGTCAGGCTCCAGACAGCTGG 1037  
DB 1 CCGCCTCTGGGTTCAAGGATTCCTCTGTCAGGCTCCAGACAGCTGG 51  
RESULT 91  
AA176817  
ID AA176817 standard; DNA; 51 BP.  
XX  
XX AA176817;  
XX  
XX 09-NOV-2001 (first entry)  
XX  
XX Human silent SNP containing nucleic acid SEQ:3758.  
DE  
XX  
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KW protein therapy; vaccine; probe; diagnostic assay; detection;  
KW quantitation; restorative therapy; polymorphic; ds.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200140521-A2.  
XX  
XX 07-JUN-2001.  
PD  
XX  
XX 30-NOV-2000; 2000WO-US032758.  
PF  
XX  
XX 30-NOV-1999; 99US-0168138P.  
PR  
XX 29-NOV-2000; 2000US-00726173.  
PR  
XX  
XX (CURA-) CURAGEN CORP.  
PA  
XX  
XX Shimkets RA, Leach M;  
PI  
XX  
XX WPI; 2001-356160/37.  
DR  
XX  
XX Polymorphic nucleic acid sequences, useful in genetic testing and  
PT therapy.  
XX  
XX Claim 1; Page 1201; 2653pp; English.  
XX

CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (i), which contain single nucleotide polymorphisms (SNPs).  
CC AAM53114 to AAM53329 represent peptides related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (i) and the polypeptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides. For  
CC example, (i) may be used to treat disorders by rectifying mutations or  
CC deletions in a patient's genome that affect the activity of polypeptides  
CC by expressing inactive proteins or to supplement the patient's own  
CC production of polypeptide. Additionally, (i) and its complementary  
CC sequences may also be used as DNA probes in diagnostic assays to detect  
CC and quantitate the presence of similar nucleic acids in samples, and  
CC therefore which patients may be in need of restorative therapy. The  
CC polypeptides encoded by (i) may be used as antigens in the production of  
CC antibodies specific for polymorphic polypeptides. The antibodies may also  
CC be used to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples  
XX  
XX Sequence 51 BP; 8 A; 17 C; 13 G; 13 T; 0 U; 0 Other;  
SQ  
XX  
XX Query Match 4.3%; Score 42.6; DB 1; Length 51;  
XX Best Local Similarity 91.8%; Pred. No. 1.8e+02;  
XX Matches 45; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 193 TTCTCCATGTGTGTCAGGCTGTGTCGAACCTCCGACCTCAGATGATCC 241  
DB 1 TTGCGCATGTGTGCGCAGGCTGTGTCGAACCTCCTGACCTCAGATGATCC 49  
RESULT 92  
AD112541/c  
ID AD112541 standard; DNA; 44 BP.  
XX  
XX AD112541;  
XX  
XX 22-APR-2004 (first entry)  
XX  
XX Mutant human BRCA1 genomic DNA resulting from deletion 3 Segid 24.  
DE  
XX  
XX de; cancer; human; tumour suppressor;  
KW breast cancer susceptibility gene 1; BRCA1; repetitive Alu;  
KW ovarian cancer; recombination; mutant.  
XX  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO2003104474-A2.  
XX  
XX 18-DEC-2003.  
PD  
XX  
XX 09-JUN-2003; 2003WO-US018098.  
PF  
XX  
XX 07-JUN-2002; 2002US-0387132P.  
PR  
XX 09-AUG-2002; 2002US-0402430P.  
PR  
XX  
XX (MYRI-) MYRIAD GENETICS INC.  
PA  
XX  
XX Scholl T, Hendrickson BC, Ward B, Pruse D;  
PI  
XX  
XX WPI; 2004-062369/06.  
DR  
XX  
XX Predicting a predisposition to cancer in a patient comprising detecting a  
PT deletion in the BRCA1 gene that results from the unequal crossover  
PT between a pair of repetitive sequences in the BRCA1 gene.  
XX  
XX Disclosure; SEQ ID NO 24; 59pp; English.  
XX  
XX This invention relates to a novel method for predicting a predisposition  
CC to cancer in a patient by detecting large deletions in the human tumour  
CC suppressor gene identified as the breast cancer susceptibility gene 1  
CC (BRCA1). Specifically, it refers to deletions that result from the  
CC unequal crossover between a pair of repetitive Alu sequences in the BRCA1

CC gene, such that the recombined nucleotide sequence containing the  
CC deletion indicates a predisposition to breast and ovarian cancer. The  
CC present invention describes newly discovered deletion mutations that are  
CC believed to be deleterious and cause significant alterations in the  
CC structure or biochemical function of BRCA1. Accordingly, it provides  
CC methods for detecting such mutants, as well as identifying and screening  
CC for cytostatic compounds useful for treating or preventing cancers  
CC associated with a BRCA1 genetic variant. This polynucleotide is a mutant  
CC human BRCA1 genomic DNA fragment that arises as a result of a  
CC recombinational event (deletion 3), which causes the omission of exons 16  
CC and 17, given in an exemplification of the invention.

XX SQ Sequence 44 BP; 11 A; 12 C; 14 G; 7 T; 0 U; 0 Other;

Query Match 4.3%; Score 42.4; DB 1; Length 44;  
Best Local Similarity 97.7%; Pred. No. 1.6e+02;  
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 833 TTGTGATCTGCTCGGCTCCCAAGTGTGGATTACAG 876  
DB 44 TTGTGATCTGCTCGGCTCCCAAGTGTGGATTACAG 1

RESULT 93

AAH38364/C  
ID AAH38364 standard; DNA; 51 BP.

XX AC AAH38364;

XX DT 14-AUG-2001 (first entry)

XX DE Human SNP flanking oligonucleotide SEQ ID 1160.

XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
XX SNP; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;  
XX Leesh-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;  
XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
XX inflammation; forensic investigation; paternity analysis; ds.

XX OS Homo sapiens.

XX PN WO200129262-A2.

XX PD 26-APR-2001.

XX PF 13-OCT-2000; 2000MO-US028436.

XX PR 15-OCT-1999; 99US-0160096P.

XX PA (ORCH-) ORCHID BIOSCIENCES INC.

XX PI Picoult-Newburg L, Pohl M;

XX DR WPI; 2001-290930/30.

XX PT New genotyping oligonucleotide, useful for detecting the presence,  
XX PT absence or identity of single polynucleotide polymorphism in a nucleic  
XX PT acid sample.

XX PS Claim 1; Page 55; 83pp; English.

XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
XX primer extension (SNPE) primers, and the sequences of regions flanking  
XX sites of single nucleotide polymorphisms SNPs. The present invention  
XX includes kits for determining the presence or absence of a SNP, using the  
XX oligonucleotides of the invention. The PCR primers are used to amplify a  
XX SNP flanking sequence, the SNP primer is used as a genotyping primer.  
XX The oligonucleotides are useful for genotyping a nucleic acid sample by  
XX performing a single-nucleotide primer extension reaction. The  
XX oligonucleotides are useful for determining the presence, absence or  
XX identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
XX assess by association analysis the genotype of an individual or group of

CC individuals, having a pathological phenotypic trait suspected of being  
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
CC agammaglobulinaemia, diabetes insipidus, Leesh-Nyhan syndrome, muscular  
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,  
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
CC traits also include symptoms of or susceptibility to multifactorial  
CC diseases, including, rheumatoid arthritis, multiple sclerosis,  
CC diseases, including, cancer, nervous system diseases and infection by pathogenic  
CC microorganism. The method is also useful in forensic investigations and  
CC paternity analysis. The present sequence represents a fragment of human  
CC DNA flanking the site of a single nucleotide polymorphism

XX SQ Sequence 51 BP; 8 A; 14 C; 17 G; 12 T; 0 U; 0 Other;

Query Match 4.3%; Score 42.4; DB 1; Length 51;  
Best Local Similarity 97.7%; Pred. No. 1.8e+02;  
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 854 CTCCCAAGTGTGGATTACAGGCGTGAAGCCACACGCCGCGC 897  
DB 51 CTCCCAAGTGTGGATTACAGGCGTGAAGCCACACGCCGCGC 8

RESULT 94

AAZ69411/C  
ID AAZ69411 standard; DNA; 47 BP.

XX AC AAZ69411;

XX DT 10-SEP-2001 (first entry)

XX DE Human map-related biallelic marker SEQ ID NO:3767.

XX Human genome; biallelic marker; high density disequilibrium map;  
XX genomic map; haplotype; phenotype; polymorphic base; genotyping;  
XX genotyping; hybridisation; identification; characterisation; diagnosis;  
XX single nucleotide polymorphism; SNP; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Variation replace(24,T)

XX FT /\*tag= a

XX FT /standard\_name= "single nucleotide polymorphism"

XX PN WO9954500-A2.

XX PD 28-OCT-1999.

XX PF 21-APR-1999; 99WO-1B000822.

XX PR 21-APR-1998; 98US-0082614P.

XX PR 23-NOV-1998; 98US-0109732P.

XX PA (GENET ) GENSET.

XX PI Cohen D, Blumenfeld M, Chumakov I;

XX DR WPI; 2000-013267/01.

XX PT Novel biallelic markers used to construct a high density disequilibrium  
XX PT map of the human genome.

XX PS Claim 3; Page 1034; 2745pp; English.

XX AAZ65654 to AAZ69578 represent human biallelic markers from the present  
XX invention, which contain a polymorphic base at position 24 of their  
XX nucleotide sequences. AAZ6579 to AAZ77440 represent amplification  
XX primers for the biallelic markers. The biallelic markers of the invention  
XX have a variety of uses: they can be used for high density mapping of the  
XX human genome, and in complex association studies and haplotyping studies  
XX which are useful in determining the genetic basis for disease states.

CC Compositions and methods of the invention can also be useful for the  
CC identification of the targets for the development of pharmaceutical  
CC agents and diagnostic methods, as well as the characterisation of the  
CC differential efficacious responses to and side effects from  
CC pharmaceutical agents acting on a disease as well as other treatment.  
CC N.B. The SEQ ID NOS 2852, 2813, 2974, 3035, 3096, 3157, 3227, 3297 and  
CC 3367, are not actually given a sequence in the Sequence Listing from the  
CC present invention

XX SQ Sequence 47 BP; 13 A; 8 C; 19 G; 7 T; 0 U; 0 Other;

Query Match 4.3%; Score 42.2; DB 1; Length 47;  
Best Local Similarity 93.6%; Pred. No. 1.7e+02;  
Matches 44; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 673 GCTCACTGCACCTCTGCTCCCGGTTCAAGTATTCTCTCCGCC 719  
DB 47 GCTCACTGCACCTCTGCTCCCGGTTCAAGTATTCTCTCCGCC 1

RESULT 95  
AA174450/c  
ID AA174450 standard; DNA; 51 BP.

XX AA174450;  
XX  
DT 09-NOV-2001 (first entry)  
XX

DE Human silent SNP containing nucleic acid SEQ.1391.

XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KW protein therapy; vaccine; probe; diagnostic assay; detection;  
KW quantitation; restorative therapy; polymorphic; ds.

XX Homo sapiens.

XX WO200140521-A2.

XX 07-JUN-2001.

PF 30-NOV-2000; 2000MO-US032758.

PR 30-NOV-1999; 99US-0168138P.

PR 29-NOV-2000; 2000US-00726173.

XX (CURA-) CURAGEN CORP.

PI Shimkets RA, Leach M;

XX WPI; 2001-356160/37.

PT Polymorphic nucleic acid sequences, useful in genetic testing and  
XX therapy.

XX Claim 1; Page 479; 2653pp; English.

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).  
CC AA173060 to AA173329 represent peptide sequences related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (I) and the polypeptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides. For  
CC example, (I) may be used to treat disorders by rectifying mutations or  
CC deletions in a patient's genome that affect the activity of polypeptides  
CC by expressing inactive proteins or to supplement the patients own  
CC production of polypeptide. Additionally, (I) and its complementary  
CC sequences may also be used as DNA probes in diagnostic assays to detect  
CC and quantitate the presence of similar nucleic acids in samples, and  
CC therefore which patients may be in need of restorative therapy. The  
CC polypeptides encoded by (I) may be used as antigens in the production of  
CC antibodies specific for polymorphic polypeptides. The antibodies may also  
CC be used to down regulate expression and activity. The antibodies may also

CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples

XX SQ Sequence 51 BP; 10 A; 11 C; 19 G; 11 T; 0 U; 0 Other;

Query Match 4.3%; Score 42.2; DB 1; Length 51;  
Best Local Similarity 93.6%; Pred. No. 1.9e+02;  
Matches 44; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 369 TCCACCTGCCTCAGCCTCCCAAGTCTGGATTACAGGCGTGCAC 415  
DB 49 TCCCTGCTCAGCCTCCCAAGTCTGGATTACAGGCGATGCACC 3

RESULT 96  
AA176248/c  
ID AA176248 standard; DNA; 51 BP.

XX AA176248;  
XX

DT 09-NOV-2001 (first entry)

DE Human silent SNP containing nucleic acid SEQ.1389.

XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KW protein therapy; vaccine; probe; diagnostic assay; detection;  
KW quantitation; restorative therapy; polymorphic; ds.

XX Homo sapiens.

XX WO200140521-A2.

XX 07-JUN-2001.

PF 30-NOV-2000; 2000MO-US032758.

PR 30-NOV-1999; 99US-0168138P.

PR 29-NOV-2000; 2000US-00726173.

XX (CURA-) CURAGEN CORP.

PI Shimkets RA, Leach M;

XX WPI; 2001-356160/37.

PT Polymorphic nucleic acid sequences, useful in genetic testing and  
XX therapy.

XX Claim 1; Page 1026; 2653pp; English.

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).  
CC AA173060 to AA173329 represent peptide sequences related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (I) and the polypeptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides. For  
CC example, (I) may be used to treat disorders by rectifying mutations or  
CC deletions in a patient's genome that affect the activity of polypeptides  
CC by expressing inactive proteins or to supplement the patients own  
CC production of polypeptide. Additionally, (I) and its complementary  
CC sequences may also be used as DNA probes in diagnostic assays to detect  
CC and quantitate the presence of similar nucleic acids in samples, and  
CC therefore which patients may be in need of restorative therapy. The  
CC polypeptides encoded by (I) may be used as antigens in the production of  
CC antibodies specific for polymorphic polypeptides. The antibodies may also  
CC be used to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples

XX SQ Sequence 51 BP; 15 A; 10 C; 18 G; 8 T; 0 U; 0 Other;

Query Match 4.3%; Score 42.2; DB 1; Length 51;

Best Local Similarity 93.6%; Pred. No. 1.9e+02;  
Matches 44; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 667 ATCTTGCTCACTGACACCTCTGCTCCCGGTTCAATATTCCTCC 713  
DB 47 ATCTTGCTCACTGACACCTCTGCTCCCGGTTCAATATTCCTCC 1

## RESULT 97

AA175601/C  
ID AA175601 standard; DNA; 51 BP.

XX AA175601;

DT 09-NOV-2001 (first entry)

XX Human silent SNP containing nucleic acid SEQ:2542.

DE Human; single nucleotide polymorphism; SNP; genome; gene therapy;

KW protein therapy; vaccine; probe; diagnostic assay; detection;

KW quantitation; restorative therapy; polymorphic; ds.

XX Homo sapiens.

OS WO200140521-A2.

PN 07-JUN-2001.

PD 30-NOV-2000; 2000WO-US032758.

PF 30-NOV-1999; 99US-0168138P.

PR 29-NOV-2000; 2000US-00726173.

XX (CURA-) CURAGEN CORP.

XX Shinkets RA, Leach M;

PI WPI; 2001-356160/37.

DR Polymorphic nucleic acid sequences, useful in genetic testing and

PT therapy.

PS Claim 1; Page 829; 2653pp; English.

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide

CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

CC AA173114 to AA1753129 represent peptides related to human polymorphic

CC polynucleotide sequences. The sequences can be used in gene and protein

CC therapy, and in vaccine production. (I) and the polypeptides encoded by

CC them may be used in the prevention, diagnosis and treatment of diseases

CC associated with inappropriate expression of polymorphic polypeptides. For

CC example, (I) may be used to treat disorders by rectifying mutations or

CC deletions in a patient's genome that affect the activity of polypeptides

CC by expressing inactive proteins or to supplement the activity of polypeptides

CC production of polypeptide. Additionally, (I) and its complementary

CC sequences may also be used as DNA probes in diagnostic assays to detect

CC and quantitate the presence of similar nucleic acids in samples, and

CC therefore which patients may be in need of restorative therapy. The

CC polypeptides encoded by (I) may be used as antigens in the production of

CC antibodies specific for polymorphic polypeptides. The antibodies may also

CC be used to down regulate expression and activity. The antibodies may also

CC be used as diagnostic agents for detecting the presence of polymorphic

CC polypeptides in samples

XX SQ Sequence 51 BP; 13 A; 13 C; 16 G; 9 T; 0 U; 0 Other;

OY Query Match 4.3%; Score 42.2; DB 1; Length 51;

DB Best Local Similarity 93.6%; Pred. No. 1.9e+02;

Matches 44; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 634 ACTGTGTACCCAGGCTGAGTGCAGTGGCGCAATCTTGGCTCACTG 680

DB 48 ACTGTGTGCGCCAGGCTGAGTGCAGTGGCGCAATCTTGGCTCACTG 2

## RESULT 98

ACC84458  
ID ACC84458 standard; DNA; 42 BP.

XX ACC84458;

DT 28-AUG-2003 (first entry)

DE NTP peptide encoding sequence #5.

XX Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;

KW neural thread protein; NTP; tumour; ds.

XX Unidentified.

OS WO2003008443-A2.

PN 30-JAN-2003.

PD 19-JUL-2002; 2002WO-CA001105.

PF 19-JUL-2001; 2001US-0306150P.

PR 19-JUL-2001; 2001US-0306151P.

PR 16-NOV-2001; 2001US-0331477P.

XX (NYMO-) NYMOX CORP.

XX Averbach PA;

PI WPI; 2003-247999/24.

DR P-PSDB; ABR63253.

XX Novel neural thread protein peptide, referred as cell death peptide,

PT useful for treating prostatic hyperplasia, psoriasis, eczema, dermatosis,

PS atherosclerosis, cosmetic modification to skin, throat, mouth, muscle.

XX Disclosure; Page 16; 77pp; English.

XX The present invention relates to a neural thread protein (NTP) peptide

CC referred to as cell death peptide. Thought to be cytostatic,

CC antibacterial, immunosuppressive and antiinflammatory. It is useful for

CC treating a condition in a patient requiring removal or destruction of

CC cells, for treating a condition such as benign or malignant tumor,

CC inflammatory disease, autoimmune disease and infectious disease. The

CC peptide useful for treatment is derived from the amino acid sequence for

CC a pancreatic thread protein. The peptide is conjugated, linked or bound

CC to a molecule chosen from antibody or its fragment, antibody-like binding

CC molecule, where the molecule has a higher affinity for binding to a tumor

CC or other target than binding to other cells. Treatment using NTP peptides

CC can remove benign tumors with less risk and fewer of the undesirable side

CC effects of surgery. The present sequence is an NTP encoding sequence

XX SQ Sequence 42 BP; 8 A; 15 C; 10 G; 9 T; 0 U; 0 Other;

OY Query Match 4.2%; Score 42; DB 1; Length 42;

DB Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 369 TCCACCTGCTCAGCTCCCAAGTGTGAGTTACAGGCT 410

DB 1 TCCACCTGCTCAGCTCCCAAGTGTGAGTTACAGGCT 42

RESULT 99

ACC84457

ID ACC84457 standard; DNA; 42 BP.

XX ACC84457;

AC 28-AUG-2003 (first entry)

DT

XX





CC individuals. Single nucleotide polymorphisms (SNPs) tend to occur with  
CC great frequency throughout the genome and may be located close to loci of  
CC interest. Such variations can cause or be closely linked to pathological  
CC conditions (genetic diseases). Hence the SNPs of the invention may be  
CC useful in the development of compounds with cytostatic,  
CC immunosuppressive, antiinflammatory, neuroprotective or antimicrobial  
CC activities. Regulators of metabolic pathways such as fatty acid  
CC metabolism, glycolysis, and amino acid metabolism may also be developed.  
CC The compounds may be useful for treating a subject suffering from or at  
CC risk for a pathology associated with the presence of a sequence  
CC polymorphism. SNP detection is also useful in paternity analysis and  
CC forensic application. Polymorphisms may contribute to the phenotype of an  
CC organism and phenotypic traits include genetic diseases such as  
CC autoimmune diseases, cancer, diseases of the nervous system and infection  
CC by pathogenic microorganisms. The present sequence is the sequence  
CC surrounding and including a human SNP of the invention.

XX Sequence 51 BP; 12 A; 11 C; 17 G; 11 T; 0 U; 0 Other;

Query Match 4.2%; Score 42; DB 1; Length 51;  
Best Local Similarity 90.0%; Pred. No. 1.9e+02;  
Matches 45; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 356 TGAGCTCAAGCAGTCCAGCTGCTCAGCTCCCAAGTGTGGATTACA 405  
DB 50 TCAGCTCAAGTATCCAGCTGCTCGGCTCCCAAGTGTGGATTACA 1

RESULT 104  
AAL27794/C  
ID AAL27794 standard; DNA; 51 BP.  
XX  
XX AAL27794;

XX 24-JAN-2002 (first entry)

XX Human SNP oligonucleotide #1002.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cyostatic;  
XX neuroprotective; antitubercial; gene therapy; vaccine; amylose; cancer;  
XX amyloid protein; angiotensin; apoptosis related protein; cadherin;  
XX cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
XX complement related protein; cytochrome; kinesin; cytokine; interferon;  
XX interleukin; G-protein coupled receptor; thioesterase; inflammation;  
XX multifactorial disease; autoimmune disease; infection;  
XX nervous system disease; ss.

XX Homo sapiens.

XX MO200147944-A2.

XX 05-JUL-2001.

XX 28-DEC-2000; 2000WO-US035498.

XX 28-DEC-1999; 99US-0173419P.

XX 27-DEC-2000; 2000US-00173419.

XX (CURA-) CURAGEN CORP.

XX Shinkets RA, Leach M;

XX WPI; 2001-465210/50.

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
XX oncogenes and histones, useful for diagnosing and treating, e.g. cancer,  
XX autoimmune diseases and infections.

XX Claim 1; Page 1666; 4143pp; English.

XX The present invention relates to oligonucleotides encoding polymorphic  
XX variants of proteins related to amylases, amyloid proteins, angiotensin,  
XX apoptosis related proteins, cadherin, cyclin, polymerase, oncogene,

CC histones, kinases, colony stimulating factors, complement related  
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-  
CC protein coupled receptors and thioesterases. The present sequence is one  
CC such oligonucleotide. The oligonucleotides and the peptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of the proteins listed above.

CC Disorders that may be prevented, diagnosed and/or treated include  
CC multifactorial diseases with a genetic component, such as autoimmune  
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer  
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
CC leukaemia), diseases of the nervous system and an infection of pathogenic  
CC organisms

XX Sequence 51 BP; 10 A; 13 C; 16 G; 12 T; 0 U; 0 Other;

Query Match 4.2%; Score 42; DB 1; Length 51;  
Best Local Similarity 90.0%; Pred. No. 1.9e+02;  
Matches 45; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 994 CCGGGCTCAAGGAGTTCCTGCTCAGCTCCCAAGCAGCTGGATTAC 1043  
DB 51 CAGGGCTCAAGGAATCCTCTCTCAGCTCCCAAGGAGCTGGATTAC 2

RESULT 105  
AAI73932  
ID AAI73932 standard; DNA; 51 BP.  
XX  
XX AAI73932;

XX 09-NOV-2001 (first entry)

XX Human silent SNP containing nucleic acid SEQ.873.

XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
XX protein therapy; vaccine; probe; diagnostic assay; detection;  
XX quantitation; restorative therapy; polymorphic; ds.

XX Homo sapiens.

XX MO200140521-A2.

XX 07-JUN-2001.

XX 30-NOV-2000; 2000WO-US032758.

XX 30-NOV-1999; 99US-0168138P.

XX 29-NOV-2000; 2000US-00726173.

XX (CURA-) CURAGEN CORP.

XX Shinkets RA, Leach M;

XX WPI; 2001-356160/37.

XX Polymorphic nucleic acid sequences, useful in genetic testing and  
XX therapy.

XX Claim 1; Page 321; 2653pp; English.

XX AAI73060 to AAI79867 represent isolated human polymorphic polymorphic  
XX sequences (I), which contain single nucleotide polymorphisms (SNPs).  
XX AAI53114 to AAI53139 represent peptides related to human polymorphic  
XX polymorphic nucleic acid sequences. The sequences can be used in gene and protein  
XX therapy, and in vaccine production. (I) and the polymorphisms encoded by  
XX them may be used in the prevention, diagnosis and treatment of diseases  
XX associated with inappropriate expression of polymorphic polymorphisms. For  
XX example, (I) may be used to treat disorders by rectifying mutations or  
XX deletions in a patient's genome that affect the activity of polymorphisms  
XX by expressing inactive proteins or to supplement the patients own  
XX production of polymorphisms. Additionally, (I) and its complementary  
XX sequences may also be used as DNA probes in diagnostic assays to detect

CC	and quantitate the presence of similar nucleic acids in samples, and
CC	therefore which patients may be in need of restorative therapy. The
CC	polypeptides encoded by (I) may be used as antigens in the production of
CC	antibodies specific for polymorphic polypeptides. The antibodies may also
CC	be used to down regulate expression and activity. The antibodies may also
CC	be used as diagnostic agents for detecting the presence of polymorphic
CC	polypeptides in samples
XX	
XX	Sequence 51 BP; 12 A; 15 C; 12 G; 12 T; 0 U; 0 Other;
XX	
XX	Query Match 4.2%; Score 42; DB 1; Length 51;
XX	Best Local Similarity 90.0%; Pred. No. 1.9e+02;
XX	Matches 45; Conservative 0; Mismatches 5; Indels 0; Gaps 0
OY	356 TGAGCTCAAGCAGTCCACCTGCTCCTCAGCTCCCAAGTCTGGATTACA 405
DB	1 TGGGCTCAAGTATCACCCTGCTCCTCAGCTCCAAAGTCTGGATTACA 50
XX	
XX	RESULT 106
ID	AA179551
AC	AA179551 standard; DNA; 51 BP.
XX	AA179551;
XX	09-NOV-2001 (first entry)
DE	Human silent SNP containing nucleic acid SEQ:6492.
XX	
KW	Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW	protein therapy; vaccine; probe; diagnostic assay; detection;
KW	quadrification; restorative therapy; polymorphic; ds.
OS	Homo sapiens.
XX	
PN	WO200140521-A2.
PD	07-JUN-2001.
PF	30-NOV-2000; 2000WO-US032758.
PR	30-NOV-1999; 99US-0168138P.
PR	29-NOV-2000; 2000US-00726173.
PA	(CURA-) CURAGEN CORP.
PI	Shimkets RA, Leach M;
DR	WPI, 2001-356160/37.
XX	
XX	polymorphic nucleic acid sequences, useful in genetic testing and
PT	therapy.
XX	
PS	Claim 1; Page 2493; 2653pp; English.
XX	
XX	AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC	sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC	AA173114 to AA175332 represent peptides related to human polymorphic
CC	polynucleotide sequences. The sequences can be used in gene and protein
CC	therapy, and in vaccine production. (I) and the polypeptides encoded by
CC	them may be used in the prevention, diagnosis and treatment of diseases
CC	associated with inappropriate expression of polymorphic polypeptides. For
CC	example, (I) may be used to treat disorders by rectifying mutations or
CC	deletions in a patient's genome that affect the activity of polypeptides
CC	by expressing inactive proteins or to supplement the patients own
CC	production of polypeptide. Additionally, (I) and its complementary
CC	sequences may also be used as DNA probes in diagnostic assays to detect
CC	and quantitate the presence of similar nucleic acids in samples, and
CC	therefore which patients may be in need of restorative therapy. The
CC	polypeptides encoded by (I) may be used as antigens in the production of
CC	antibodies specific for polymorphic polypeptides. The antibodies may also
CC	be used to down regulate expression and activity. The antibodies may also
CC	be used as diagnostic agents for detecting the presence of polymorphic.

[illegible]





XX 09-NOV-2001 (first entry)  
 XX Human silent SNP containing nucleic acid SEQ:5241.  
 DE  
 XX  
 XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
 KM protein therapy; vaccine; probe; diagnostic assay; detection;  
 KM quantitation; restorative therapy; polymorphic; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200140521-A2.  
 PN  
 XX  
 XX 07-JUN-2001.  
 PD  
 XX  
 XX 30-NOV-2000; 2000WO-US032758.  
 PF  
 XX 30-NOV-1999; 99US-0168138P.  
 PR 29-NOV-2000; 2000US-00726173.  
 XX  
 XX (CURA-) CURAGEN CORP.  
 PA  
 XX Shinkets RA, Leach M;  
 PI WPI; 2001-356160/37.  
 DR  
 XX Polymorphic nucleic acid sequences, useful in genetic testing and  
 PT therapy.  
 XX  
 XX Claim 1; Page 2114; 2653pp; English.  
 PS  
 XX AAT73060 to AAT79867 represent isolated human polymorphic polynucleotide  
 CC sequences (I), which contain single nucleotide polymorphisms (SNPs).  
 CC AAM53114 to AAM53329 represent peptide sequences related to human polymorphic  
 CC polynucleotide sequences. The sequences can be used in gene and protein  
 CC therapy, and in vaccine production. (I) and the polypeptides encoded by  
 CC them may be used in the prevention, diagnosis and treatment of diseases  
 CC associated with inappropriate expression of polymorphic polypeptides. For  
 CC example, (I) may be used to treat disorders by rectifying mutations or  
 CC deletions in a patient's genome that affect the activity of polypeptides  
 CC by expressing inactive proteins or to supplement the patient's own  
 CC production of polypeptide. Additionally, (I) and its complementary  
 CC sequences may also be used as DNA probes in diagnostic assays to detect  
 CC and quantitate the presence of similar nucleic acids in samples, and  
 CC therefore which patients may be in need of restorative therapy. The  
 CC polypeptides encoded by (I) may be used as antigens in the production of  
 CC antibodies specific for polymorphic polypeptides. The antibodies may also  
 CC be used to down regulate expression and activity. The antibodies may also  
 CC be used as diagnostic agents for detecting the presence of polymorphic  
 CC polypeptides in samples  
 CC  
 SQ Sequence 51 BP; 12 A; 17 C; 14 G; 8 T; 0 U; 0 Other;  
 Query Match 4.2%; Score 42; DB 1; Length 51;  
 Best Local Similarity 90.0%; Pred. No. 1.9e+02;  
 Matches 45; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 847 CCTGGCCTCCCAAGTGTGGATTACAGGCGTACGCCACACCCCGG 896  
 DB 2 CCTGGCCTCCCAAGTGTGGATTACAGGCGTACGCCACACCCCGG 51  
 RESULT 111  
 AAT73860  
 ID AAT73860 standard; DNA; 51 BP.  
 XX  
 XX AAT73860;  
 AC  
 XX 09-NOV-2001 (first entry)  
 DT  
 XX Human silent SNP containing nucleic acid SEQ:801.  
 DE  
 XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
 KM

KM protein therapy; vaccine; probe; diagnostic assay; detection;  
 KM quantitation; restorative therapy; polymorphic; ds.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200140521-A2.  
 PN  
 XX 07-JUN-2001.  
 PD  
 XX  
 XX 30-NOV-2000; 2000WO-US032758.  
 PF  
 XX 30-NOV-1999; 99US-0168138P.  
 PR 29-NOV-2000; 2000US-00726173.  
 XX  
 XX (CURA-) CURAGEN CORP.  
 PA  
 XX Shinkets RA, Leach M;  
 PI WPI; 2001-356160/37.  
 DR  
 XX Polymorphic nucleic acid sequences, useful in genetic testing and  
 PT therapy.  
 XX  
 XX Claim 1; Page 299; 2653pp; English.  
 PS  
 XX AAT73060 to AAT79867 represent isolated human polymorphic polynucleotide  
 CC sequences (I), which contain single nucleotide polymorphisms (SNPs).  
 CC AAM53114 to AAM53329 represent peptide sequences related to human polymorphic  
 CC polynucleotide sequences. The sequences can be used in gene and protein  
 CC therapy, and in vaccine production. (I) and the polypeptides encoded by  
 CC them may be used in the prevention, diagnosis and treatment of diseases  
 CC associated with inappropriate expression of polymorphic polypeptides. For  
 CC example, (I) may be used to treat disorders by rectifying mutations or  
 CC deletions in a patient's genome that affect the activity of polypeptides  
 CC by expressing inactive proteins or to supplement the patient's own  
 CC production of polypeptide. Additionally, (I) and its complementary  
 CC sequences may also be used as DNA probes in diagnostic assays to detect  
 CC and quantitate the presence of similar nucleic acids in samples, and  
 CC therefore which patients may be in need of restorative therapy. The  
 CC polypeptides encoded by (I) may be used as antigens in the production of  
 CC antibodies specific for polymorphic polypeptides. The antibodies may also  
 CC be used to down regulate expression and activity. The antibodies may also  
 CC be used as diagnostic agents for detecting the presence of polymorphic  
 CC polypeptides in samples  
 CC  
 SQ Sequence 51 BP; 9 A; 16 C; 13 G; 13 T; 0 U; 0 Other;  
 Query Match 4.2%; Score 42; DB 1; Length 51;  
 Best Local Similarity 90.0%; Pred. No. 1.9e+02;  
 Matches 45; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 638 TGTACCCAGGCTGAGTGCAGTGGCGCAATCTTGGCTCACTGCAACTC 687  
 DB 1 TGTACCCAGGCTGAGTGCAGTGGCGCAATCTTGGCTCACTGCAACTC 50  
 RESULT 112  
 AAT73760  
 ID AAT73760 standard; DNA; 51 BP.  
 XX  
 XX AAT73760;  
 AC  
 XX 09-NOV-2001 (first entry)  
 DT  
 XX Human silent SNP containing nucleic acid SEQ:701.  
 DE  
 XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
 KM protein therapy; vaccine; probe; diagnostic assay; detection;  
 KM quantitation; restorative therapy; polymorphic; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200140521-A2.  
 PN

XX 07-JUN-2001.  
PD 30-NOV-2000; 2000MO-US032758.  
XX 30-NOV-1999; 99US-0168138P.  
PF 29-NOV-2000; 2000US-00726173.  
PR (CURA-) CURAGEN CORP.  
XX Shinkets RA, Leach M;  
XX WPI; 2001-356160/37.  
XX Polymorphic nucleic acid sequences, useful in genetic testing and  
PT therapy.  
PS Claim 1; Page 268; 2653pp; English.  
XX  
XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).  
CC AA173114 to AA175332 represent peptides related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (I) and the polypeptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides. For  
CC example, (I) may be used to treat disorders by rectifying mutations or  
CC deletions in a patient's genome that affect the activity of polypeptides  
CC by expressing inactive proteins or to supplement the patients own  
CC production of polypeptide. Additionally, (I) and its complementary  
CC sequences may also be used as DNA probes in diagnostic assays to detect  
CC and quantitate the presence of similar nucleic acids in samples, and  
CC therefore which patients may be in need of restorative therapy. The  
CC polypeptides encoded by (I) may be used as antigens in the production of  
CC antibodies specific for polymorphic polypeptides. The antibodies may also  
CC be used to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples  
XX  
SQ Sequence 51 BP; 9 A; 19 C; 13 G; 10 T; 0 U; 0 Other;  
Query Match 4.2%; Score 42; DB 1; Length 51;  
Best Local Similarity 90.0%; Pred. No. 1.9e+02;  
Matches 45; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 648 GGTGAGTGCAGTGGGCAATCTTGCTCACTGCAACCTTGCTCCCG 697  
DB 1 GCTGAGTGCAGTGAATGCAATCTGCTCACTGCAACCTTGCTCCCG 50  
RESULT 113  
AA177806  
ID AA177806 standard; DNA; 51 BP.  
XX  
AC AA177806;  
XX  
DT 09-NOV-2001 (first entry)  
XX  
DE Human silent SNP containing nucleic acid SEQ:4747.  
XX  
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KM protein therapy; vaccine; probe; diagnostic assay; detection;  
KM quantitation; restorative therapy; polymorphic; ds.  
XX  
OS Homo sapiens.  
XX  
XX WO200140521-A2.  
XX  
XX 07-JUN-2001.  
PD  
PF 30-NOV-2000; 2000MO-US032758.  
XX  
PR 30-NOV-1999; 99US-0168138P.  
XX

PR 29-NOV-2000; 2000US-00726173.  
XX (CURA-) CURAGEN CORP.  
XX Shinkets RA, Leach M;  
XX WPI; 2001-356160/37.  
XX Polymorphic nucleic acid sequences, useful in genetic testing and  
PT therapy.  
PS Claim 1; Page 1963; 2653pp; English.  
XX  
XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).  
CC AA173114 to AA175332 represent peptides related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (I) and the polypeptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides. For  
CC example, (I) may be used to treat disorders by rectifying mutations or  
CC deletions in a patient's genome that affect the activity of polypeptides  
CC by expressing inactive proteins or to supplement the patients own  
CC production of polypeptide. Additionally, (I) and its complementary  
CC sequences may also be used as DNA probes in diagnostic assays to detect  
CC and quantitate the presence of similar nucleic acids in samples, and  
CC therefore which patients may be in need of restorative therapy. The  
CC polypeptides encoded by (I) may be used as antigens in the production of  
CC antibodies specific for polymorphic polypeptides. The antibodies may also  
CC be used to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples  
XX  
SQ Sequence 51 BP; 7 A; 22 C; 9 G; 13 T; 0 U; 0 Other;  
Query Match 4.2%; Score 42; DB 1; Length 51;  
Best Local Similarity 90.0%; Pred. No. 1.9e+02;  
Matches 45; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 672 GGCTCACTGCAACCTTGCTCCCGGTTCAAGTATTTCTGCCCCAG 721  
DB 2 GGCTCACTGCAATCTTGCTCCCGGTTCAAGTATTTCTGCCCCAG 51  
RESULT 114  
AA173533/c  
ID AA173533 standard; DNA; 51 BP.  
XX  
AC AA173533;  
XX  
DT 09-NOV-2001 (first entry)  
XX  
DE Human silent SNP containing nucleic acid SEQ:474.  
XX  
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KM protein therapy; vaccine; probe; diagnostic assay; detection;  
KM quantitation; restorative therapy; polymorphic; ds.  
XX  
OS Homo sapiens.  
XX  
XX WO200140521-A2.  
XX  
XX 07-JUN-2001.  
PD  
PF 30-NOV-2000; 2000MO-US032758.  
XX  
PR 30-NOV-1999; 99US-0168138P.  
XX  
PR 29-NOV-2000; 2000US-00726173.  
XX (CURA-) CURAGEN CORP.  
XX Shinkets RA, Leach M;  
XX PI

DR WPI; 2001-356160/37.  
 XX Polymorphic nucleic acid sequences, useful in genetic testing and  
 PT therapy.  
 PS Claim 1; Page 199; 2653pp; English.  
 CC AAT73060 to AAT7867 represent isolated human polymorphic polynucleotide  
 CC sequences (I), which contain single nucleotide polymorphisms (SNPs).  
 CC AAM53114 to AAM53329 represent peptides related to human polymorphic  
 CC polynucleotide sequences. The sequences can be used in gene and protein  
 CC therapy, and in vaccine production. (I) and the polypeptides encoded by  
 CC them may be used in the prevention, diagnosis and treatment of diseases  
 CC associated with inappropriate expression of polymorphic polypeptides. For  
 CC example, (I) may be used to treat disorders by rectifying mutations or  
 CC deletions in a patient's genome that affect the activity of polypeptides  
 CC by expressing inactive proteins or to supplement the patients own  
 CC production of polypeptide. Additionally, (I) and its complementary  
 CC and quantitate the presence of similar nucleic acids in samples, and  
 CC therefore which patients may be in need of restorative therapy. The  
 CC polypeptides encoded by (I) may be used as antigens in the production of  
 CC antibodies specific for polymorphic polypeptides. The antibodies may also  
 CC be used to down regulate expression and activity. The antibodies may also  
 CC be used as diagnostic agents for detecting the presence of polymorphic  
 CC polypeptides in samples  
 CC  
 SQ Sequence 51 BP; 9 A; 14 C; 19 G; 9 T; 0 U; 0 Other;  
 Query Match 4.2%; Score 42; DB 1; Length 51;  
 Best Local Similarity 90.0%; Pred. No. 1.9e+02;  
 Matches 45; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 Oy 842 GCGTCGCTCGGCTCCCAAGTCGCGATTACAGGCGCCACCCAG 891  
 Db 50 GCCCGCTCGGCTCCCAAGTCGCGGATTACAGGCTTGAATCACCAG 1  
 RESULT 115  
 ABL00195  
 ID ABL00195 standard; DNA; 51 BP.  
 XX  
 AC ABL00195;  
 XX  
 DT 05-MAR-2002 (first entry)  
 XX  
 DE Human silent noncoding SNP oligonucleotide SEQ ID NO:186.  
 XX  
 KM Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic;  
 KM immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;  
 KM autoimmune disease; inflammation; cancer; nervous system disease;  
 KM infection; polymorphic protein; de.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200138586-A2.  
 XX  
 PD 31-MAY-2001.  
 XX  
 PF 22-NOV-2000; 2000WO-US032311.  
 XX  
 PR 24-NOV-1999; 99US-0167383P.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Shinkels RA, Leach M;  
 XX  
 DR WPI; 2001-355949/37.  
 XX  
 PT Isolated human nucleic acids comprising one or more single nucleotide  
 PT polymorphisms, useful for treating a subject suffering from a pathology,  
 PT e.g. autoimmune diseases, ascribed to the presence of a sequence  
 PT polymorphism.

XX  
 PS Claim 1; Page 303; 674pp; English.  
 CC ABL00010 to ABL01104 represent human nucleic acid oligonucleotides  
 CC comprising one or more single nucleotide polymorphisms (SNPs). ABB56531  
 CC to ABB56903 represent human peptides encoded by some of the SNP  
 CC oligonucleotides. The sequences from the present invention can have  
 CC immunosuppressive, cytostatic, antiinflammatory, neuroprotective and  
 CC antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides  
 CC and antibodies from the present invention can be used for treating a  
 CC subject suffering from, at risk for, or suspected of, suffering from a  
 CC pathology ascribed to the presence of a sequence polymorphism. The  
 CC pathology may be autoimmune diseases, inflammation, cancer, diseases of  
 CC the nervous system, and infection by pathogenic microorganisms. The SNPs  
 CC are also useful for determining which forms of a characterized  
 CC polymorphism are present in individuals. The antibodies may be used in  
 CC the detection, quantitation and/or cellular or tissue localisation of a  
 CC polymorphic protein (e.g., for use in measuring levels of the polymorphic  
 CC protein within appropriate physiological samples)  
 CC  
 SQ Sequence 51 BP; 8 A; 23 C; 8 G; 12 T; 0 U; 0 Other;  
 Query Match 4.2%; Score 42; DB 1; Length 51;  
 Best Local Similarity 90.0%; Pred. No. 1.9e+02;  
 Matches 45; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 Oy 981 CAACCTGCTGCTCCGCGCTCAAGGATTCCTCTCTCAGCCTCCAG 1030  
 Db 1 CAACCTCGCTCCCGAGTTCAACGATTCCTCTCTCAGCCTCCAG 50  
 RESULT 116  
 AD112525/C  
 ID AD112525 standard; DNA; 48 BP.  
 XX  
 AC AD112525;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE Human BRCA1 DNA junction sequence comprising large deletion SegID 5.  
 XX  
 KM ds; cancer; human; tumour suppressor;  
 KM breast cancer susceptibility gene 1; BRCA1; repetitive Alu;  
 KM ovarian cancer; junction sequence; recombination; mutant.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003104474-A2.  
 XX  
 PD 18-DEC-2003.  
 XX  
 PF 09-JUN-2003; 2003WO-US018098.  
 XX  
 PR 07-JUN-2002; 2002US-0387132P.  
 PR 09-AUG-2002; 2002US-0402430P.  
 XX  
 PA (MYRI-) MYRIAD GENETICS INC.  
 XX  
 PI Scholl T, Hendrickson BC, Ward B, Pruss D;  
 XX  
 DR WPI; 2004-062369/06.  
 XX  
 PT Predicting a predisposition to cancer in a patient comprising detecting a  
 PT deletion in the BRCA1 gene that results from the unequal crossover  
 PT between a pair of repetitive sequences in the BRCA1 gene.  
 XX  
 PS Claim 16; SEQ ID NO 5; 59pp; English.  
 XX  
 CC This invention relates to a novel method for predicting a predisposition  
 CC to cancer in a patient by detecting large deletions in the human tumour  
 CC suppressor gene identified as the breast cancer susceptibility gene 1  
 CC (BRCA1). Specifically, it refers to deletions that result from the  
 CC unequal crossover between a pair of repetitive Alu sequences in the BRCA1

CC gene, such that the recombinant nucleotide sequence containing the  
CC deletion indicates a predisposition to breast and ovarian cancer. The  
CC present invention describes newly discovered deletion mutations that are  
CC believed to be deleterious and cause significant alterations in the  
CC structure or biochemical function of BRCA1. Accordingly, it provides  
CC methods for detecting such mutants, as well as identifying and screening  
CC for cytostatic compounds useful for treating or preventing cancers  
CC associated with a BRCA1 genetic variant. This polynucleotide is a DNA  
CC fragment representing a junction sequence that arises as a result of a  
CC recombination event in human BRCA1 that causes the omission of exons 15  
CC and 16, given in an exemplification of the invention.

XX SQ Sequence 48 BP; 13 A; 12 C; 14 G; 9 T; 0 U; 0 Other;

Query Match 4.2%; Score 41.6; DB 1; Length 48;  
Best Local Similarity 91.7%; Pred. No. 1.9e+02;  
Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 696 GGGTCAAGTATTTCTCTGCCCCAGCCCTCTGAGTACTGAGACTAC 743  
DB 48 GGGTCAAGCATCTCTCTGCTCAGCCCTCTGAGTACTGAGACTAC 1

RESULT 117

AA175849  
ID AA175849 standard; DNA; 51 BP.

XX AC AA175849;

XX DT 09-NOV-2001 (first entry)

XX DE Human silent SNP containing nucleic acid SEQ:2790.

XX KM Human; single nucleotide polymorphism; SNP; genome; gene therapy;

XX KW protein therapy; vaccine; probe; diagnostic assay; detection;

XX KM quantitation; restorative therapy; polymorphic; ds.

XX OS Homo sapiens.

XX PN MO200140521-A2.

XX PD 07-JUN-2001.

XX PF 30-NOV-2000; 2000WO-US032758.

XX PR 30-NOV-1999; 99US-0168138P.

XX PR 29-NOV-2000; 2000US-00726173.

XX PA (CURA-) CURAGEN CORP.

XX PI Shimkete RA, Leach M;

XX DR WPI; 2001-356160/37.

XX PT Polymorphic nucleic acid sequences, useful in genetic testing and

XX therapy.

XX PS Claim 1; Page 904; 2653pp; English.

XX CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide

XX CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide

XX CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide

XX CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

XX CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide

CC polypeptides encoded by (1) may be used as antigens in the production of  
CC antibodies specific for polymorphic polypeptides. The antibodies may also  
CC be used to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples

XX SQ Sequence 51 BP; 12 A; 21 C; 6 G; 12 T; 0 U; 0 Other;

Query Match 4.2%; Score 41.6; DB 1; Length 51;  
Best Local Similarity 91.7%; Pred. No. 2e+02;  
Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 966 AATCTCGCTCACTGCAACCTCTGCTCCGGGCTCAAGCATCTCC 1013  
DB 4 AATCTCGCTCACTGCAACCTCTGCTCCGGGCTCAAGCATCTCC 51

RESULT 118

ABL00141/C  
ID ABL00141 standard; DNA; 51 BP.

XX AC ABL00141;

XX DT 05-MAR-2002 (first entry)

XX DE Human silent noncoding SNP oligonucleotide SEQ ID NO:132.

XX KM Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic;

XX KM immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;

XX KM autoimmune disease; inflammation; cancer; nervous system disease;

XX KM infection; polymorphic protein; ds.

XX OS Homo sapiens.

XX PN MO200138586-A2.

XX PD 31-MAY-2001.

XX PF 22-NOV-2000; 2000WO-US032311.

XX PR 24-NOV-1999; 99US-0167383P.

XX PA (CURA-) CURAGEN CORP.

XX PI Shimkete RA, Leach M;

XX DR WPI; 2001-355949/37.

XX PT Isolated human nucleic acids comprising one or more single nucleotide

XX PT polymorphisms, useful for treating a subject suffering from a pathology,

XX PT e.g. autoimmune diseases, ascribed to the presence of a sequence

XX PT polymorphism.

XX PS Claim 1; Page 286; 674pp; English.

XX CC ABL00010 to ABL01104 represent human nucleic acid oligonucleotides

XX CC comprising one or more single nucleotide polymorphisms (SNPs). ABB56531

XX CC to ABB56903 represent human peptides encoded by some of the SNP

XX CC oligonucleotides. The sequences from the present invention can have

XX CC immunosuppressive, cytostatic, antiinflammatory, neuroprotective and

XX CC antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides

XX CC and antibodies from the present invention can be used for treating a

XX CC subject suffering from, at risk for, or suspected of, suffering from a

XX CC pathology ascribed to the presence of a sequence polymorphism. The

XX CC pathology may be autoimmune diseases, inflammation, cancer, diseases of

XX CC the nervous system, and infection by pathogenic microorganisms. The SNPs

XX CC are also useful for determining which forms of a characterized

XX CC polymorphism are present in individuals. The antibodies may be used in

XX CC the detection, quantitation and/or cellular or tissue localization of a

XX CC polymorphic protein (e.g., for use in measuring levels of the polymorphic

XX CC protein within appropriate physiological samples)

XX SQ Sequence 51 BP; 14 A; 12 C; 16 G; 9 T; 0 U; 0 Other;

Query Match 4.2%; Score 41.6; DB 1; Length 51;  
Best Local Similarity 91.7%; Pred. No. 2e+02; 4; Indels 0; Gaps 0;  
Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Dy 194 TCTCCATGTTGGTCAGGCTGCTCGAACTCCGACCTCAGATGATCC 241  
Db 51 TCTCCATGTTGGTCAGGCTGCTCGAACTCCGACCTCAGATGATCC 4

## RESULT 119

AAA77442  
ID AAA77442 standard; cDNA; 51 BP.

AC AAA77442;

DT 16-NOV-2000 (first entry)

DE Human Aluubfamily SQ gene polymorphic site, SEQ ID NO:1125.

KM Human; single nucleotide polymorphism; SNP; detection; identification;  
KW gene therapy; ss.

XX Homo sapiens.

XX OS

XX Key Location/Qualifiers  
FH replace(26,C)  
FT variation /\*tag= a

XX WO200029623-A2.

XX 25-MAY-2000.

XX 17-NOV-1999; 99WO-US027293.

XX 17-NOV-1998; 98US-0109024P.

XX 16-NOV-1999; 99US-00443199.

XX (CURA-) CURAGEN CORP.

XX Shinkets RA, Leach MD;

XX WPI; 2000-387826/33.

XX P-PSDB; AAB11761.

PT Human nucleic acids containing single nucleotide polymorphisms, useful  
for treating a subject suffering, or at risk from a pathology due to the  
presence of a sequence polymorphism.

PS Claim 1; Page 498; 543pp; English.

XX Sequences AAA76318-A77509 represent 1192 human nucleic acid sequences  
CC which contain single nucleotide polymorphisms (SNPs). Sequences 1 to 1112  
CC (AAA76318-A77429) are consecutive pairs of nucleotides which contain  
CC silent SNPs. Sequences 1113 to 1192 (AAA77430-A77509) are consecutive  
CC pairs of nucleotides containing SNPs which result in changes in the  
CC corresponding amino acid sequences (AAB11749-B11828). The SNPs in  
CC sequences 1113 to 1128 (AAA77430-A77445) lead to conservative amino acid  
CC changes, while those in sequences 1129 to 1186 (AAA77446-A77503) result  
CC in non-conservative changes. The SNPs in sequences 1187 to 1192  
CC (AAA77504-A77509) generate frameshift mutations. The invention also  
CC relates to a method of detecting a polymorphic site in a nucleic acid and  
CC a method of determining the relatedness of two nucleic acids. It also  
CC encompasses peptides containing polymorphic sites, antibodies raised  
CC against such peptides, and a method of detecting polymorphic  
CC proteins/peptides using the antibodies. The nucleic acids are useful for  
CC gene therapy of an individual having, suspected of having, or at risk of  
CC developing a pathological condition due to the presence of a sequence  
CC polymorphism. Such treatment would comprise administration of the wild-  
CC type nucleic acid sequence. Antibodies raised against polymorphic  
CC peptides can also be used in the treatment of such individuals  
XX Sequence 51 BP; 8 A; 8 C; 15 G; 20 T; 0 U; 0 Other;

Query Match 4.2%; Score 41.4; DB 1; Length 51;  
Best Local Similarity 88.2%; Pred. No. 2e+02; 6; Indels 0; Gaps 0;  
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Dy 1071 TTTTGATTTTTCATTAGAGCGGGGTTTCACCATATTGTCAGGCTGCT 1121  
Db 1 TTTTGATTTTTCATTAGAGAGAGCGGGGTTTCACCATATTGTCAGGCTGCT 51

## RESULT 120

AAA76988/c  
ID AAA76988 standard; cDNA; 51 BP.

AC AAA76988;

DT 16-NOV-2000 (first entry)

DE Human clone cg42924993 polymorphic site, SEQ ID NO:671.

KM Human; single nucleotide polymorphism; SNP; detection; identification;  
KW gene therapy; ss.

XX Homo sapiens.

XX OS

XX Key Location/Qualifiers  
FH replace(26,G)  
FT variation /\*tag= a

XX WO200029623-A2.

XX 25-MAY-2000.

XX 17-NOV-1999; 99WO-US027293.

XX 17-NOV-1998; 98US-0109024P.

XX 16-NOV-1999; 99US-00443199.

XX (CURA-) CURAGEN CORP.

XX Shinkets RA, Leach MD;

XX WPI; 2000-387826/33.

PT Human nucleic acids containing single nucleotide polymorphisms, useful  
for treating a subject suffering, or at risk from a pathology due to the  
presence of a sequence polymorphism.

PS Claim 1; Page 360; 543pp; English.

XX Sequences AAA76318-A77509 represent 1192 human nucleic acid sequences  
CC which contain single nucleotide polymorphisms (SNPs). Sequences 1 to 1112  
CC (AAA76318-A77429) are consecutive pairs of nucleotides which contain  
CC silent SNPs. Sequences 1113 to 1192 (AAA77430-A77509) are consecutive  
CC pairs of nucleotides containing SNPs which result in changes in the  
CC corresponding amino acid sequences (AAB11749-B11828). The SNPs in  
CC sequences 1113 to 1128 (AAA77430-A77445) lead to conservative amino acid  
CC changes, while those in sequences 1129 to 1186 (AAA77446-A77503) result  
CC in non-conservative changes. The SNPs in sequences 1187 to 1192  
CC (AAA77504-A77509) generate frameshift mutations. The invention also  
CC relates to a method of detecting a polymorphic site in a nucleic acid and  
CC a method of determining the relatedness of two nucleic acids. It also  
CC encompasses peptides containing polymorphic sites, antibodies raised  
CC against such peptides, and a method of detecting polymorphic  
CC proteins/peptides using the antibodies. The nucleic acids are useful for  
CC gene therapy of an individual having, suspected of having, or at risk of  
CC developing a pathological condition due to the presence of a sequence  
CC polymorphism. Such treatment would comprise administration of the wild-  
CC type nucleic acid sequence. Antibodies raised against polymorphic  
CC peptides can also be used in the treatment of such individuals  
XX Sequence 51 BP; 20 A; 15 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 4.2%; Score 41.4; DB 1; Length 51;  
 Best Local Similarity 88.2%; Pred. No. 2e+02;  
 Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 1071 TTTTGTATTTTCATAGAGCGGGGTTTCACATATTTGTGAGGCTGCT 1121  
 51 TTTTGTATTTTCATAGAGCGGGGTTTCACATATTTGTGAGGCTGCT 1

RESULT 121  
 AAA77021/C  
 ID AAA77021 standard; cDNA; 51 BP.  
 AC AAA77021;  
 XX  
 XX  
 16-NOV-2000 (first entry)

Human clone CG43089031 polymorphic site, SEQ ID NO:704.  
 Human; single nucleotide polymorphism; SNP; detection; identification;  
 gene therapy; ss.  
 Homo sapiens.

Key Location/Qualifiers  
 FH replace(26,A)  
 FT /\*tag= a

WO200029623-A2.

25-MAY-2000.

17-NOV-1999; 99WO-US027293.

17-NOV-1998; 98US-0109024P.

16-NOV-1999; 99US-00443199.

(CURA-) CURAGEN CORP.

Shinkets RA, Leach MD;

WPI; 2000-387826/33.

Human nucleic acids containing single nucleotide polymorphisms, useful  
 for treating a subject suffering, or at risk from a pathology due to the  
 presence of a sequence polymorphism.

Claim 1; Page 370; 543pp; English.

Sequences AAA76318-A77509 represent 1192 human nucleic acid sequences  
 which contain single nucleotide polymorphisms (SNPs). Sequences 1 to 112  
 (AAA76318-A77429) are consecutive pairs of nucleotides which contain  
 silent SNPs. Sequences 113 to 1192 (AAA77430-A77509) are consecutive  
 pairs of nucleotides containing SNPs which result in changes in the  
 corresponding amino acid sequences (AAB11749-B11828). The SNPs in  
 sequences 113 to 1128 (AAA77430-A77445) lead to conservative amino acid  
 changes, while those in sequences 1129 to 1166 (AAA77446-A77503) result  
 in non-conservative changes. The SNPs in sequences 1167 to 1192  
 (AAA77504-A77509) generate frameshift mutations. The invention also  
 relates to a method of detecting a polymorphic site in a nucleic acid and  
 a method of determining the relatedness of two nucleic acids. It also  
 encompasses peptides containing polymorphic sites, antibodies raised  
 against such peptides, and a method of detecting polymorphic  
 proteins/peptides using the antibodies. The nucleic acids are useful for  
 gene therapy of an individual having, suspected of having, or at risk of  
 developing a pathological condition due to the presence of a sequence  
 polymorphism. Such treatment would comprise administration of the wild-  
 type nucleic acid sequence. Antibodies raised against polymorphic  
 peptides can also be used in the treatment of such individuals

Sequence 51 BP; 12 A; 14 C; 16 G; 9 T; 0 U; 0 Other;

Query Match 4.2%; Score 41.4; DB 1; Length 51;

Best Local Similarity 88.2%; Pred. No. 2e+02;  
 Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 853 CTTCCCAAGTCTGGATTACAGCGGTGACACACCGCCGCTTATTT 903  
 51 CTTCCCAAGTCTGGATTATAGCGGTGACACACCGCCGCTTATTT 1

RESULT 122  
 ADCl6930/C  
 ID ADCl6930 standard; DNA; 51 BP.  
 AC ADCl6930;  
 XX  
 XX  
 18-DEC-2003 (first entry)

Human single nucleotide polymorphism (SNP) region Seq ID32.

sequence polymorphism analysis; human identity; human relatedness;  
 single nucleotide polymorphism; SNP; genetic disease; cytostatic;  
 immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;  
 fatty acid metabolism; glycolysis; amino acid metabolism;  
 paternity analysis; forensic; autoimmune disease; cancer; nervous system;  
 infection; pathogenic microorganism; human; ds.

Homo sapiens.

Key Location/Qualifiers  
 FH replace(26,T)  
 FT /\*tag= a  
 FT /standard\_name="single nucleotide polymorphism"

WO200029622-A2.

25-MAY-2000.

17-NOV-1999; 99WO-US027283.

17-NOV-1998; 98US-0109024P.

16-NOV-1999; 99US-00443199.

(CURA-) CURAGEN CORP.

Shinkets RA, Leach MD;

WPI; 2000-39731/34.

Novel polynucleotide and polypeptide including one or more single  
 nucleotide polymorphisms, useful for diagnosing and treating conditions  
 associated with the presence of sequence polymorphism in humans and  
 animals.

Claim 1; SEQ ID NO 32; 187pp; English.

This invention relates to novel isolated nucleotide sequences which  
 comprise 217 defined polymorphic sequences. Sequence polymorphism-based  
 analysis of nucleic acid sequences can augment or replace previously  
 known methods for determining the identity and relatedness of  
 individuals. Single nucleotide polymorphisms (SNPs) tend to occur with  
 great frequency throughout the genome and may be located close to loci of  
 interest. Such variations can cause or be closely linked to pathological  
 conditions (genetic diseases). Hence the SNPs of the invention may be  
 useful in the development of compounds with cytostatic,  
 immunosuppressive, antiinflammatory, neuroprotective or antimicrobial  
 activities. Regulators of metabolic pathways such as fatty acid  
 metabolism, glycolysis, and amino acid metabolism may also be developed.  
 The compounds may be useful for treating a subject suffering from or at  
 risk for a pathology associated with the presence of a sequence  
 polymorphism. SNP detection is also useful in paternity analysis and  
 forensic application. Polymorphisms may contribute to the phenotype of an  
 organism and phenotypic traits include genetic diseases such as  
 autoimmune diseases, cancer, diseases of the nervous system and infection  
 by pathogenic microorganisms. The present sequence is the sequence

CC surrounding and including a human SNP of the invention.

XX Sequence 51 BP; 12 A; 15 C; 14 G; 10 T; 0 U; 0 Other;

SO Query Match 4.2%; Score 41.4; DB 1; Length 51;

Best Local Similarity 88.2%; Pred. No. 2e+02;

Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

1087 GAGGCGGGGTTTACATATTGTCAGGCTGTCCTCAAACTCCAGCTCA 1137  
DB 51 GAGACGGGGTTTCACCATATTGCGCGGATGCTCTCGAACTCTGACCTCA 1

RESULT 123

AA176193/c  
ID AA176193 standard; DNA; 51 BP.

AA176193;

09-NOV-2001 (first entry)

Human silent SNP containing nucleic acid SEQ:3134.

Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
protein therapy; vaccine; probe; diagnostic assay; detection;  
quantitation; restorative therapy; polymorphic; ds.

Homo sapiens.

MO200140521-A2.

07-JUN-2001.

30-NOV-2000; 2000MO-US032758.

30-NOV-1999; 99US-0168138P.

29-NOV-2000; 2000US-00726173.

(CURA-) CURAGEN CORP.

Shimkets RA, Leach M;

WPI; 2001-356160/37.

Polymorphic nucleic acid sequences, useful in genetic testing and

therapy.

Claim 1; Page 1009; 2653pp; English.

AA173060 to AA179867 represent isolated human polymorphic polynucleotide

sequences (I), which contain single nucleotide polymorphisms (SNPs).

AA173060 to AA173329 represent peptides related to human polymorphic

polynucleotide sequences. The sequences can be used in gene and protein

therapy, and in vaccine production. (I) and the polypeptides encoded by

them may be used in the prevention, diagnosis and treatment of diseases

associated with inappropriate expression of polymorphic polypeptides. For

example, (I) may be used to treat disorders by rectifying mutations or

deletions in a patient's genome that affect the activity of polypeptides

by expressing inactive proteins or to supplement the patient's own

production of polypeptide. Additionally, (I) and its complementary

sequences may also be used as DNA probes in diagnostic assays to detect

and quantitate the presence of similar nucleic acids in samples, and

therefore which patients may be in need of restorative therapy. The

polypeptides encoded by (I) may be used as antigens in the production of

antibodies specific for polymorphic polypeptides. The antibodies may also

be used to down regulate expression and activity. The antibodies may also

be used as diagnostic agents for detecting the presence of polymorphic

polypeptides in samples

Sequence 51 BP; 13 A; 16 C; 13 G; 9 T; 0 U; 0 Other;

Query Match 4.2%; Score 41.4; DB 1; Length 51;

Best Local Similarity 88.2%; Pred. No. 2e+02;

Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 177 TTAGTAGAGATGAGTTTCTTCATGTTGGTCAGGCTGTCGAACTCCCG 227

DB 51 TTAGTAGAGAGAGGGGTTTCACCATGCTGCGCGGATGCTCTCGAACTCTG 1

RESULT 124

AA173061/c  
ID AA173061 standard; DNA; 51 BP.

AA173061;

09-NOV-2001 (first entry)

Human silent SNP containing nucleic acid SEQ:2.

Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
protein therapy; vaccine; probe; diagnostic assay; detection;  
quantitation; restorative therapy; polymorphic; ds.

Homo sapiens.

MO200140521-A2.

07-JUN-2001.

30-NOV-2000; 2000MO-US032758.

30-NOV-1999; 99US-0168138P.

29-NOV-2000; 2000US-00726173.

(CURA-) CURAGEN CORP.

Shimkets RA, Leach M;

WPI; 2001-356160/37.

Polymorphic nucleic acid sequences, useful in genetic testing and

therapy.

Claim 1; Page 54; 2653pp; English.

AA173060 to AA179867 represent isolated human polymorphic polynucleotide

sequences (I), which contain single nucleotide polymorphisms (SNPs).

AA173060 to AA173329 represent peptides related to human polymorphic

polynucleotide sequences. The sequences can be used in gene and protein

therapy, and in vaccine production. (I) and the polypeptides encoded by

them may be used in the prevention, diagnosis and treatment of diseases

associated with inappropriate expression of polymorphic polypeptides. For

example, (I) may be used to treat disorders by rectifying mutations or

deletions in a patient's genome that affect the activity of polypeptides

by expressing inactive proteins or to supplement the patient's own

production of polypeptide. Additionally, (I) and its complementary

sequences may also be used as DNA probes in diagnostic assays to detect

and quantitate the presence of similar nucleic acids in samples, and

therefore which patients may be in need of restorative therapy. The

polypeptides encoded by (I) may be used as antigens in the production of

antibodies specific for polymorphic polypeptides. The antibodies may also

be used to down regulate expression and activity. The antibodies may also

be used as diagnostic agents for detecting the presence of polymorphic

polypeptides in samples

Sequence 51 BP; 12 A; 11 C; 22 G; 6 T; 0 U; 0 Other;

Query Match 4.2%; Score 41.4; DB 1; Length 51;

Best Local Similarity 88.2%; Pred. No. 2e+02;

Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 684 CTTCTGCTCCCGGTTTCAATATTCTCTGCTCCCGGAGCTCTCGAGTAGC 734

DB 51 CTTCTGCTCCCGGTTTCAATATTCTCTGCTCCCGGAGCTCTCGAGTAGC 1



RESULT 125  
AA174775  
ID AA174775 standard; DNA; 51 BP.  
XX  
AC AA174775;  
XX  
DT 09-NOV-2001 (first entry)  
XX  
DE Human silent SNP containing nucleic acid SEQ:1716.  
XX  
KM Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KW protein therapy; vaccine; probe; diagnostic assay; detection;  
KM quantitation; restorative therapy; polymorphic; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200140521-A2.  
XX  
PD 07-JUN-2001.  
XX  
PF 30-NOV-2000; 2000WO-US032758.  
XX  
PR 30-NOV-1999; 99US-0168138P.  
XX  
PR 29-NOV-2000; 2000US-00726173.  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
PI Shimketa RA, Leach M;  
XX  
DR WPI; 2001-356160/37.  
XX  
PT polymorphic nucleic acid sequences, useful in genetic testing and  
PT therapy.  
XX  
PS Claim 1; Page 579; 2653pp; English.  
XX  
XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).  
CC AA173114 to AA175329 represent peptides related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (I) and the polypeptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides. For  
CC example, (I) may be used to treat disorders by rectifying mutations or  
CC deletions in a patient's genome that affect the activity of polypeptides  
CC by expressing inactive proteins or to supplement the patients own  
CC production of polypeptide. Additionally, (I) and its complementary  
CC sequences may also be used as DNA probes in diagnostic assays to detect  
CC and quantitate the presence of similar nucleic acids in samples, and  
CC therefore which patients may be in need of restorative therapy. The  
CC polypeptides encoded by (I) may be used as antigens in the production of  
CC antibodies specific for polymorphic polypeptides. The antibodies may also  
CC be used to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples  
XX  
SQ Sequence 51 BP; 11 A; 21 C; 12 G; 7 T; 0 U; 0 Other;  
Query Match 4.2%; Score 41.4; DB 1; Length 51;  
Best Local Similarity 88.2%; Pred. No. 2e+02;  
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
OY 997 GGCTCAAGCATCTCTGCTCAGCTCCCAAGCAGCTGGATTACGGC 1047  
DB 1 GGCTCAAGCATCTCTCGCTCAGCTCCCAAGCAGCTGGACTACAGGC 51  
RESULT 126  
AA173736/C  
ID AA173736 standard; DNA; 51 BP.  
XX  
AC AA173736;

XX  
DT 09-NOV-2001 (first entry)  
XX  
DE Human silent SNP containing nucleic acid SEQ:677.  
XX  
AC Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KW protein therapy; vaccine; probe; diagnostic assay; detection;  
KM quantitation; restorative therapy; polymorphic; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200140521-A2.  
XX  
PD 07-JUN-2001.  
XX  
PF 30-NOV-2000; 2000WO-US032758.  
XX  
PR 30-NOV-1999; 99US-0168138P.  
XX  
PR 29-NOV-2000; 2000US-00726173.  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
PI Shimketa RA, Leach M;  
XX  
DR WPI; 2001-356160/37.  
XX  
PT polymorphic nucleic acid sequences, useful in genetic testing and  
PT therapy.  
XX  
PS Claim 1; Page 261; 2653pp; English.  
XX  
XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).  
CC AA173114 to AA175329 represent peptides related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (I) and the polypeptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides. For  
CC example, (I) may be used to treat disorders by rectifying mutations or  
CC deletions in a patient's genome that affect the activity of polypeptides  
CC by expressing inactive proteins or to supplement the patients own  
CC production of polypeptide. Additionally, (I) and its complementary  
CC sequences may also be used as DNA probes in diagnostic assays to detect  
CC and quantitate the presence of similar nucleic acids in samples, and  
CC therefore which patients may be in need of restorative therapy. The  
CC polypeptides encoded by (I) may be used as antigens in the production of  
CC antibodies specific for polymorphic polypeptides. The antibodies may also  
CC be used to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples  
XX  
SQ Sequence 51 BP; 18 A; 11 C; 11 G; 11 T; 0 U; 0 Other;  
Query Match 4.2%; Score 41.4; DB 1; Length 51;  
Best Local Similarity 88.2%; Pred. No. 2e+02;  
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
OY 1052 GCCACCAACCCCGCTAATTTTGTATTTTCATTAGAGCGGTTTCACC 1102  
DB 51 GCCATCACACCCGGCTAATTTTGTATTTTGTATAGACGGGTTTCATC 1  
RESULT 127  
AA176185/C  
ID AA176185 standard; DNA; 51 BP.  
XX  
AC AA176185;  
XX  
DT 09-NOV-2001 (first entry)  
XX  
DE Human silent SNP containing nucleic acid SEQ:3126.  
XX  
AC Human; single nucleotide polymorphism; SNP; genome; gene therapy;

KM protein therapy; vaccine; probe; diagnostic assay; detection;  
KM quantitation; restorative therapy; polymorphic; ds.  
XX Homo sapiens.  
OS WO200140521-A2.  
XX  
XX PD 07-JUN-2001.  
XX  
XX PE 30-NOV-2000; 2000WO-US032758.  
XX  
XX PR 30-NOV-1999; 99US-0168138P.  
XX PR 29-NOV-2000; 2000US-00726173.  
XX  
XX PA (CURA-) CURAGEN CORP.  
XX  
XX PI Shinkets RA, Leach M;  
XX DR WPI; 2001-356160/37.  
XX  
XX PT Polymorphic nucleic acid sequences, useful in genetic testing and  
XX therapy.  
XX  
XX PS Claim 1; Page 1007; 2653pp; English.  
XX  
XX CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
XX sequences (I), which contain single nucleotide polymorphisms (SNPs).  
XX CC AA53114 to AA53329 represent peptides related to human polymorphic  
XX polynucleotide sequences. The sequences can be used in gene and protein  
XX therapy, and in vaccine production. (I) and the polypeptides encoded by  
XX them may be used in the prevention, diagnosis and treatment of diseases  
XX associated with inappropriate expression of polymorphic polypeptides. For  
XX example, (I) may be used to treat disorders by rectifying mutations or  
XX deletions in a patient's genome that affect the activity of polypeptides  
XX by expressing inactive proteins or to supplement the patients own  
XX production of polypeptide. Additionally, (I) and its complementary  
XX sequences may also be used as DNA probes in diagnostic assays to detect  
XX and quantitate the presence of similar nucleic acids in samples, and  
XX therefore which patients may be in need of restorative therapy. The  
XX polypeptides encoded by (I) may be used as antigens in the production of  
XX antibodies specific for polymorphic polypeptides. The antibodies may also  
XX be used to down regulate expression and activity. The antibodies may also  
XX be used as diagnostic agents for detecting the presence of polymorphic  
XX polypeptides in samples  
XX  
SQ Sequence 51 BP; 17 A; 16 C; 9 G; 9 T; 0 U; 0 Other;  
Query Match 4.2%; Score 41.4; DB 1; Length 51;  
Best Local Similarity 88.2%; Pred. No. 2e+02;  
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
CY 170 TTTTATTAGTAGAGTGGAGTTCTCCATGTTGGTGAAGCTGCTCGA 220  
DB 51 TGTATTTTAGTAGAGCGGGTTTCACCATGTGGCCAGGCTGCTCGA 1  
RESULT 128  
AA174502/C  
ID AA174502 standard; DNA; 51 BP.  
XX  
XX AC AA174502;  
XX  
XX DT 09-NOV-2001 (first entry)  
XX  
XX DE Human silent SNP containing nucleic acid SEQ:1443.  
XX  
XX KM Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
XX KM protein therapy; vaccine; probe; diagnostic assay; detection;  
XX KM quantitation; restorative therapy; polymorphic; ds.  
OS Homo sapiens.  
XX  
XX PF WO200140521-A2.  
XX  
XX PR

XX  
XX PD 07-JUN-2001.  
XX  
XX PE 30-NOV-2000; 2000WO-US032758.  
XX  
XX PR 30-NOV-1999; 99US-0168138P.  
XX PR 29-NOV-2000; 2000US-00726173.  
XX  
XX PA (CURA-) CURAGEN CORP.  
XX  
XX PI Shinkets RA, Leach M;  
XX DR WPI; 2001-356160/37.  
XX  
XX PT Polymorphic nucleic acid sequences, useful in genetic testing and  
XX therapy.  
XX  
XX PS Claim 1; Page 495; 2653pp; English.  
XX  
XX CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
XX sequences (I), which contain single nucleotide polymorphisms (SNPs).  
XX CC AA53114 to AA53329 represent peptides related to human polymorphic  
XX polynucleotide sequences. The sequences can be used in gene and protein  
XX therapy, and in vaccine production. (I) and the polypeptides encoded by  
XX them may be used in the prevention, diagnosis and treatment of diseases  
XX associated with inappropriate expression of polymorphic polypeptides. For  
XX example, (I) may be used to treat disorders by rectifying mutations or  
XX deletions in a patient's genome that affect the activity of polypeptides  
XX by expressing inactive proteins or to supplement the patients own  
XX production of polypeptide. Additionally, (I) and its complementary  
XX sequences may also be used as DNA probes in diagnostic assays to detect  
XX and quantitate the presence of similar nucleic acids in samples, and  
XX therefore which patients may be in need of restorative therapy. The  
XX polypeptides encoded by (I) may be used as antigens in the production of  
XX antibodies specific for polymorphic polypeptides. The antibodies may also  
XX be used to down regulate expression and activity. The antibodies may also  
XX be used as diagnostic agents for detecting the presence of polymorphic  
XX polypeptides in samples  
XX  
SQ Sequence 51 BP; 13 A; 16 C; 12 G; 10 T; 0 U; 0 Other;  
Query Match 4.2%; Score 41.4; DB 1; Length 51;  
Best Local Similarity 88.2%; Pred. No. 2e+02;  
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
CY 178 TAGTAGAGTAGAGTTCATGCTGCTGAGCTGGTGAAGTCCCGA 228  
DB 51 TAGTAGAGTAGAGTGGGTTTCACCATGCTGGCCAGGCTGCTGA 1  
RESULT 129  
AA176499  
ID AA176499 standard; DNA; 51 BP.  
XX  
XX AC AA176499;  
XX  
XX DT 09-NOV-2001 (first entry)  
XX  
XX DE Human silent SNP containing nucleic acid SEQ:1440.  
XX  
XX KM Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
XX KM protein therapy; vaccine; probe; diagnostic assay; detection;  
XX KM quantitation; restorative therapy; polymorphic; ds.  
OS Homo sapiens.  
XX  
XX PF WO200140521-A2.  
XX  
XX PD 07-JUN-2001.  
XX  
XX PR 30-NOV-2000; 2000WO-US032758.  
XX  
XX PF 30-NOV-1999; 99US-0168138P.  
XX  
XX PR

PR 29-NOV-2000; 2000US-00726173.  
XX (CURA-) CURAGEN CORP.  
PA Shimkets RA, Leach M;  
XX WPI, 2001-356160/37.  
XX Polymorphic nucleic acid sequences, useful in genetic testing and  
PT therapy.  
PS Claim 1; Page 1103; 2653pp; English.  
XX AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide  
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).  
CC AAM53114 to AAM53329 represent peptides related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (I) and the polypeptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides. For  
CC example, (I) may be used to treat disorders by rectifying mutations or  
CC deletions in a patient's genome that affect the activity of polypeptides  
CC by expressing inactive proteins or to supplement the patients own  
CC production of polypeptide. Additionally, (I) and its complementary  
CC sequences may also be used as DNA probes in diagnostic assays to detect  
CC and quantitate the presence of similar nucleic acids in samples, and  
CC therefore which patients may be in need of restorative therapy. The  
CC polypeptides encoded by (I) may be used as antigens in the production of  
CC antibodies specific for polymorphic polypeptides. The antibodies may also  
CC be used to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples  
SQ Sequence 51 BP; 10 A; 22 C; 11 G; 8 T; 0 U; 0 Other;  
Query Match 4.2%; Score 41.4; DB 1; Length 51;  
Best Local Similarity 88.2%; Pred. No. 2e+02; Indels 0; Gaps 0;  
Matches 45; Conservative 0; Mismatches 6;  
OY 216 CTCGAACCTCCGACCTCAGATGATCCCTCCGCTCGGCGCTCCCAAGTGCT 266  
DB 1 CTCGAACCTCCGACCTCAGATGATCCGACCGCGCGCTCCCAAGTGCT 51  
RESULT 130  
AAI79633/C  
ID AAI79633 standard; DNA; 51 BP.  
XX AAI79633;  
AC  
XX  
DT 09-NOV-2001 (first entry)  
XX  
DE Human silent SNP containing nucleic acid SEQ.6574.  
XX  
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KM protein therapy; vaccine; probe; diagnostic assay; detection;  
KM quantitation; restorative therapy; polymorphic; ds.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200140521-A2.  
PN  
XX  
XX 07-JUN-2001.  
PD  
XX 30-NOV-2000; 2000MO-US032758.  
PF  
XX 30-NOV-1999; 99US-0168138P.  
PR 29-NOV-2000; 2000US-00726173.  
XX  
XX (CURA-) CURAGEN CORP.  
PA  
XX Shimkets RA, Leach M;  
PI  
XX

DR WPI, 2001-356160/37.  
XX Polymorphic nucleic acid sequences, useful in genetic testing and  
PT therapy.  
PS Claim 1; Page 2518; 2653pp; English.  
XX AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide  
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).  
CC AAM53114 to AAM53329 represent peptides related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (I) and the polypeptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides. For  
CC example, (I) may be used to treat disorders by rectifying mutations or  
CC deletions in a patient's genome that affect the activity of polypeptides  
CC by expressing inactive proteins or to supplement the patients own  
CC production of polypeptide. Additionally, (I) and its complementary  
CC sequences may also be used as DNA probes in diagnostic assays to detect  
CC and quantitate the presence of similar nucleic acids in samples, and  
CC therefore which patients may be in need of restorative therapy. The  
CC polypeptides encoded by (I) may be used as antigens in the production of  
CC antibodies specific for polymorphic polypeptides. The antibodies may also  
CC be used to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples  
SQ Sequence 51 BP; 17 A; 14 C; 11 G; 9 T; 0 U; 0 Other;  
Query Match 4.2%; Score 41.4; DB 1; Length 51;  
Best Local Similarity 88.2%; Pred. No. 2e+02; Indels 0; Gaps 0;  
Matches 45; Conservative 0; Mismatches 6;  
OY 1085 TAGAGCGGGGTTTACCATATTTGTACAGCTGCTCTCAACTCTGACT 1135  
DB 51 TAGAGCGGGGTTTACCATATTTGTAGCTGCTCTCAACTCTGACT 1  
RESULT 131  
AAI79539/C  
ID AAI79539 standard; DNA; 51 BP.  
XX AAI79539;  
AC  
XX  
DT 09-NOV-2001 (first entry)  
XX  
DE Human silent SNP containing nucleic acid SEQ.6480.  
XX  
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KM protein therapy; vaccine; probe; diagnostic assay; detection;  
KM quantitation; restorative therapy; polymorphic; ds.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200140521-A2.  
PN  
XX  
XX 07-JUN-2001.  
PD  
XX 30-NOV-2000; 2000MO-US032758.  
PF  
XX 30-NOV-1999; 99US-0168138P.  
PR 29-NOV-2000; 2000US-00726173.  
XX  
XX (CURA-) CURAGEN CORP.  
PA  
XX Shimkets RA, Leach M;  
PI  
XX WPI, 2001-356160/37.  
DR  
XX Polymorphic nucleic acid sequences, useful in genetic testing and  
PT therapy.  
PS Claim 1; Page 2490; 2653pp; English.

XX AAT73060 to AAT79867 represent isolated human polymorphic polynucleotide  
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).  
CC AAM53114 to AAM53329 represent peptides related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (I) and the polypeptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides. For  
CC example, (I) may be used to treat disorders by rectifying mutations or  
CC deletions in a patient's genome that affect the activity of polypeptides  
CC by expressing inactive proteins or to supplement the patients own  
CC production of polypeptide. Additionally, (I) and its complementary  
CC sequences may also be used as DNA probes in diagnostic assays to detect  
CC and quantitate the presence of similar nucleic acids in samples, and  
CC therefore which patients may be in need of restorative therapy. The  
CC polypeptides encoded by (I) may be used as antigens in the production of  
CC antibodies specific for polymorphic polypeptides. The antibodies may also  
CC be used to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples  
XX

SO Sequence 51 BP; 13 A; 10 C; 20 G; 8 T; 0 U; 0 Other;

Query Match 4.2%; Score 41.4; DB 1; Length 51;  
Best Local Similarity 88.2%; Pred. No. 2e+02;  
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 970 TCGGCTCACTGACACTGCTGCTCCGGGCTCAAGCGATTCTCTCTCA 1020  
DB 51 TCGGCTCGCTGACAGCTGCTCTCCGGGCTCAAGCGATTCTCTCTCA 1

RESULT 132  
AAT76814  
ID AAT76814 standard; DNA; 51 BP.  
XX  
AC AAT76814;  
XX  
DT 09-NOV-2001 (first entry)  
XX  
DE Human silent SNP containing nucleic acid SEQ:3755.  
XX  
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KM protein therapy; vaccine; probe; diagnostic assay; detection;  
KW quantitation; restorative therapy; polymorphic; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200140521-A2.  
XX  
PD 07-JUN-2001.  
XX  
PF 30-NOV-2000; 2000WO-US032758.  
XX  
PR 30-NOV-1999; 99US-0168138P.  
PR 29-NOV-2000; 2000US-00726173.  
XX  
XX (CURA-) CURAGEN CORP.  
XX  
PI Shinkets RA, Leach M;  
XX  
DR WPI; 2001-356160/37.  
XX  
PT Polymorphic nucleic acid sequences, useful in genetic testing and  
PT therapy.  
XX  
PS Claim 1; Page 1200; 2653pp; English.  
XX  
CC AAT73060 to AAT79867 represent isolated human polymorphic polynucleotide  
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).  
CC AAM53114 to AAM53329 represent peptides related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (I) and the polypeptides encoded by

CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides. For  
CC example, (I) may be used to treat disorders by rectifying mutations or  
CC deletions in a patient's genome that affect the activity of polypeptides  
CC by expressing inactive proteins or to supplement the patients own  
CC production of polypeptide. Additionally, (I) and its complementary  
CC sequences may also be used as DNA probes in diagnostic assays to detect  
CC and quantitate the presence of similar nucleic acids in samples, and  
CC therefore which patients may be in need of restorative therapy. The  
CC polypeptides encoded by (I) may be used as antigens in the production of  
CC antibodies specific for polymorphic polypeptides. The antibodies may also  
CC be used to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples  
XX

SO Sequence 51 BP; 9 A; 9 C; 15 G; 18 T; 0 U; 0 Other;

Query Match 4.2%; Score 41.4; DB 1; Length 51;  
Best Local Similarity 88.2%; Pred. No. 2e+02;  
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 172 TTTTGTAGTAGATGAGATTCTCCATGTTGCTGAGGCTGCTCGAAC 222  
DB 1 TTTTGTAGTAGACAGAGGTTTCGCAATGTTGCTGAGGCTGCTCGAAC 51

RESULT 133  
AAT76092/c  
ID AAT76092 standard; DNA; 51 BP.  
XX  
AC AAT76092;  
XX  
DT 09-NOV-2001 (first entry)  
XX  
XX Human silent SNP containing nucleic acid SEQ:3033.  
DE  
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KM protein therapy; vaccine; probe; diagnostic assay; detection;  
KW quantitation; restorative therapy; polymorphic; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200140521-A2.  
XX  
PD 07-JUN-2001.  
XX  
PF 30-NOV-2000; 2000WO-US032758.  
XX  
PR 30-NOV-1999; 99US-0168138P.  
PR 29-NOV-2000; 2000US-00726173.  
XX  
XX (CURA-) CURAGEN CORP.  
XX  
PI Shinkets RA, Leach M;  
XX  
DR WPI; 2001-356160/37.  
XX  
PT Polymorphic nucleic acid sequences, useful in genetic testing and  
PT therapy.  
XX  
PS Claim 1; Page 978; 2653pp; English.  
XX  
CC AAT73060 to AAT79867 represent isolated human polymorphic polynucleotide  
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).  
CC AAM53114 to AAM53329 represent peptides related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (I) and the polypeptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides. For  
CC example, (I) may be used to treat disorders by rectifying mutations or  
CC deletions in a patient's genome that affect the activity of polypeptides  
CC by expressing inactive proteins or to supplement the patients own  
CC production of polypeptide. Additionally, (I) and its complementary

CC sequences may also be used as DNA probes in diagnostic assays to detect  
CC and quantitate the presence of similar nucleic acids in samples, and  
CC therefore which patients may be in need of restorative therapy. The  
CC polypeptides encoded by (1) may be used as antigens in the production of  
CC antibodies specific for polymorphic polypeptides. The antibodies may also  
CC be used to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples

XX Sequence 51 BP; 12 A; 8 C; 23 G; 8 T; 0 U; 0 Other;

Query Match 4.2%; Score 41.4; DB 1; Length 51;

Best Local Similarity 88.2%; Pred. No. 2e+02;

Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 974 CTCACGCAACCTCTCCCTCCGGGCTCAAGGATTCCTCTGCTCAGCCT 1024  
DB 51 CTCACGCAACCTCTCCCTCCGGGCTCAAGGATTCCTCTGCTCAGCCT 1

RESULT 134

AA179838/c

ID AA179838 standard; DNA; 51 BP.

XX AA179838;

DT 09-NOV-2001 (first entry)

DE Human nonconservative amino acid changing SNP nucleic acid SEQ:6779.

XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;

KW protein therapy; vaccine; probe; diagnostic assay; detection;

KM quantitation; restorative therapy; polymorphic; ds.

XX Homo sapiens.

XX WO200140521-A2.

XX 07-JUN-2001.

XX 30-NOV-2000; 2000MO-US032758.

XX 30-NOV-1999; 99US-0168138P.

XX 29-NOV-2000; 2000US-00726173.

XX (CURA-) CURAGEN CORP.

XX Shimketa RA, Leach M;

XX WPI; 2001-356160/37.

PT Polymorphic nucleic acid sequences, useful in genetic testing and

XX therapy.

PS Claim 1; Page 2579; 2653pp; English.

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide

CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

CC AA173060 to AA179867 represent peptides related to human polymorphic

CC polynucleotide sequences. The sequences can be used in gene and protein

CC therapy, and in vaccine production. (1) and the polypeptides encoded by

CC them may be used in the prevention, diagnosis and treatment of diseases

CC associated with inappropriate expression of polymorphic polypeptides. For

CC example, (1) may be used to treat disorders by rectifying mutations or

CC deletions in a patient's genome that affect the activity of polypeptides

CC be used as diagnostic agents for detecting the presence of polymorphic

CC polypeptides in samples

XX Sequence 51 BP; 10 A; 13 C; 17 G; 11 T; 0 U; 0 Other;

XX Query Match 4.2%; Score 41.4; DB 1; Length 51;

Best Local Similarity 88.2%; Pred. No. 2e+02;

Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 835 GTGATCTGCTGCTCTCCGCTCCCAAGTCTGGAGTTACAGCGCTGAGCC 885  
DB 51 GTGATCTGCTGCTCTCCGCTCCCAAGTCTGGAGTTACAGCGCTGAGCC 1

RESULT 135

AA176541/c

ID AA176541 standard; DNA; 51 BP.

XX AA176541;

DT 09-NOV-2001 (first entry)

DE Human silent SNP containing nucleic acid SEQ:3482.

XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;

KW protein therapy; vaccine; probe; diagnostic assay; detection;

KM quantitation; restorative therapy; polymorphic; ds.

XX Homo sapiens.

XX WO200140521-A2.

XX 07-JUN-2001.

XX 30-NOV-2000; 2000MO-US032758.

XX 30-NOV-1999; 99US-0168138P.

XX 29-NOV-2000; 2000US-00726173.

XX (CURA-) CURAGEN CORP.

XX Shimketa RA, Leach M;

XX WPI; 2001-356160/37.

PT Polymorphic nucleic acid sequences, useful in genetic testing and

XX therapy.

PS Claim 1; Page 1116; 2653pp; English.

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide

CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

CC AA173060 to AA179867 represent peptides related to human polymorphic

CC polynucleotide sequences. The sequences can be used in gene and protein

CC therapy, and in vaccine production. (1) and the polypeptides encoded by

CC them may be used in the prevention, diagnosis and treatment of diseases

CC associated with inappropriate expression of polymorphic polypeptides. For

CC example, (1) may be used to treat disorders by rectifying mutations or

CC deletions in a patient's genome that affect the activity of polypeptides

CC by expressing inactive proteins or to supplement the patients own

CC be used as diagnostic agents for detecting the presence of polymorphic

CC polypeptides in samples

XX Sequence 51 BP; 10 A; 13 C; 17 G; 11 T; 0 U; 0 Other;

XX Query Match 4.2%; Score 41.4; DB 1; Length 51;

Best Local Similarity 88.2%; Pred. No. 2e+02;

Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 835 GTGATCTGCTGCTCTCCGCTCCCAAGTCTGGAGTTACAGCGCTGAGCC 885  
DB 51 GTGATCTGCTGCTCTCCGCTCCCAAGTCTGGAGTTACAGCGCTGAGCC 1

RESULT 135

AA176541/c

ID AA176541 standard; DNA; 51 BP.

XX AA176541;

DT 09-NOV-2001 (first entry)

DE Human silent SNP containing nucleic acid SEQ:3482.

XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;

KW protein therapy; vaccine; probe; diagnostic assay; detection;

KM quantitation; restorative therapy; polymorphic; ds.

XX Homo sapiens.

XX WO200140521-A2.

XX 07-JUN-2001.

XX 30-NOV-2000; 2000MO-US032758.

XX 30-NOV-1999; 99US-0168138P.

XX 29-NOV-2000; 2000US-00726173.

XX (CURA-) CURAGEN CORP.

XX Shimketa RA, Leach M;

XX WPI; 2001-356160/37.

PT Polymorphic nucleic acid sequences, useful in genetic testing and

XX therapy.

PS Claim 1; Page 1116; 2653pp; English.

XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide

CC sequences (1), which contain single nucleotide polymorphisms (SNPs).

CC AA173060 to AA179867 represent peptides related to human polymorphic

CC polynucleotide sequences. The sequences can be used in gene and protein

CC therapy, and in vaccine production. (1) and the polypeptides encoded by

CC them may be used in the prevention, diagnosis and treatment of diseases

CC associated with inappropriate expression of polymorphic polypeptides. For

CC example, (1) may be used to treat disorders by rectifying mutations or

CC deletions in a patient's genome that affect the activity of polypeptides

CC by expressing inactive proteins or to supplement the patients own

Best Local Similarity 88.2%; Pred. No. 2e+02; Mismatches 6; Indels 0; Gaps 0;  
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
692 TCCGGGGTTCAGTATTCCTGCGCCGACCTCTGAGTACGTGGAGCTA 742  
51 TCTGGGCTCAAGTATCTCTGCTGAGTCTCTGAGTACGTGGAGCTA 1

RESULT 136  
AA179697/c  
ID AA179697 standard; DNA; 51 BP.

AA179697;  
09-NOV-2001 (first entry)

Human conservative amino acid changing SNP nucleic acid SEQ:6638.

Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
protein therapy; vaccine; probe; diagnostic assay; detection;  
quantitation; restorative therapy; polymorphic; ds.

Homo sapiens.

WO200140521-A2.

07-JUN-2001.

30-NOV-2000; 2000WO-US032758.

30-NOV-1999; 99US-0168138P.

29-NOV-2000; 2000US-00726173.

(CURA-) CURAGEN CORP.

Shinkets RA, Leach M;

WPI; 2001-356160/37.

Polymorphic nucleic acid sequences, useful in genetic testing and  
therapy.

Claim 1; Page 2537; 2653pp; English.

AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
sequences (I), which contain single nucleotide polymorphisms (SNPs).  
AA173060 to AA173329 represent peptides related to human polymorphic  
polynucleotide sequences. The sequences can be used in gene and protein  
therapy, and in vaccine production. (I) and the polypeptides encoded by  
them may be used in the prevention, diagnosis and treatment of diseases  
associated with inappropriate expression of polymorphic polypeptides. For  
example, (I) may be used to treat disorders by rectifying mutations or  
deletions in a patient's genome that affect the activity of polypeptides  
by expressing inactive proteins or to supplement the patient's own  
production of polypeptide. Additionally, (I) and its complementary  
sequences may also be used as DNA probes in diagnostic assays to detect  
and quantitate the presence of similar nucleic acids in samples, and  
therefore which patients may be in need of restorative therapy. The  
polypeptides encoded by (I) may be used as antigens in the production of  
antibodies specific for polymorphic polypeptides. The antibodies may also  
be used to down regulate expression and activity. The antibodies may also  
be used as diagnostic agents for detecting the presence of polymorphic  
polypeptides in samples

Sequence 51 BP; 10 A; 12 C; 18 G; 11 T; 0 U; 0 Other;

Query Match 4.2%; Score 41.4; DB 1; Length 51;  
Best Local Similarity 88.2%; Pred. No. 2e+02;  
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

1025 CCCAAGCAGCTGGGATTACGGGACCTCCACCAACCCCGTATTTTGG 1075  
51 CCCAAGTACGTGGATTACAGGCGCCGCCACACGACCCAGCTATTTTGG 1

RESULT 137  
AA174778  
ID AA174778 standard; DNA; 51 BP.

AA174778;

09-NOV-2001 (first entry)

Human silent SNP containing nucleic acid SEQ:1719.

Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
protein therapy; vaccine; probe; diagnostic assay; detection;  
quantitation; restorative therapy; polymorphic; ds.

Homo sapiens.

WO200140521-A2.

07-JUN-2001.

30-NOV-2000; 2000WO-US032758.

30-NOV-1999; 99US-0168138P.

29-NOV-2000; 2000US-00726173.

(CURA-) CURAGEN CORP.

Shinkets RA, Leach M;

WPI; 2001-356160/37.

Polymorphic nucleic acid sequences, useful in genetic testing and  
therapy.

Claim 1; Page 580; 2653pp; English.

AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
sequences (I), which contain single nucleotide polymorphisms (SNPs).  
AA173060 to AA173329 represent peptides related to human polymorphic  
polynucleotide sequences. The sequences can be used in gene and protein  
therapy, and in vaccine production. (I) and the polypeptides encoded by  
them may be used in the prevention, diagnosis and treatment of diseases  
associated with inappropriate expression of polymorphic polypeptides. For  
example, (I) may be used to treat disorders by rectifying mutations or  
deletions in a patient's genome that affect the activity of polypeptides  
by expressing inactive proteins or to supplement the patient's own  
production of polypeptide. Additionally, (I) and its complementary  
sequences may also be used as DNA probes in diagnostic assays to detect  
and quantitate the presence of similar nucleic acids in samples, and  
therefore which patients may be in need of restorative therapy. The  
polypeptides encoded by (I) may be used as antigens in the production of  
antibodies specific for polymorphic polypeptides. The antibodies may also  
be used to down regulate expression and activity. The antibodies may also  
be used as diagnostic agents for detecting the presence of polymorphic  
polypeptides in samples

Sequence 51 BP; 9 A; 21 C; 13 G; 8 T; 0 U; 0 Other;

Query Match 4.2%; Score 41.4; DB 1; Length 51;  
Best Local Similarity 88.2%; Pred. No. 2e+02;  
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

847 CCTGGGCTCCCAAGTCTGGGATTACAGGCGCTGACCCACGCGCCGCG 897  
1 CCTGGGCTCCCAATTCCTGGGACTACAGGCGTGAACCACTGACCCGCGC 51

RESULT 138  
AA173250/c  
ID AA173250 standard; DNA; 51 BP.

Query Match	4.2%	Score 41.4	DB 1	Length 51
Best Local Similarity	88.2%	Pred No. 2e+02	6	Indels 0
Matches 45	Conservative 0	Mismatches 6	Indels 0	Gaps 0
Db	956 GCATATGCGCCAAATCTCGGCTCACTGCAACCTCTGCTCCCGGAGCTCAAGC	1006		
YY				
51	GCATATGCGCCAAATCTCGGCTCACTGCAACCTCTGCTCCCGGAGCTCAAGC	1		
RESULT 139				
AA179700/c				
ID	AA179700	standard; DNA; 51 BP.		
XX				
AC	AA179700;			
XX				
DT	09-NOV-2001	(first entry)		
XX				
DE	Human conservative amino acid changing SNP nucleic acid SEQ:6641.			

KW	Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW	protein therapy; vaccine; probe; diagnostic assay; detection;
KW	quantitation; restorative therapy; polymorphic; ds.
XX	
XX	Homo sapiens.
OS	
PN	WO200140521-A2.
XX	
PD	07-JUN-2001.
XX	
PF	30-NOV-2000; 2000WO-US032758.
PR	30-NOV-1999; 99US-0168138P.
PR	29-NOV-2000; 2000US-00726173.
XX	
PA	(CURA-) CURAGEN CORP.
XX	
PI	Shimkets RA, Leach M;
DR	WPI; 2001-356160/37.
XX	
PT	Polymorphic nucleic acid sequences, useful in genetic testing and
PT	therapy.
XX	
PS	Claim 1; Page 2538; 2653pp; English.
XX	
CC	AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC	sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC	AA173114 to AA175329 represent peptides related to human polymorphic
CC	polynucleotide sequences. The sequences can be used in gene and protein
CC	therapy, and in vaccine production. (I) and the polypeptides encoded by
CC	them may be used in the prevention, diagnosis and treatment of diseases
CC	associated with inappropriate expression of polymorphic polypeptides. For
CC	example, (I) may be used to treat disorders by rectifying mutations or
CC	deletions in a patient's genome that affect the activity of polypeptides
CC	by expressing inactive proteins or to supplement the patient's own
CC	production of polypeptide. Additionally, (I) and its complementary
CC	sequences may also be used as DNA probes in diagnostic assays to detect
CC	and quantitate the presence of similar nucleic acids in samples, and
CC	therefore which patients may be in need of restorative therapy. The
CC	polypeptides encoded by (I) may be used as antigens in the production of
CC	antibodies specific for polymorphic polypeptides. The antibodies may also
CC	be used to down regulate expression and activity. The antibodies may also
CC	be used as diagnostic agents for detecting the presence of polymorphic
CC	polypeptides in samples
SQ	
SQ	Sequence 51 BP; 10 A; 12 C; 17 G; 12 T; 0 U; 0 Other;
QY	
QY	Query Match 4.2%; Score 41.4; DB 1; Length 51;
QY	Best Local Similarity 88.2%; Pred. No. 2e+02;
QY	Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY	836 TGAATGCTGCTGCTGAGCTCCCAAGTGTGGATTACAGCGGTAGGCCA 886
QY	51 TGATCGCGCCATCTGCGCTCCCAAAATGTGGATTACAGGCATAGGCCA 1
RESULT 140	
AA178386	
ID	AA178386 standard; DNA; 51 BP.
XX	
AC	AA178386;
XX	
DT	09-NOV-2001 (first entry)
XX	
DE	Human silent SNP containing nucleic acid SEQ:5327.
XX	
KW	Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW	protein therapy; vaccine; probe; diagnostic assay; detection;
KW	quantitation; restorative therapy; polymorphic; ds.
OS	
OS	Homo sapiens.





XX WPI; 2001-356160/37.  
XX Polymorphic nucleic acid sequences, useful in genetic testing and  
PT therapy.  
XX  
XX Claim 1; Page 2563; 2653pp; English.  
XX  
XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).  
CC AA173114 to AA175329 represent peptide sequences related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (I) and the polypeptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides. For  
CC example, (I) may be used to treat disorders by rectifying mutations or  
CC deletions in a patient's genome that affect the activity of polypeptides  
CC by expressing inactive proteins or to supplement the patient's own  
CC production of polypeptide. Additionally, (I) and its complementary  
CC sequences may also be used as DNA probes in diagnostic assays to detect  
CC and quantitate the presence of similar nucleic acids in samples, and  
CC therefore which patients may be in need of restorative therapy. The  
CC polypeptides encoded by (I) may be used as antigens in the production of  
CC antibodies specific for polymorphic polypeptides. The antibodies may also  
CC be used to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples  
XX  
XX Sequence 51 BP; 11 A; 12 C; 19 G; 9 T; 0 U; 0 Other;  
SQ  
XX  
XX Query Match 4.2%; Score 41.4; DB 1; Length 51;  
XX Best Local Similarity 88.2%; Pred. No. 2e+02; 6; Indels 0; Gaps 0;  
XX Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 989 GCGTCCCGGCGCTCAAGGATTCCTGCTCAGCCTCCAGACGCTGGGA 1039  
DB 51 GCGTCCCGGCGCTCAAGGATTCCTGCTCAGCCTCCAGACGCTGGGA 1  
XX  
XX RESULT 143  
XX AAH90585/c  
XX ID AAH90585 standard; cDNA; 51 BP.  
XX  
XX AAH90585;  
AC  
XX  
XX 08-OCT-2001 (first entry)  
DT  
XX  
XX Human clone cg43080072 SNP site, SEQ ID NO:465.  
DE  
XX  
XX Human; single nucleotide polymorphism; SNP; detection; identification;  
XX gene therapy; genetic disorder; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX Key Location/Qualifiers  
XX FT replace(26,C)  
XX FT /\*tag= a  
XX FT /standard\_name= "single nucleotide polymorphism"  
XX  
XX WO200147942-A2.  
XX  
XX 05-JUL-2001.  
XX  
XX 27-DEC-2000; 2000WO-US035387.  
XX  
XX 27-DEC-1999; 99US-00472865.  
XX  
XX (CURA-) CURAGEN CORP.  
XX  
XX Shimkets RA, Leach M;  
XX  
XX WPI; 2001-425617/45.  
XX

PT New polynucleotides containing single nucleotide polymorphisms, for  
PT detecting the presence of polymorphism, detecting a polymorphic site, and  
PT treating a patient suffering from a pathology ascribed to the  
XX polymorphism.  
XX  
XX Claim 1; Page 109; 295pp; English.  
XX  
XX Sequences AAH90121-AAH90700 represent 580 human cDNA sequences which  
CC contain single nucleotide polymorphisms (SNPs). Sequences 1 to 568  
CC (AAH90121-AAH90688) are consecutive pairs of nucleotides which contain  
CC silent SNPs. Sequences 569 to 580 (AAH90689-AAH90700) are consecutive  
CC pairs of nucleotides containing SNPs which result in changes in the  
CC corresponding amino acid sequences (AAG64751-AAG64762). The SNPs in  
CC sequences 569 to 574 (AAH90689-AAH90694) lead to conservative amino acid  
CC changes, while those in sequences 575 to 578 (AAH90695-AAH90698) result  
CC in non-conservative changes. The SNP in sequences 579 and 580 (AAH90699-  
CC AAH90700) generates a frameshift mutation. The invention also relates to  
CC a method of detecting a polymorphic site in a nucleic acid and a method  
CC of determining the relatedness of two nucleic acids. It also encompasses  
CC peptides containing polymorphic sites, antibodies raised against such  
CC peptides, and a method of detecting polymorphic proteins/peptides using  
CC the antibodies. The nucleic acids are useful for gene therapy of an  
CC individual having, suspected of having, or at risk of developing a  
CC pathological condition due to the presence of a sequence polymorphism.  
CC Such treatment would comprise administration of the wild-type nucleic  
CC acid sequence. Antibodies raised against polymorphic peptides can also be  
CC used in the treatment of such individuals  
XX  
XX Sequence 51 BP; 12 A; 14 C; 15 G; 10 T; 0 U; 0 Other;  
SQ  
XX  
XX Query Match 4.2%; Score 41.4; DB 1; Length 51;  
XX Best Local Similarity 88.2%; Pred. No. 2e+02; 6; Indels 0; Gaps 0;  
XX Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 836 TGATCGCTGCGCTCGGCGCTCCCAAGTGTGCTGATTACAGCGGTAGCCA 886  
DB 51 TGATCGCTGCGCTCGGCGCTCCCAAGTGTGCTGATTACAGCGGTAGCCA 1  
XX  
XX RESULT 144  
XX AAH89405  
XX ID AAH89405 standard; DNA; 51 BP.  
XX  
XX AAH89405;  
AC  
XX  
XX 01-OCT-2001 (first entry)  
DT  
XX  
XX Human coding sequence polymorphic site SEQ ID NO: 186.  
DE  
XX  
XX Human; single nucleotide polymorphism; SNP; paternity test;  
XX forensic test; aberrant protein expression; ds.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200151670-A2.  
XX  
XX 19-JUL-2001.  
XX  
XX 05-JAN-2001; 2001WO-US000322.  
XX  
XX 07-JAN-2000; 2000US-0174962P.  
XX  
XX (CURA-) CURAGEN CORP.  
XX  
XX Shimkets RA, Leach MD;  
XX  
XX WPI; 2001-451871/48.  
XX  
XX P-PSDB; AAM00292.  
XX  
XX Isolated human polynucleotides containing single nucleotide  
XX polymorphisms, useful for the treatment and diagnosis of e.g. cancer,  
XX infection and diabetes.  
XX

PS Claim 1; Page 159; 475bp; English.  
XX  
CC The present invention relates to human nucleic acids containing single  
CC nucleotide polymorphisms (SNPs). These can be used in forensic and  
CC paternity tests, and to aid in the treatment of diseases associated with  
CC aberrant protein expression, including cancer, amyloidosis, diabetes,  
CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,  
CC glomerulonephritis, haemolytic anaemia, thrombocytopenia, arthritis,  
CC meningitis, muscular disorders, dementia, neurological diseases, tubercu  
CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,  
CC osteoporosis, pathogenic infections, hypercholesterolemia, obesity or  
CC autoimmunity. The present sequence is a polymorphism-containing  
CC oligonucleotide fragment of the invention  
SQ Sequence 51 BP; 9 A; 21 C; 9 G; 12 T; 0 U; 0 Other;  
  
Query Match 4.2%; Score 41.4; DB 1; Length 51;  
Best Local Similarity 88.2%; Pred. No. 2e+02; Mismatches 6; Indels 0; Gaps 0;  
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
  
OY 663 CGCATCTTGCTGCTCAACCTCTGCTCCCGGATTCAAGTATTCTCC 713  
DB 1 CACGATCTTGCTGCTCAACCTCTGCTCCCGGATTCAAGTATTCTCC 51  
  
RESULT 145  
AAH89485/C  
ID AAH89485 standard; DNA; 51 BP.  
XX  
AC AAH89485;  
XX  
DT 01-OCT-2001 (first entry)  
XX  
DE Human coding sequence polymorphic site SEQ ID NO: 266.  
XX  
KM Human; single nucleotide polymorphism; SNP; paternity test;  
KM forensic test; aberrant protein expression; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200151670-A2.  
XX  
PD 19-JUL-2001.  
XX  
PF 05-JAN-2001; 2001WO-US000322.  
XX  
PR 07-JAN-2000; 2000US-0174962P.  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
PI Shinkets RA, Leach MD;  
XX  
PI MPI: 2001-451871/48.  
DR P-PSDB; AAM00370.  
XX  
PT Isolated human polynucleotides containing single nucleotide  
PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,  
PT infection and diabetes.  
XX  
PS Claim 1; Page 180; 475bp; English.  
XX  
CC The present invention relates to human nucleic acids containing single  
CC nucleotide polymorphisms (SNPs). These can be used in forensic and  
CC paternity tests, and to aid in the treatment of diseases associated with  
CC aberrant protein expression, including cancer, amyloidosis, diabetes,  
CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,  
CC glomerulonephritis, haemolytic anaemia, thrombocytopenia, arthritis,  
CC meningitis, muscular disorders, dementia, neurological diseases, tubercu  
CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,  
CC osteoporosis, pathogenic infections, hypercholesterolemia, obesity or  
CC autoimmunity. The present sequence is a polymorphism-containing  
CC oligonucleotide fragment of the invention  
SQ

SQ Sequence 51 BP; 15 A; 12 C; 12 G; 12 T; 0 U; 0 Other;  
  
Query Match 4.2%; Score 41.4; DB 1; Length 51;  
Best Local Similarity 88.2%; Pred. No. 2e+02; Mismatches 6; Indels 0; Gaps 0;  
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
  
OY 1080 TTCAATGAGCGGGGTTTACCAATATTGTGACGGTGTCTCAACTCCT 1130  
DB 51 TTGATGAGACAGAGGTTTACCAATATTGTGACGGTGTCTCAACTCCT 1  
  
RESULT 146  
AAH89514/C  
ID AAH89514 standard; DNA; 51 BP.  
XX  
AC AAH89514;  
XX  
DT 01-OCT-2001 (first entry)  
XX  
DE Human coding sequence polymorphic site SEQ ID NO: 295.  
XX  
KM Human; single nucleotide polymorphism; SNP; paternity test;  
KM forensic test; aberrant protein expression; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200151670-A2.  
XX  
PD 19-JUL-2001.  
XX  
PF 05-JAN-2001; 2001WO-US000322.  
XX  
PR 07-JAN-2000; 2000US-0174962P.  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
PI Shinkets RA, Leach MD;  
XX  
PI MPI: 2001-451871/48.  
DR P-PSDB; AAM00397.  
XX  
PT Isolated human polynucleotides containing single nucleotide  
PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,  
PT infection and diabetes.  
XX  
PS Claim 1; Page 188; 475bp; English.  
XX  
CC The present invention relates to human nucleic acids containing single  
CC nucleotide polymorphisms (SNPs). These can be used in forensic and  
CC paternity tests, and to aid in the treatment of diseases associated with  
CC aberrant protein expression, including cancer, amyloidosis, diabetes,  
CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,  
CC glomerulonephritis, haemolytic anaemia, thrombocytopenia, arthritis,  
CC meningitis, muscular disorders, dementia, neurological diseases, tubercu  
CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,  
CC osteoporosis, pathogenic infections, hypercholesterolemia, obesity or  
CC autoimmunity. The present sequence is a polymorphism-containing  
CC oligonucleotide fragment of the invention  
SQ  
Sequence 51 BP; 7 A; 13 C; 22 G; 9 T; 0 U; 0 Other;  
  
Query Match 4.2%; Score 41.4; DB 1; Length 51;  
Best Local Similarity 88.2%; Pred. No. 2e+02; Mismatches 6; Indels 0; Gaps 0;  
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
  
OY 844 CTGCTCGGCTCCCAAGTCTGGATTACAGCGTGAGCCACACGCCC 894  
DB 51 CTGCTCGGCTCCCAAGTCTGGATTACAGCGTGAGCCACACGCCC 1  
  
RESULT 147  
AAH89519/C  
ID AAH89519 standard; DNA; 51 BP.



PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,  
PT infection and diabetes.  
XX  
PS Claim 1; Page 198; 475pp; English.  
XX  
CC The present invention relates to human nucleic acids containing single  
CC nucleotide polymorphisms (SNPs). These can be used in forensic and  
CC paternity tests, and to aid in the treatment of diseases associated with  
CC aberrant protein expression, including cancer, amyloidosis, diabetes,  
CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,  
CC glomerulonephritis, haemolytic anaemia, thrombocytopenia, arthritis,  
CC meningitis, muscular disorders, dementia, neurological diseases, tubercous  
CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or  
CC autoimmunity. The present sequence is a polymorphism-containing  
CC oligonucleotide fragment of the invention  
XX  
SQ Sequence 51 BP; 14 A; 14 C; 14 G; 9 T; 0 U; 0 Other;  
  
Query Match 4.2%; Score 41.4; DB 1; Length 51;  
Best Local Similarity 88.2%; Pred. No. 2e+02;  
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
  
Qy 1086 AGAGCGGGGTTTACCAATTGTCAGGCTGCTCAAACTCTGACCTC 1136  
Db 51 AGAGCGGGGTTTACCAATTGTCAGGCTGCTCAAACTCTGACCTC 1  
  
RESULT 150  
AAH89472  
ID AAH89472 standard; DNA; 51 BP.  
XX  
AC AAH89472;  
XX  
DT 01-OCT-2001 (first entry)  
XX  
DE Human coding sequence polymorphic site SEQ ID NO: 253.  
XX  
KW Human; single nucleotide polymorphism; SNP; paternity test;  
KW forensic test; aberrant protein expression; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200151670-A2.  
XX  
PD 19-JUL-2001.  
XX  
PF 05-JAN-2001; 2001WO-US000322.  
XX  
PR 07-JAN-2000; 2000US-0174962P.  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
PI Shimkets RA, Leach MD;  
XX  
DR WPI; 2001-451871/48.  
DR P-Psdb; AAM00357.  
XX  
PT Isolated human polynucleotides containing single nucleotide  
PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,  
XX infection and diabetes.  
XX  
PS Claim 1; Page 177; 475pp; English.  
XX  
CC The present invention relates to human nucleic acids containing single  
CC nucleotide polymorphisms (SNPs). These can be used in forensic and  
CC paternity tests, and to aid in the treatment of diseases associated with  
CC aberrant protein expression, including cancer, amyloidosis, diabetes,  
CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,  
CC glomerulonephritis, haemolytic anaemia, thrombocytopenia, arthritis,  
CC meningitis, muscular disorders, dementia, neurological diseases, tubercous  
CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or  
CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or

CC autoimmunity. The present sequence is a polymorphism-containing  
CC oligonucleotide fragment of the invention  
XX  
SQ Sequence 51 BP; 9 A; 17 C; 13 G; 12 T; 0 U; 0 Other;  
  
Query Match 4.2%; Score 41.4; DB 1; Length 51;  
Best Local Similarity 88.2%; Pred. No. 2e+02;  
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
  
Qy 692 TCCCGGGTTTCAAGTTATTCCTCCGCCAGCCTCCTAGTAGCTGGGACTA 742  
Db 1 TCCCGGGTTTCAAGTTATTCCTCCGCCAGCCTCCTAGTAGCTGGGACTA 51  
  
RESULT 151  
ADK19818/C  
ID ADK19818 standard; DNA; 51 BP.  
XX  
AC ADK19818;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Human mannosyl transferase-related SNP region DNA SegID20.  
XX  
KW human; mannosyl transferase; anti-mannic; antidepressant; gene therapy;  
KW fusion protein; chromosome 9 fusion protein; chromosome 11 translocation;  
KW bipolar disorder; single nucleotide polymorphism; SNP; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FH replace(26,C)  
FT variation /\*tag= a  
FT /standard\_name= "Single nucleotide polymorphism"  
XX  
PN WO2003012064-A2.  
XX  
PD 13-FEB-2003.  
XX  
PE 02-AUG-2002; 2002WO-US024490.  
XX  
PR 02-AUG-2001; 2001US-00922225.  
XX  
PA (EGEA-) EGEA BIOSCIENCES INC.  
XX  
PI Evans GA;  
XX  
DR WPI; 2003-268116/26.  
XX  
PT New polypeptide comprising human mannosyl transferase, useful for  
PT diagnosing or predicting the susceptibility to a bipolar disorder and for  
PT identifying a compound that modulates the activity of a mannosyl  
PT transferase.  
XX  
PS Claim 11; SEQ ID NO 20; 147pp; English.  
XX  
CC This invention relates to a novel isolated protein which comprises a  
CC human mannosyl transferase having the same sequence as the fully defined  
CC 611- or 255-amino acid sequence or its fragment. The invention may be  
CC useful for the production of compounds with an anti-mannic or  
CC antidepressant activity whilst the disclosed sequences may be used for  
CC gene therapy. The invention also provides a human mannosyl transferase  
CC fusion protein and a chromosome 9 fusion protein, both of which result  
CC from a chromosome 11 translocation. The human mannosyl transferase and  
CC the fusion proteins are useful for diagnosing or predicting the  
CC susceptibility to a bipolar disorder and for identifying a compound that  
CC modulates the activity of a mannosyl transferase. The present sequence is  
CC that of a region of human DNA surrounding a single nucleotide  
CC polymorphism within the gene which encodes the human mannosyl transferase  
CC of the invention.  
XX  
SQ Sequence 51 BP; 13 A; 12 C; 16 G; 10 T; 0 U; 0 Other;



XX 09-NOV-2001 (first entry)  
XX  
XX Human silent SNP containing nucleic acid SEQ:3757.  
DE  
XX  
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KW protein therapy; vaccine; probe; diagnostic assay; detection;  
KW quantitation; restorative therapy; polymorphic; ds.  
XX  
XX Homo sapiens.  
OS  
XX WO200140521-A2.  
FN  
XX  
XX 07-JUN-2001.  
PD  
XX  
XX 30-NOV-2000; 2000WO-US032758.  
PF  
XX 30-NOV-1999; 99US-0168138P.  
PR 29-NOV-2000; 2000US-00726173.  
XX  
XX (CURA-) CURAGEN CORP.  
PA  
XX Shinkets RA, Leach M;  
PI WPI; 2001-356160/37.  
DR  
XX  
XX Polymorphic nucleic acid sequences, useful in genetic testing and  
PT therapy.  
PS Claim 1; Page 1200; 2653pp; English.  
XX  
XX AAT73060 to AAT79867 represent isolated human polymorphic polynucleotide  
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).  
CC AAM53114 to AAM53329 represent peptides related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (I) and the polypeptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides. For  
CC example, (I) may be used to treat disorders by rectifying mutations or  
CC deletions in a patient's genome that affect the activity of polypeptides  
CC by expressing inactive proteins or to supplement the patients own  
CC production of polypeptide. Additionally, (I) and its complementary  
CC sequences may also be used as DNA probes in diagnostic assays to detect  
CC and quantitate the presence of similar nucleic acids in samples, and  
CC therefore which patients may be in need of restorative therapy. The  
CC polypeptides encoded by (I) may be used as antigens in the production of  
CC antibodies specific for polymorphic polypeptides. The antibodies may also  
CC be used to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples  
XX  
XX  
SQ Sequence 51 BP; 8 A; 16 C; 13 G; 14 T; 0 U; 0 Other;  
Query Match 4.1%; Score 41; DB 1; Length 51;  
Best Local Similarity 89.8%; Pred. No. 2.1e+02;  
Matches 44; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
OY 193 TTCTCCATTTGTCAGGCTGCTCGAATCCCACTCAATATATCC 241  
DB 1 TTTCGCAATGTGGCCAGCGCTGCTTGAATCTCTGACCTCAGATATCC 49  
RESULT 155  
AAT79093/C  
ID AAT79093 standard; DNA; 51 BP.  
XX  
XX AAT79093;  
AC  
XX  
XX 09-NOV-2001 (first entry)  
DT  
XX Human silent SNP containing nucleic acid SEQ:6034.  
DE  
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KW

KW protein therapy; vaccine; probe; diagnostic assay; detection;  
KW quantitation; restorative therapy; polymorphic; ds.  
XX  
XX Homo sapiens.  
OS  
XX WO200140521-A2.  
FN  
XX  
XX 07-JUN-2001.  
PD  
XX  
XX 30-NOV-2000; 2000WO-US032758.  
PF  
XX 30-NOV-1999; 99US-0168138P.  
PR 29-NOV-2000; 2000US-00726173.  
XX  
XX (CURA-) CURAGEN CORP.  
PA  
XX Shinkets RA, Leach M;  
PI WPI; 2001-356160/37.  
DR  
XX  
XX Polymorphic nucleic acid sequences, useful in genetic testing and  
PT therapy.  
PS Claim 1; Page 2356; 2653pp; English.  
XX  
XX AAT73060 to AAT79867 represent isolated human polymorphic polynucleotide  
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).  
CC AAM53114 to AAM53329 represent peptides related to human polymorphic  
CC polynucleotide sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (I) and the polypeptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate expression of polymorphic polypeptides. For  
CC example, (I) may be used to treat disorders by rectifying mutations or  
CC deletions in a patient's genome that affect the activity of polypeptides  
CC by expressing inactive proteins or to supplement the patients own  
CC production of polypeptide. Additionally, (I) and its complementary  
CC sequences may also be used as DNA probes in diagnostic assays to detect  
CC and quantitate the presence of similar nucleic acids in samples, and  
CC therefore which patients may be in need of restorative therapy. The  
CC polypeptides encoded by (I) may be used as antigens in the production of  
CC antibodies specific for polymorphic polypeptides. The antibodies may also  
CC be used to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples  
XX  
XX  
SQ Sequence 51 BP; 12 A; 15 C; 16 G; 8 T; 0 U; 0 Other;  
Query Match 4.1%; Score 41; DB 1; Length 51;  
Best Local Similarity 89.8%; Pred. No. 2.1e+02;  
Matches 44; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
OY 944 CCAGCTGGAGTGCATATGCCAATCTCGGCTCACTGACCTTGGCT 992  
DB 49 CCAGCTGGAGTGCATATGTGTGATCTCGGCTCACTGACCTCGGCT 1  
RESULT 156  
AAT73524  
ID AAT73524 standard; DNA; 51 BP.  
XX  
XX AAT73524;  
AC  
XX  
XX 09-NOV-2001 (first entry)  
DT  
XX Human silent SNP containing nucleic acid SEQ:465.  
DE  
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KW protein therapy; vaccine; probe; diagnostic assay; detection;  
KW quantitation; restorative therapy; polymorphic; ds.  
XX  
XX Homo sapiens.  
OS  
XX WO200140521-A2.  
FN

XX 07-JUN-2001.  
PD 30-NOV-2000; 2000WO-US032758.  
XX 30-NOV-1999; 99US-0168138P.  
PR 29-NOV-2000; 2000US-00726173.  
XX (CURA-) CURAGEN CORP.  
XX Shimkets RA, Leach M;  
PI WPI; 2001-356160/37.  
DR Polymorphic nucleic acid sequences, useful in genetic testing and  
XX therapy.  
XX Claim 1; Page 196; 2653pp; English.  
XX AA173060 to AA179867 represent isolated human polymorphic polymorphic  
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).  
CC AA53114 to AA53329 represent peptides related to human polymorphic  
CC polymorphic sequences. The sequences can be used in gene and protein  
CC therapy, and in vaccine production. (I) and the polypeptides encoded by  
CC associated with inappropriate expression of polymorphic polypeptides. For  
CC example, (I) may be used to treat disorders by rectifying mutations or  
CC deletions in a patient's genome that affect the activity of polypeptides  
CC by expressing inactive proteins or to supplement the patients own  
CC production of polypeptide. Additionally, (I) and its complementary  
CC sequences may also be used as DNA probes in diagnostic assays to detect  
CC and quantitate the presence of similar nucleic acids in samples, and  
CC therefore which patients may be in need of restorative therapy. The  
CC polypeptides encoded by (I) may be used as antigens in the production of  
CC antibodies specific for polymorphic polypeptides. The antibodies may also  
CC be used to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of polymorphic  
CC polypeptides in samples  
XX  
SO Sequence 51 BP; 10 A; 14 C; 13 G; 14 T; 0 U; 0 Other;  
Query Match 4.1%; Score 41; DB 1; Length 51;  
Best Local Similarity 89.8%; Pred. No. 2.1e+02;  
Matches 44; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 1091 CGGGGTTTCCCATTTGTCAGGCTGCTCAAACTCCGACCTCAGG 1139  
DB 2 CGGGGTTTCCCATTTGTCAGGCTGCTCAAACTCCGACCTCAGG 50  
RESULT 157  
AAH89516/C  
ID AAH89516 standard; DNA; 51 BP.  
XX  
AC AAH89516;  
XX  
DT 01-OCT-2001 (first entry)  
XX  
DE Human coding sequence polymorphic site SEQ ID NO: 297.  
XX  
XX Human; single nucleotide polymorphism; SNP; paternity test;  
KM forensic test; aberrant protein expression; de.  
XX  
OS Homo sapiens.  
XX  
XX WO200151670-A2.  
XX  
XX 19-JUL-2001.  
XX  
XX 05-JAN-2001; 2001WO-US000322.  
XX  
XX 07-JAN-2000; 2000US-0174962P.  
XX

PA (CURA-) CURAGEN CORP.  
XX Shimkets RA, Leach MD;  
PI WPI; 2001-451871/48.  
DR P-PSDB; AA000399.  
XX  
XX Isolated human polymorphic sequences containing single nucleotide  
PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,  
PT infection and diabetes.  
XX  
PS Claim 1; Page 189; 475pp; English.  
XX  
XX The present invention relates to human nucleic acids containing single  
CC nucleotide polymorphisms (SNPs). These can be used in forensic and  
CC paternity tests, and to aid in the treatment of diseases associated with  
CC aberrant protein expression, including cancer, amyloidosis, diabetes,  
CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,  
CC glomerulonephritis, haemolytic anaemia, thrombocytopaenia, arthritis,  
CC meningitis, muscular disorders, dementia, neurological diseases, tubercous  
CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,  
CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or  
CC autoimmunity. The present sequence is a polymorphism-containing  
CC oligonucleotide fragment of the invention  
XX  
SQ Sequence 51 BP; 11 A; 10 C; 20 G; 10 T; 0 U; 0 Other;  
Query Match 4.1%; Score 41; DB 1; Length 51;  
Best Local Similarity 89.8%; Pred. No. 2.1e+02;  
Matches 44; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 990 CTTCCCGGGCTCAAGCATTTCTGTCAGCTTCCCAAGCACTGGG 1038  
DB 49 CTTCCCGGGCTCAAGCATTTCTGTCAGCTTCCCAAGCACTGGG 1  
RESULT 158  
AAH38408/C  
ID AAH38408 standard; DNA; 51 BP.  
XX  
AC AAH38408;  
XX  
DT 14-AUG-2001 (first entry)  
XX  
DE Human SNP flanking oligonucleotide SEQ ID 1204.  
XX  
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
KM SNPs; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;  
KM Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;  
KM polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
KM acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
KM inflammation; forensic investigation; paternity analysis; ds.  
XX  
OS Homo sapiens.  
XX  
XX WO200129262-A2.  
XX  
XX 26-APR-2001.  
XX  
XX 13-OCT-2000; 2000WO-US028436.  
XX  
XX 15-OCT-1999; 99US-0160096P.  
XX  
XX (ORCH-) ORCHID BIOSCIENCES INC.  
XX  
XX Picoult-Newburg L, Pohl M;  
XX  
XX WPI; 2001-290930/30.  
XX  
XX New genotyping oligonucleotide, useful for detecting the presence,  
PT absence or identity of single polymorphic polymorphism in a nucleic  
PT acid sample.  
XX

PS Claim 1; Page 56; 83pp; English.

CC Sequences AAH371205 - AAH40944 represent PCR primers, single nucleotide  
CC primer extension (SNPE) primers, and the sequences of regions flanking  
CC sites of single nucleotide polymorphisms SNPs. The present invention  
CC includes kits for determining the presence or absence of a SNP, using the  
CC oligonucleotides of the invention. The PCR primers are used to amplify a  
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.  
CC The oligonucleotides are useful for genotyping a nucleic acid sample by  
CC performing a single-nucleotide primer extension reaction. The  
CC oligonucleotides are useful for determining the presence, absence or  
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
CC assess by association analysis the genotype of an individual or group of  
CC individuals, having a pathological phenotypic trait suspected of being  
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
CC agammaglobulinemia, diabetes insipidus, Leech-Nyhan syndrome, muscular  
CC dystrophy, familial hypercholesterolemia, polycystic kidney disease,  
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
CC traits also include symptoms of or susceptibility to multifactorial  
CC disease of which a component is or may be genetic, such as autoimmune  
CC diseases, including, Rheumatoid arthritis, multiple sclerosis,  
CC inflammation, cancer, nervous system diseases and infection by pathogenic  
CC microorganism. The method is also useful in forensic investigations and  
CC paternity analysis. The present sequence represents a fragment of human  
CC DNA flanking the site of a single nucleotide polymorphism  
XX  
XQ Sequence 51 BP; 12 A; 11 C; 17 G; 10 T; 0 U; 1 Other;

SQ Sequence 51 BP; 12 A; 11 C; 17 G; 10 T; 0 U; 1 Other;

Query Match	4.1%	Score 41	DB 1	Length 51
Best Local Similarity	86.3%	Pred. NO. 2.1e+02		
Matches 44	Conservative 1	Mismatches 6	Indels 0	Gaps 0

```

OY      1024 TCCCAAGCAGCTGGGATTACGGGACCTGCCACCAACACCCCGCTAATTTTT 1074
         ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      51  TCCTRAGTACTGGGATTACAGCACCTGCCACCAACGCCCGGCTAATTTTT 1

```

RESULT 159  
AAH40504/C  
ID AAH40504 standard; DNA; 51 BP.

AC AAH40504;

DT 14-AUG-2001 (first entry)

Human SNP flanking oligonucleotide SEQ ID 3300.

KM single nucleotide polymorphism; SNP; single nucleotide primer extension; SNP; genotyping; agammaglobulinaemia; diabetes insipidus; cancer; Leech-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia; polycystic kidney disease; osteogenesis imperfecta; autoimmune disease; acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis; inflammation; forensic investigation; paternity analysis; da-

OS Homo sapiens.

PN WO200129262-A2.

PD 26-APR-2001.

PF 13-OCT-2000; 2000WO-US028436.

PR 15-OCT-1999; 99US-0160096P.

PA (ORCH-) ORCHID BIOSCIENCES INC.

PI Picoult-Newburg L, Pohl M;

DR WPI; 2001-290930/30.

PT New genotyping oligonucleotide, useful for detecting the presence,  
PT absence or identity of single polynucleotide polymorphism in a nucleic  
PT acid sample.

PS Claim 1; Page 66; 83pp; English.

SequenceAAH31205 - AAH4094 represent PCR primers, single nucleotide primer extension (SNPE) primers, and the sequences of regions flanking sites of single nucleotide polymorphisms SNPs. The present invention includes kits for determining the presence or absence of a SNP, using the oligonucleotides of the invention. The PCR primers are used to amplify a SNP flanking sequence, the SNPE primer is used as a genotyping primer. The oligonucleotides are useful for genotyping a nucleic acid sample by performing a single-nucleotide primer extension reaction. The oligonucleotides are useful for determining the presence, absence or identity of a SNP and for genotyping nucleic acid samples, for e.g. to assess by association analysis the genotype of an individual or group of individuals, having a pathological phenotypic trait suspected of being caused by one or more SNPs. Phenotypic traits include diseases e.g. agammaglobulinemia, diabetes insipidus, Lessch-Nyhan syndrome, muscular dystrophy, familial hypercholesterolemia, polycystic kidney disease, osteogenesis imperfecta and acute intermittent porphyria. Phenotypic traits also include symptoms of or susceptibility to multifactorial disease of which a component is or may be genetic such as autoimmune diseases, including, rheumatoid arthritis, multiple sclerosis, inflammation, cancer, nervous system diseases and infection by pathogenic microorganism. The method is also useful in forensic investigations and paternity analysis. The present sequence represents a fragment of human DNA flanking the site of a single nucleotide polymorphism

SQ Sequence 51 BP; 13 A; 13 C; 15 G; 9 T; 0 U; 1 Other;

Query Match	4.1%;	Score 41;	DB 1;	length 51;
Best Local Similarity	86.3%;	Prod. No. 2.1e+02;		
Matches 44;	Conservative 1;	Mismatches 6;	Indels 0;	Gaps 0;

```

Qy      1003 AGCGATTCTCCTGTCTCAGCCTCCCAAGCAGCTGGGATTACGGGCACTGC 1053
          |||||
Db      51  AGCGATTCTCCTGTCTCAGCCTCCGAGTACTGGATTACAGGCACTGC 1
          |||||

```

RESULT 160  
ABL00045/c  
ID ABL00045 standard; DNA; 51 BP.

AC ABL00045;

DT 05-MAR-2002 (first entry)

DE Human silent noncoding SNP oligonucleotide SEQ ID NO:36.

KM Human, single nucleotide polymorphism; SNP, polymorphism; cytostatic; immunosuppressive; antiinflammatory; neuroprotective; antidiabetic; autoimmune disease; inflammation; cancer; nervous system disease; infection; polymorphic protein; ds.

OS Homo sapiens.

PN WO200138586-A2.

PD 31-MAY-2001.

PF 22-NOV-2000; 2000WO-US032311.

PR 24-NOV-1999; 99US-0167383P.

PA (CURA-) CURAGEN CORP.

PI Shimkets RA, Leach M;

DR WPI; 2001-355949/37.

PT Isolated human nucleic acids comprising one or more single nucleotide polymorphisms, useful for treating a subject suffering from a pathology, e.g. autoimmune diseases, ascribed to the presence of a sequence polymorphism.







Query Match 4.1%; Score 40.4; DB 1; Length 50;  
Best Local Similarity 88.0%; Pred. No. 2.2e+02;  
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1052 GGCACACACCGCCGATTTTGTATTTTATTAGAGGCGGTTTCAC 1101  
DB 50 GGCACACACCGCCGATTTTGTATTTTATTAGAGAGAGCGGTTTCAC 1

RESULT 165  
AAV19044/c  
ID AAV19044 standard; DNA; 40 BP.  
XX  
AC AAV19044;  
XX  
DT 28-JUL-1998 (first entry)  
XX  
DE Alu PCR primer 1.  
XX  
XX PCR; primer; amplification; Alu repeat sequence; vector;  
KM circular yeast artificial chromosome; YAC; ss.  
XX  
OS Synthetic.  
XX Saccharomyces sp.  
XX  
PN WO9801573-A1.  
XX  
PD 15-JAN-1998.  
XX  
PF 09-JUL-1996; 96WO-US011478.  
XX  
PR 09-JUL-1996; 96WO-US011478.  
XX  
PA (USSR ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Resnick MA, Larionov VL, Kouprina NY, Perkins EL;  
XX  
DR WPI; 1998-110234/10.  
XX  
PT Preparation of yeast artificial chromosomes - by in vivo recombination  
XX using vector comprising yeast centromere, marker, yeast telomere and  
PT nucleic acid for recombination.  
XX  
PS Example 1; Page 45; 117pp; English.  
XX  
CC This is the nucleotide sequence for the PCR primer used in the  
CC amplification of the Alu repeat sequence, which is used to demonstrate  
CC the processes described in the invention. It involves the creation and  
CC use of circular yeast artificial chromosome (YAC) to selectively clone  
CC specific nucleic acids from a background of mixed nucleic acids by  
CC introducing the vector(s) into E. coli cells. They can be used to rapidly  
CC isolate human DNA where only a part of the sequence of DNA is known.  
CC Using the methods large fragments of DNA can be easily cloned and  
CC analysed  
XX  
SQ Sequence 40 BP; 7 A; 12 C; 13 G; 8 T; 0 U; 0 Other;  
QY Query Match 4.0%; Score 40; DB 1; Length 40;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 849 TCGGCTCCCAAGTCTGGATTACAGGCGTGAGCCACC 888  
40 TCGGCTCCCAAGTCTGGATTACAGGCGTGAGCCACC 1

XX Nucleotide sequence of an Alu PCR primer.  
DE Yeast artificial chromosome; YAC; inter-Alu PCR.  
XX Transformation-associated recombination; PCR; primer; ss.  
KM Synthetic.  
XX  
OS US6391642-B1.  
XX  
PN 21-MAY-2002.  
XX  
PD 14-APR-1998; 98US-00060023.  
XX  
PF 09-JUL-1996; 96WO-US011478.  
XX  
PR (USSR ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Resnick MA, Larionov VL, Kouprina NY, Perkins EL;  
XX  
DR WPI; 2002-49877/53.  
XX  
PT Preparing yeast artificial chromosomes, useful e.g. for cloning specific  
PT human nucleic acid, comprises recombination in yeast cells between a  
PT nucleic acid and a yeast vector.  
XX  
PS Example 1; Col 27; 50pp; English.  
XX

CC The specification describes a method for making a yeast artificial  
CC chromosome (YAC) that includes an origin of replication (ori). The method  
CC comprises incorporating into yeast cells: a population of mammalian  
CC nucleic acid; and a vector that comprises a yeast centromere, selection  
CC marker, yeast telomere and a sequence that recombines with a region of  
CC the nucleic acid, so that in vivo recombination to a YAC occurs. This  
CC method, designated transformation-associated recombination, eliminates  
CC the need for an in vitro ligation step, and makes possible selective  
CC cloning of cDNAs for which only the 3'-sequence is known. The method is  
CC used for making a YAC. The method is also used for selective cloning of  
CC mammalian, specifically human, nucleic acid from a population.  
CC particularly radiation hybrids that contain only a small fragment of a  
CC human chromosome. The present sequence represents an Alu PCR primer. It  
CC was used for inter-Alu PCR, to produce Alu profiles of YACs produced  
CC using the method of the invention  
XX

SQ Sequence 40 BP; 7 A; 12 C; 13 G; 8 T; 0 U; 0 Other;  
QY Query Match 4.0%; Score 40; DB 1; Length 40;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 849 TCGGCTCCCAAGTCTGGATTACAGGCGTGAGCCACC 888  
40 TCGGCTCCCAAGTCTGGATTACAGGCGTGAGCCACC 1

RESULT 167  
ABZ49631/c  
ID ABZ49631 standard; DNA; 41 BP.  
XX  
AC ABZ49631;  
XX  
DT 26-JUN-2003 (first entry)  
XX  
DE Human sulphotransferase SULTR1C1 gene polymorphic site, #6413.  
XX  
XX Human; drug metabolising enzyme; gene; drug metabolism; chromosome 2;  
KM polymorphic site; drug evaluation; drug screening; genotyping;  
KM genetic profiling; therapeutic customisation; adverse reaction;  
XX clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers

```
FT variation replace(21,C)
FT /*tag= a
FT /standard_name= "Single nucleotide polymorphism (SNP) "
XX
XX WO200252044-A2.
XX
XX 04-JUL-2002.
XX
XX 27-DEC-2001; 2001WO-JP011592.
XX
XX 27-DEC-2000; 2000JP-00399443.
XX 02-MAY-2001; 2001JP-00135256.
XX 27-AUG-2001; 2001JP-00256862.
XX
XX (RIKE ) RIKEN KK.
XX
XX Nakamura Y, Sekine A, Iida A, Satto S;
XX
XX WPI; 2002-583571/62.
XX
XX Identifying individuals having a polymorphism, useful for determining the
XX effectiveness or side effect of a drug or treatment protocol, comprises
XX detecting at least one polymorphism in the drug metabolizing enzyme
XX nucleic acid.
XX
XX Claim 23; Page 194; 2785SP; English.
XX
XX Sequences AB243217-AB250887 represent polymorphic sites within genes
XX encoding enzymes associated with drug metabolism. The invention relates
XX to methods and compositions for identifying individuals who have at least
XX one polymorphism in such drug metabolizing enzyme-encoding genes. The
XX polymorphisms may be identified in a nucleic acid sample using probes or
XX primers specific for a sequence selected from AB243217-AB250887 using a
XX variety of detection assays, including hybridisation assays, nucleic acid
XX arrays and PCR-based methods. The invention also encompasses methods of
XX evaluating and screening drugs using genetic polymorphism data. Genetic
XX polymorphism data, particularly that relating to single nucleotide
XX polymorphisms (SNPs), may be used in studying the relationship between
XX DNA sequence variations and human diseases, conditions, and responses to
XX drugs. SNPs are also useful as polymorphism markers for discovering genes
XX that cause or exacerbate certain diseases. SNPs are particularly useful
XX in the above respects as they are stable in populations, occur
XX frequently, and have lower mutation rates than other genome variations
XX such as repeating sequences. The detection and analysis of polymorphisms
XX in genes encoding drug metabolising enzymes allows the customisation of
XX drug therapies based upon the genetic profile of individual patients.
XX This would not only take the guesswork out of selecting the drug with the
XX greatest therapeutic effect for a particular patient, but would also
XX reduce the likelihood of adverse reactions, thereby increasing safety.
XX Methods of the invention are also useful in the drug discovery and
XX approval processes. For example, individuals could be selected for
XX clinical trials only if their genetic profiles indicate that they are
XX capable of responding to a particular drug or drug class, and previously
XX failed drug candidates could be revived if they were matched with more
XX appropriate patient populations. The methods, data and compositions of
XX the invention may therefore lead to an increase in the range of
XX possible drug targets and decreases in the number of adverse drug
XX reactions, failed drug trials, the time taken for a drug to be approved,
XX the length of time patients are on medication and the number of different
XX medications a patient needs to take before finding an effective therapy
XX
XX Sequence 41 BP; 7 A; 13 C; 14 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 4.0%; Score 40; DB 1; Length 41;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 846 GCCTCGGCTCCCAAGTCTGGATTCAGCGCTGAGCC 885
XX |||||
XX Db 40 GCCTCGGCTCCCAAGTCTGGATTCAGCGCTGAGCC 1
```

```
AB243598/C
ID AB243598 standard; DNA; 41 BP.
XX
XX AC AB243598;
XX
XX 26-JUN-2003 (first entry)
XX
XX Human sulphotransferase SULT1C1 gene polymorphic site, #382.
XX
XX Human; drug metabolising enzyme; gene; drug metabolism; chromosome 2;
XX polymorphic site; drug evaluation; drug screening; genotyping;
XX genetic profiling; therapeutic customisation; adverse reaction;
XX clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Variation replace(21,C)
XX /*tag= a
XX /standard_name= "Single nucleotide polymorphism (SNP) "
XX
XX WO200252044-A2.
XX
XX 04-JUL-2002.
XX
XX 27-DEC-2001; 2001WO-JP011592.
XX
XX 27-DEC-2000; 2000JP-00399443.
XX 02-MAY-2001; 2001JP-00135256.
XX 27-AUG-2001; 2001JP-00256862.
XX
XX (RIKE ) RIKEN KK.
XX
XX Nakamura Y, Sekine A, Iida A, Satto S;
XX
XX WPI; 2002-583571/62.
XX
XX Identifying individuals having a polymorphism, useful for determining the
XX effectiveness or side effect of a drug or treatment protocol, comprises
XX detecting at least one polymorphism in the drug metabolizing enzyme
XX nucleic acid.
XX
XX Claim 23; Page 70; 2785SP; English.
XX
XX Sequences AB243217-AB250887 represent polymorphic sites within genes
XX encoding enzymes associated with drug metabolism. The invention relates
XX to methods and compositions for identifying individuals who have at least
XX one polymorphism in such drug metabolizing enzyme-encoding genes. The
XX polymorphisms may be identified in a nucleic acid sample using probes or
XX primers specific for a sequence selected from AB243217-AB250887 using a
XX variety of detection assays, including hybridisation assays, nucleic acid
XX arrays and PCR-based methods. The invention also encompasses methods of
XX evaluating and screening drugs using genetic polymorphism data. Genetic
XX polymorphism data, particularly that relating to single nucleotide
XX polymorphisms (SNPs), may be used in studying the relationship between
XX DNA sequence variations and human diseases, conditions, and responses to
XX drugs. SNPs are also useful as polymorphism markers for discovering genes
XX that cause or exacerbate certain diseases. SNPs are particularly useful
XX in the above respects as they are stable in populations, occur
XX frequently, and have lower mutation rates than other genome variations
XX such as repeating sequences. The detection and analysis of polymorphisms
XX in genes encoding drug metabolising enzymes allows the customisation of
XX drug therapies based upon the genetic profile of individual patients.
XX This would not only take the guesswork out of selecting the drug with the
XX greatest therapeutic effect for a particular patient, but would also
XX reduce the likelihood of adverse reactions, thereby increasing safety.
XX Methods of the invention are also useful in the drug discovery and
XX approval processes. For example, individuals could be selected for
XX clinical trials only if their genetic profiles indicate that they are
XX capable of responding to a particular drug or drug class, and previously
XX failed drug candidates could be revived if they were matched with more
XX appropriate patient populations. The methods, data and compositions of
XX the invention may therefore lead to an increase in the range of
```

CC possible drug targets and decreases in the number of adverse drug  
CC reactions, failed drug trials, the time taken for a drug to be approved,  
CC the length of time patients are on medication and the number of different  
CC medications a patient needs to take before finding an effective therapy  
XX  
SQ Sequence 41 BP; 7 A; 13 C; 14 G; 7 T; 0 U; 0 Other;

Query Match 4.0%; Score 40; DB 1; Length 41;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 846 GCTCGGCTCCCAAGTGTGGATTACAGCGCTGAGCC 885  
DB 40 GCTCGGCTCCCAAGTGTGGATTACAGCGCTGAGCC 1

## RESULT 169

AAH89819  
ID AAH89819 standard; DNA; 50 BP.

XX  
AC AAH89819;

XX 01-OCT-2001 (first entry)

XX Human coding sequence polymorphic site SEQ ID NO: 600.

DE Human; single nucleotide polymorphism; SNP; paternity test;

KM forensic test; aberrant protein expression; ds.

XX Homo sapiens.

XX WO200151670-A2.

XX 19-JUL-2001;

XX 05-JAN-2001; 2001WO-US000322.

XX 07-JAN-2000; 2000US-0174962P.

XX (CUPRA-) CUPAGEN CORP.

XX Shinketsu RA, Leach MD;

XX WPI; 2001-451871/48.

XX P-PSDB; AAM00700.

XX Isolated human polynucleotides containing single nucleotide  
XX polymorphisms, useful for the treatment and diagnosis of e.g. cancer,  
XX infection and diabetes.

XX Claim 1; Page 277; 475pp; English.

XX The present invention relates to human nucleic acids containing single  
XX nucleotide polymorphisms (SNPs). These can be used in forensic and  
XX paternity tests, and to aid in the treatment of diseases associated with  
XX aberrant protein expression, including cancer, amyloidosis, diabetes,  
XX Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,  
XX glomerulonephritis, haemolytic anaemia, thrombocytopaenia, arthritis,  
XX meningitis, muscular disorders, dementia, neurological diseases, tuberculous  
XX sclerosis, male infertility, hypercalcaemia, blood pressure disorders,  
XX osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or  
XX autoimmunity. The present sequence is a polymorphism-containing  
XX oligonucleotide fragment of the invention

XX Sequence 50 BP; 14 A; 12 C; 9 G; 15 T; 0 U; 0 Other;

Query Match 4.0%; Score 40; DB 1; Length 50;  
Best Local Similarity 89.6%; Pred. No. 2.4e+02;  
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1052 GCCACCGACCCCGCTAATTTTGTATTTTCATTAGAGGGGTTTC 1099  
DB 3 GCCACCGACCCCGCTAATTTTGTATTTTAAATAGAGCGGGATTTC 50

RESULT 170  
ACC84472  
ID ACC84472 standard; DNA; 39 BP.

XX ACC84472;

XX 28-AUG-2003 (first entry)

XX NTP peptide encoding sequence #19.

XX Cycostatic; Antibacterial; Immunosuppressive; Antiinflammatory;  
XX neutral thread protein; NTP; tumour; ds.

XX Unidentified.

XX WO2003008443-A2.

XX 30-JAN-2003.

XX 19-JUL-2002; 2002WO-CA001105.

XX 19-JUL-2001; 2001US-0306150P.

XX 19-JUL-2001; 2001US-0306161P.

XX 16-NOV-2001; 2001US-0331477P.

XX (NYMO-) NYMOX CORP.

XX Averbach PA;

XX WPI; 2003-247999/24.

XX P-PSDB; ABR63267.

XX Novel neural thread protein peptide, referred as cell death peptide,  
XX useful for treating prostatic hyperplasia, psoriasis, eczema, dermatosis,  
XX atherosclerosis, cosmetic modification to skin, throat, mouth, muscle.  
XX Disclosure; Page 19; 77pp; English.

XX The present invention relates to a neural thread protein (NTP) peptide  
XX referred to as cell death peptide. Thought to be cytostatic,  
XX antibacterial, immunosuppressive and antiinflammatory. It is useful for  
XX treating a condition in a patient requiring removal or destruction of  
XX cells, for treating a condition such as benign or malignant tumor,  
XX inflammatory disease, autoimmune disease and infectious disease. The  
XX peptide useful for treatment is derived from the amino acid sequence for  
XX a pancreatic thread protein. The peptide is conjugated, antibody-like binding  
XX to a molecule chosen from antibody or its fragment, antibody-like binding  
XX or other target than binding to other cells. Treatment using NTP peptides  
XX can remove benign tumors with less risk and fewer of the undesirable side  
XX effects of surgery. The present sequence is an NTP encoding sequence

XX Sequence 39 BP; 6 A; 13 C; 12 G; 8 T; 0 U; 0 Other;

Query Match 3.9%; Score 39; DB 1; Length 39;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 843 CCTGCTCGGCTCCCAAGTGTGGATTACAGCGCTG 881  
DB 1 CCTGCTCGGCTCCCAAGTGTGGATTACAGCGCTG 39

## RESULT 171

ACC84471  
ID ACC84471 standard; DNA; 39 BP.

XX ACC84471;

XX 28-AUG-2003 (first entry)

DE NTP peptide encoding sequence #18.  
XX  
XX Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;  
KW neural thread protein; NTP; tumour; ds.  
XX  
XX Unidentified.  
XX  
XX WO200308443-A2.  
XX  
XX 30-JAN-2003.  
XX  
XX 19-JUL-2002; 2002WO-CA001105.  
XX  
XX 19-JUL-2001; 2001US-0306150P.  
XX 19-JUL-2001; 2001US-0306161P.  
XX 16-NOV-2001; 2001US-0331477P.  
XX  
XX (NTMO-) NYMOX CORP.  
XX  
XX Averbach PA;  
XX  
XX WPI; 2003-247999/24.  
XX P-PSDB; ABR63266.  
XX  
XX Novel neural thread protein peptide, referred as cell death peptide,  
PT useful for treating prostatic hyperplasia, psoriasis, eczema, dermatosis,  
PT atherosclerosis, cosmetic modification to skin, throat, mouth, muscle.  
XX  
XX Disclosure; Page 19; 77pp; English.  
XX  
XX The present invention relates to a neural thread protein (NTP) peptide  
CC referred to as cell death peptide. Thought to be cytostatic,  
CC antibacterial, immunosuppressive and antiinflammatory. It is useful for  
CC treating a condition in a patient requiring removal or destruction of  
CC cells, for treating a condition such as benign or malignant tumor,  
CC inflammatory disease, autoimmune disease and infectious disease. The  
CC peptide useful for treatment is derived from the amino acid sequence for  
CC a pancreatic thread protein. The peptide is conjugated, linked or bound  
CC to a molecule chosen from antibody or its fragment, antibody-like binding  
CC molecule, where the molecule has a higher affinity for binding to a tumor  
CC or other target than binding to other cells. Treatment using NTP peptides  
CC can remove benign tumors with less risk and fewer of the undesirable side  
CC effects of surgery. The present sequence is an NTP encoding sequence  
CC  
XX  
SQ Sequence 39 BP; 10 A; 14 C; 9 G; 6 T; 0 U; 0 Other;  
  
Query Match 3.9%; Score 39; DB 1; Length 39;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 537 CCTGCTCAGCCTCCCAAGTAGCTGGACCAAGACATG 575  
Db 1 CCTGCTCAGCCTCCCAAGTAGCTGGACCAAGACATG 39  
  
RESULT 172  
ABA96813  
ID ABA96813 standard; DNA; 41 BP.  
XX  
XX ABA96813;  
XX  
XX 30-APR-2002 (first entry)  
XX  
XX Human uteroglobin 9 probe, SEQ ID NO:9.  
XX  
XX Human, uteroglobin 9; recombinant production; malignant tumour; cancer;  
KW blood disease; HIV infection; gene therapy; human immunodeficiency virus;  
KW immune disorder; inflammatory condition; cytostatic; anti-HIV;  
KW antiinflammatory; immunomodulator; probe; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200198337-A1.  
XX  
XX PN

XX  
XX 27-DEC-2001.  
XX  
XX 14-MAY-2001; 2001WO-CN000756.  
XX  
XX 16-MAY-2000; 2000CN-00115717.  
XX  
XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.  
XX  
XX Mao Y, Xie Y;  
XX  
XX WPI; 2002-090430/12.  
XX  
XX Human uteroglobin 9 and encoding polynucleotide, used in diagnosis and  
PT treatment of malignant tumors, hemopathy, human immunodeficiency virus  
PT infection, immunological diseases and inflammation.  
XX  
XX Example 6; Page 19; 35pp; Chinese.  
XX  
XX The invention relates to human uteroglobin 9 (AAMS49078), nucleic acids  
CC encoding it (ABA96807), and a method for the recombinant production of  
CC uteroglobin 9. The protein has a molecular weight of 9 KD. The present  
CC invention additionally discloses an antagonist of uteroglobin 9 for  
CC therapeutic use, and an antibody which specifically binds to uteroglobin  
CC 9. Uteroglobin 9, and nucleotides which encode it may be used for  
CC treating a variety of diseases, such as malignant tumours, blood  
CC diseases, HIV (human immunodeficiency virus) infection, immune disorders  
CC and inflammatory conditions. The protein may also be used to screen for  
CC modulators of its activity or for peptide fingerprinting identification.  
CC The polynucleotide can be used as a primer for nucleic acid amplification  
CC reactions or as a probe for hybridisation reactions, or in producing gene  
CC chips or microarrays. Sequences ABA96812-ABA96813 represent human  
CC uteroglobin 9 probes used in an exemplification of the invention  
XX  
SQ Sequence 41 BP; 4 A; 10 C; 13 G; 14 T; 0 U; 0 Other;  
  
Query Match 3.8%; Score 37.8; DB 1; Length 41;  
Best Local Similarity 95.1%; Pred. No. 2.6e+02;  
Matches 39; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 187 TGGAGTTTCTCCATGTTGTCAGGCTGCTCCAACTCCG 227  
Db 1 TGGAGTTTCTCCATGTTGTCAGGCTGCTCCAACTCCG 41  
  
RESULT 173  
ABA96812  
ID ABA96812 standard; DNA; 41 BP.  
XX  
XX ABA96812;  
XX  
XX 30-APR-2002 (first entry)  
XX  
XX Human uteroglobin 9 probe, SEQ ID NO:8.  
XX  
XX Human, uteroglobin 9; recombinant production; malignant tumour; cancer;  
KW blood disease; HIV infection; gene therapy; human immunodeficiency virus;  
KW immune disorder; inflammatory condition; cytostatic; anti-HIV;  
KW antiinflammatory; immunomodulator; probe; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200198337-A1.  
XX  
XX 27-DEC-2001.  
XX  
XX 14-MAY-2001; 2001WO-CN000756.  
XX  
XX 16-MAY-2000; 2000CN-00115717.  
XX  
XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.  
XX  
XX Mao Y, Xie Y;  
XX  
XX PI

XX WPI; 2002-090430/12.  
DR Human uteroglobin 9 and encoding polynucleotide, used in diagnosis and  
XX treatment of malignant tumors, hemopathy, human immunodeficiency virus  
PT infection, immunological diseases and inflammation.  
PS Example 6; Page 19; 35pp; Chinese.  
XX The invention relates to human uteroglobin 9 (AA0549078), nucleic acids  
CC encoding it (AB096807), and a method for the recombinant production of  
CC uteroglobin 9. The protein has a molecular weight of 9 kD. The present  
CC invention additionally discloses an antagonist of uteroglobin 9 for  
CC therapeutic use, and an antibody which specifically binds to uteroglobin  
CC 9. Uteroglobin 9, and nucleotides which encode it may be used for  
CC treating a variety of diseases, such as malignant tumours, blood  
CC diseases, HIV (human immunodeficiency virus) infection, immune disorders  
CC and inflammatory conditions. The protein may also be used to screen for  
CC modulators of its activity or for peptide fingerprinting identification.  
CC The polynucleotide can be used as a primer for nucleic acid amplification  
CC reactions or as a probe for hybridisation reactions, or in producing gene  
CC chips or microarrays. Sequences AB096812-AB096813 represent human  
CC uteroglobin 9 probes used in an exemplification of the invention  
XX  
SQ Sequence 41 BP; 4 A; 10 C; 13 G; 14 T; 0 U; 0 Other;  
XX  
Query Match 3.8%; Score 37.8; DB 1; Length 41;  
Best Local Similarity 95.1%; Pred. No. 2.6e+02;  
Matches 39; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
XX  
QY 187 TGGAGTTTCTCCATGTTGTGTCAGGCTGCTCGAAGTCCCG 227  
Db 1 TGGGGTTTCTCCATGTTGTGTCAGGCTGCTCGAAGTCTCG 41  
XX  
RESULT 174  
AB244526  
ID AB244526 standard; DNA; 41 BP.  
XX  
AC AB244526;  
XX  
DT 26-JUN-2003 (first entry)  
XX  
DE Human neuropathy target esterase NTE gene polymorphic site, #1310.  
XX  
KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 19;  
KW polymorphic site; drug evaluation; drug screening; genotyping;  
KW genetic profiling; therapeutic customisation; adverse reaction;  
KW clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT variation replace(21,G)  
FT /\*tag= a  
FT /standard\_name= "Single nucleotide polymorphism (SNP)"  
XX  
PN WO200252044-A2.  
XX  
PD 04-JUL-2002.  
XX  
PF 27-DEC-2001; 2001WO-JP011592.  
XX  
PR 27-DEC-2000; 2000JP-00399443.  
PR 02-MAY-2001; 2001JP-00135256.  
PR 27-AUG-2001; 2001JP-00256862.  
XX  
XX (RIKE ) RIKEN KK.  
XX  
XX Nakamura Y, Sekine A, Iida A, Saito S;  
XX  
XX WPI; 2002-583571/62.  
XX

PT Identifying individuals having a polymorphism, useful for determining the  
PT effectiveness or side effect of a drug or treatment protocol, comprises  
PT detecting at least one polymorphism in the drug metabolizing enzyme  
XX nucleic acid.  
PS Claim 23; Page 85; 2785pp; English.  
XX  
XX Sequences AB243217-AB250887 represent polymorphic sites within genes  
CC encoding enzymes associated with drug metabolism. The invention relates  
CC to methods and compositions for identifying individuals who have at least  
CC one polymorphism in such drug metabolising enzyme-encoding genes. The  
CC polymorphisms may be identified in a nucleic acid sample using probes or  
CC primers specific for a sequence selected from AB243217-AB250887 using a  
CC variety of detection assays, including hybridisation assays, nucleic acid  
CC arrays and PCR-based methods. The invention also encompasses methods of  
CC evaluating and screening drugs using genetic polymorphism data. Genetic  
CC polymorphisms (SNPs) may be used in studying the relationship between  
CC DNA sequence variations and human diseases, conditions, and responses to  
CC drugs. SNPs are also useful as polymorphism markers for discovering genes  
CC that cause or exacerbate certain diseases. SNPs are particularly useful  
CC in the above respects as they are stable in populations, occur  
CC frequently, and have lower mutation rates than other genome variations  
CC such as repeating sequences. The detection and analysis of polymorphisms  
CC in genes encoding drug metabolising enzymes allows the customisation of  
CC drug therapies based upon the genetic profile of individual patients.  
CC This would not only take the guesswork out of selecting the drug with the  
CC greatest therapeutic effect for a particular patient, but would also  
CC reduce the likelihood of adverse reactions, thereby increasing safety.  
CC Methods of the invention are also useful in the drug discovery and  
CC approval processes. For example, individuals could be selected for  
CC clinical trials only if their genetic profiles indicate that they are  
CC capable of responding to a particular drug or drug class, and previously  
CC failed drug candidates could be revived if they were matched with more  
CC appropriate patient populations. The methods, data and compositions of  
CC the invention may therefore lead to an increase in the range of  
CC possible drug targets and decreases in the number of adverse drug  
CC reactions, failed drug trials, the time taken for a drug to be approved,  
CC the length of time patients are on medication and the number of different  
CC medications a patient needs to take before finding an effective therapy  
XX  
SQ Sequence 41 BP; 7 A; 16 C; 7 G; 11 T; 0 U; 0 Other;  
XX  
Query Match 3.8%; Score 37.8; DB 1; Length 41;  
Best Local Similarity 95.1%; Pred. No. 2.6e+02;  
Matches 39; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
XX  
QY 676 CACTGCAACCTCGCTCCCGGTTCAAGTTATTCCTCCGC 716  
Db 1 CACTGCAACCTCGCTCCCGGTTCAAGTTATTCCTCCGC 41  
XX  
RESULT 175  
AB250785  
ID AB250785 standard; DNA; 41 BP.  
XX  
AC AB250785;  
XX  
DT 26-JUN-2003 (first entry)  
XX  
DE Human neuropathy target esterase NTE gene polymorphic site, #7567.  
XX  
KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 19;  
KW polymorphic site; drug evaluation; drug screening; genotyping;  
KW genetic profiling; therapeutic customisation; adverse reaction;  
KW clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.  
XX  
XX Homo sapiens.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT variation replace(21,G)  
FT /\*tag= a  
FT /standard\_name= "Single nucleotide polymorphism (SNP)"  
XX



XX MO20025044-A2.  
 XX  
 XX 04-JUN-2002.  
 XX  
 XX 27-DEC-2001; 2001WO-JP011592.  
 XX  
 XX 27-DEC-2000; 2000JP-00399443.  
 XX 02-MAY-2001; 2001JP-00135256.  
 XX 27-AUG-2001; 2001JP-00256862.  
 XX  
 XX (RIKEN ) RIKEN KK.  
 XX  
 XX Nakamura Y, Sekine A, Iida A, Satto S;  
 XX  
 XX WPI; 2002-583571/62.  
 XX  
 XX Identifying individuals having a polymorphism, useful for determining the  
 XX effectiveness or side effect of a drug or treatment protocol, comprises  
 XX detecting at least one polymorphism in the drug metabolizing enzyme  
 XX nucleic acid.  
 XX  
 XX Claim 23; Page 221; 2785pp; English.  
 XX  
 XX Sequences AB243217-AB250887 represent polymorphic sites within genes  
 XX encoding enzymes associated with drug metabolism. The invention relates  
 XX to methods and compositions for identifying individuals who have at least  
 XX one polymorphism in such drug metabolizing enzyme-encoding genes. The  
 XX polymorphisms may be identified in a nucleic acid sample using probes or  
 XX primers specific for a sequence selected from AB243217-AB250887 using a  
 XX variety of detection assays, including hybridization assays, nucleic acid  
 XX arrays and PCR-based methods. The invention also encompasses methods of  
 XX evaluating and screening drugs using genetic polymorphism data. Genetic  
 XX polymorphism data, particularly that relating to single nucleotide  
 XX polymorphisms (SNPs), may be used in studying the relationship between  
 XX DNA sequence variations and human diseases, conditions, and responses to  
 XX drugs. SNPs are also useful as polymorphism markers for discovering genes  
 XX that cause or exacerbate certain diseases. SNPs are particularly useful  
 XX in the above respects as they are stable in populations, occur  
 XX frequently, and have lower mutation rates than other genome variations  
 XX such as repeating sequences. The detection and analysis of polymorphisms  
 XX in genes encoding drug metabolizing enzymes allows the customization of  
 XX drug therapies based upon the genetic profile of individual patients.  
 XX This would not only take the guesswork out of selecting the drug with the  
 XX greatest therapeutic effect for a particular patient, but would also  
 XX reduce the likelihood of adverse reactions, thereby increasing safety.  
 XX Methods of the invention are also useful in the drug discovery and  
 XX approval processes. For example, individuals could be selected for  
 XX clinical trials only if their genetic profiles indicate that they are  
 XX capable of responding to a particular drug or drug class, and previously  
 XX failed drug candidates could be revived if they were matched with more  
 XX appropriate patient populations. The methods, data and compositions of  
 XX the invention may therefore lead to an increase in the range of  
 XX possible drug targets and decreases in the number of adverse drug  
 XX reactions, failed drug trials, the time taken for a drug to be approved,  
 XX the length of time patients are on medication and the number of different  
 XX medications a patient needs to take before finding an effective therapy  
 XX  
 XX Sequence 41 BP; 7 A; 16 C; 7 G; 11 T; 0 U; 0 Other;  
 XX  
 XX Query Match 3.8%; Score 37.8; DB 1; Length 41;  
 XX Best Local Similarity 95.1%; Pred. No. 2.6e+02;  
 XX Matches 39; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 XX  
 XX 676 CACTGCAACCTGCTCCCGGTTCAAGTTATTTCTCTGCG 716  
 XX |||||||  
 XX 1 CACTGCAACCTGCTCCCGGTTCAAGTTATTTCTCTGCG 41  
 XX  
 XX RESULT 176  
 XX AD112521  
 XX ID AD112521 standard; DNA; 42 BP.  
 XX

AC AD112521;  
 XX  
 XX 22-APR-2004 (first entry)  
 XX  
 XX Human BRCA1 DNA junction sequence comprising large deletion Segid 1.  
 XX  
 XX ds; cancer; human; tumour suppressor;  
 XX breast cancer susceptibility gene 1; BRCA1; repetitive Alu;  
 XX ovarian cancer; junction sequence; recombination; mutant.  
 XX  
 XX Homo sapiens.  
 XX  
 XX WO2003104474-A2.  
 XX  
 XX 18-DEC-2003.  
 XX  
 XX 09-JUN-2003; 2003WO-US018098.  
 XX  
 XX 07-JUN-2002; 2002US-0387132P.  
 XX 09-AUG-2002; 2002US-0402430P.  
 XX  
 XX (MYRI-) MYRIAD GENETICS INC.  
 XX  
 XX Scholl T, Hendrickson BC, Ward B, Pruss D;  
 XX  
 XX WPI; 2004-062369/06.  
 XX  
 XX Predicting a predisposition to cancer in a patient comprising detecting a  
 XX deletion in the BRCA1 gene that results from the unequal crossover  
 XX between a pair of repetitive sequences in the BRCA1 gene.  
 XX  
 XX Claim 16; SEQ ID NO 1; 59pp; English.  
 XX  
 XX This invention relates to a novel method for predicting a predisposition  
 XX to cancer in a patient by detecting large deletions in the human tumour  
 XX suppressor gene identified as the breast cancer susceptibility gene 1  
 XX (BRCA1). Specifically, it refers to deletions that result from the  
 XX unequal crossover between a pair of repetitive Alu sequences in the BRCA1  
 XX gene, such that the recombinant nucleotide sequence containing the  
 XX deletion indicates a predisposition to breast and ovarian cancer. The  
 XX present invention describes newly discovered deletion mutations that are  
 XX believed to be deleterious and cause significant alterations in the  
 XX structure or biochemical function of BRCA1. Accordingly, it provides  
 XX methods for detecting such mutants, as well as identifying and screening  
 XX for cytostatic compounds useful for treating or preventing cancers  
 XX associated with a BRCA1 genetic variant. This polynucleotide is a DNA  
 XX fragment representing a junction sequence that arises as a result of a  
 XX recombination event in human BRCA1 that causes the omission of exons 16  
 XX and 17, given in an exemplification of the invention.  
 XX  
 XX Sequence 42 BP; 8 A; 12 C; 12 G; 10 T; 0 U; 0 Other;  
 XX  
 XX Query Match 3.8%; Score 37.8; DB 1; Length 42;  
 XX Best Local Similarity 95.1%; Pred. No. 2.6e+02;  
 XX Matches 39; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 XX  
 XX 848 CTCGGCCTCCCAAGTGCTGGATTACAGGCGTACGACAC 888  
 XX |||||||  
 XX 2 CTCGGCCTCCCAAGTGCTGGATTACAGGCGTACGACATC 42  
 XX  
 XX RESULT 177  
 XX AA268006  
 XX ID AA268006 standard; DNA; 47 BP.  
 XX  
 XX AA268006;  
 XX  
 XX 10-SEP-2001 (first entry)  
 XX  
 XX Human map-related biallelic marker SEQ ID NO:2353.  
 XX  
 XX Human genome; biallelic marker; high density disequilibrium map;  
 XX genomic map; haplotype; phenotype; polymorphic base; genotyping;  
 XX



KW	haplotyping; hybridisation; identification; characterisation; diagnosis;
KM	single nucleotide polymorphism; SNP; ds.
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	variation replace(24,A)
FT	/tag= a
XX	
FN	/standard_name= "single nucleotide polymorphism"
PD	
PD	28-OCT-1999.
PF	
PF	21-APR-1999; 99WO-IB000822.
PR	
PR	21-APR-1998; 98US-0082614P.
PR	23-NOV-1998; 98US-0109732P.
PA	(BEST ) GENSET.
P1	
P1	Cohen D, Blumenfeld M, Chumakov I;
XX	
DR	WPI; 2000-013267/01.
XX	
PT	Novel biallelic markers used to construct a high density disequilibrium
PT	map of the human genome.
PS	
PS	Claim 3; Page 732; 2745pp; English.
XX	
CC	AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC	invention, which contain a polymorphic base at position 24 of their
CC	nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC	primers for the biallelic markers. The biallelic markers of the invention
CC	have a variety of uses: they can be used for high density mapping of the
CC	human genome, and in complex association studies and haplotyping studies
CC	which are useful in determining the genetic basis for disease states.
CC	Compositions and methods of the invention can also be useful for the
CC	identification of the targets for the development of pharmaceutical
CC	agents and diagnostic methods, as well as the characterisation of the
CC	differential efficacious responses to and side effects from
CC	pharmaceutical agents acting on a disease as well as other treatment.
CC	N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC	3367, are not actually given a sequence in the Sequence Listing from the
XX	present invention
SO	
SO	Sequence 47 BP; 9 A; 16 C; 11 G; 11 T; 0 U; 0 Other;
Query Match	3.8%; Score 37.6; DB 1; Length 47;
Best Local Similarity	90.9%; Pred. No. 2.9e+02;
Matches	40; Conservative 0; Mismatches 4; Indels 0; Gaps 0
OY	
OY	1006 GATTCTCCTGCTTCACAGCTTCCCAAGCAGCGGTGAATTAAGGGCAC 1049
ID	2 GATTCTCCTGCTTCACAGCTTCCCAAGCAGCGGTGAATTAAGGCAC 45
ABZ43589/C	
ABZ43589 standard; DNA; 41 BP.	
ABZ43589;	
26-JUN-2003 (first entry)	
Human cerebroside transferase CST gene polymorphic site, #373.	
Human; drug metabolising enzyme; gene; drug metabolism; chromosome 22;	
polymorphic site; drug evaluation; drug screening; genotyping;	
genetic profiling; therapeutic customisation; adverse reaction;	
clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.	
Homo sapiens.	

Key	Location/Qualifiers
FT	variation
FT	replace (21,A)
FT	/*tag= a
FT	/standard_name= "Single nucleotide polymorphism (SNP) "
FN	
FN	MO200252044-A2.
PD	
PD	04-JUL-2002.
XX	
XX	27-DEC-2001; 2001WO-JP011592.
XX	
XX	27-DEC-2000; 2000JP-00399443.
PR	02-MAY-2001; 2001JP-00135256.
PR	27-AUG-2001; 2001JP-00256862.
XX	
PA	(RIKE ) RIKEN KK.
PI	
XX	Nakamura Y, Sekine A, Iida A, Saito S;
XX	WPI; 2002-583571/62.
DR	
XX	
PT	Identifying individuals having a polymorphism, useful for determining the effectiveness or side effect of a drug or treatment protocol, comprises detecting at least one polymorphism in the drug metabolizing enzyme
PT	nucleic acid.
XX	
XX	Claim 23; Page 70; 2785pp; English.
PS	
CC	Sequences AB243217-AB250887 represent polymorphic sites within genes encoding enzymes associated with drug metabolism. The invention relates to methods and compositions for identifying individuals who have at least one polymorphism in such drug metabolizing enzyme-encoding genes. The polymorphisms may be identified in a nucleic acid sample using probes or primers specific for a sequence selected from AB243217-AB250887 using a variety of detection assays, including hybridisation assays, nucleic acid arrays and PCR-based methods. The invention also encompasses methods of evaluating and screening drugs using genetic polymorphism data. Genetic polymorphism data, particularly that relating to single nucleotide polymorphisms (SNPs), may be used in studying the relationship between DNA sequence variations and human diseases, conditions, and responses to drugs. SNPs are also useful as polymorphism markers for discovering genes that cause or exacerbate certain diseases. SNPs are particularly useful in the above respects as they are stable in populations, occur frequently, and have lower mutation rates than other genome variations such as repeating sequences. The detection and analysis of polymorphisms in genes encoding drug metabolising enzymes allows the customisation of drug therapies based upon the genetic profile of individual patients. This would not only take the guesswork out of selecting the drug with the greatest therapeutic effect for a particular patient, but would also reduce the likelihood of adverse reactions, thereby increasing safety. Methods of the invention are also useful in the drug discovery and approval processes. For example, individuals could be selected for clinical trials only if their genetic profiles indicate that they are capable of responding to a particular drug or drug class, and previously failed drug candidates could be revived if they were matched with more appropriate patient populations. The methods, data and compositions of the invention may therefore lead to an increase in the range of possible drug targets and decreases in the number of adverse drug reactions, failed drug trials, the time taken for a drug to be approved, the length of time patients are on medication and the number of different medications a patient needs to take before finding an effective therapy
CC	
CC	Sequence 41 BP; 9 A; 11 C; 13 G; 8 T; 0 U; 0 Other;
XX	
QY	Query Match 3.7%; Score 36.2; DB 1; Length 41;
QY	Best Local Similarity 92.7%; Pred. No. 3.1e+02;
QY	Matches 38; Conservative 0; Mismatches 3; Indels 0; Gaps 0
DB	198 CATTGTTGGTCAAGCGTGTCTGCAACTCCCGACCTCAGATGA 238
DB	41 CATTGTGGCCAGGCTGTTCTGCAACTCTCTGACTCTGACGCA 1

RESULT 179  
 ABZ4509  
 ID ABZ4509 standard; DNA; 41 BP.  
 XX  
 AC ABZ4509;  
 XX  
 DT 26-JUN-2003 (first entry)  
 XX  
 DE Human ATP-binding cassette ABCA7 gene polymorphic site, #2293.  
 XX  
 KM Human; drug metabolizing enzyme; gene; drug metabolism; chromosome 19;  
 KM polymorphic site; drug evaluation; drug screening; genotyping;  
 KM genetic profiling; therapeutic customisation; adverse reaction;  
 KM clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FT Key Location/Qualifiers  
 FT variation replace(21,T)  
 FT /\*tag= a  
 FT /standard\_name= "Single nucleotide polymorphism (SNP)"  
 XX  
 PN WO200252044-A2.  
 XX  
 PD 04-JUL-2002.  
 XX  
 PF 27-DEC-2001; 2001WO-JP011592.  
 XX  
 PR 27-DEC-2000; 2000JP-00399443.  
 PR 02-MAY-2001; 2001JP-00135256.  
 PR 27-AUG-2001; 2001JP-00256862.  
 XX  
 PA (RIKE ) RIKEN KK.  
 XX  
 PI Nakamura Y, Sekine A, Iida A, Saito S;  
 XX  
 DR WPI; 2002-583571/62.  
 XX  
 PT Identifying individuals having a polymorphism, useful for determining the  
 PT effectiveness or side effect of a drug or treatment protocol, comprises  
 PT detecting at least one polymorphism in the drug metabolizing enzyme  
 PT nucleic acid.  
 XX  
 PS Claim 23; Page 102; 2785pp; English.  
 XX  
 CC Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes  
 CC encoding enzymes associated with drug metabolism. The invention relates  
 CC to methods and compositions for identifying individuals who have at least  
 CC one polymorphism in such drug metabolizing enzyme-encoding genes. The  
 CC polymorphisms may be identified in a nucleic acid sample using probes or  
 CC primers specific for a sequence selected from ABZ43217-ABZ50887 using a  
 CC variety of detection assays, including hybridisation assays, nucleic acid  
 CC arrays and PCR-based methods. The invention also encompasses methods of  
 CC evaluating and screening drugs using genetic polymorphism data. Genetic  
 CC polymorphism data, particularly that relating to single nucleotide  
 CC polymorphisms (SNPs), may be used in studying the relationship between  
 CC DNA sequence variations and human diseases, conditions, and responses to  
 CC drugs. SNPs are also useful as polymorphism markers for discovering genes  
 CC that cause or exacerbate certain diseases. SNPs are particularly useful  
 CC in the above respects as they are stable in populations, occur  
 CC frequently, and have lower mutation rates than other genome variations  
 CC such as repeating sequences. The detection and analysis of polymorphisms  
 CC in genes encoding drug metabolizing enzymes allows the customisation of  
 CC drug therapies based upon the genetic profile of individual patients.  
 CC This would not only take the guesswork out of selecting the drug with the  
 CC greatest therapeutic effect for a particular patient, but would also  
 CC reduce the likelihood of adverse reactions, thereby increasing safety.  
 CC Methods of the invention are also useful in the drug discovery and  
 CC approval processes. For example, individuals could be selected for  
 CC clinical trials only if their genetic profiles indicate that they are  
 CC capable of responding to a particular drug or drug class, and previously  
 CC failed drug candidates could be revived if they were matched with more

CC appropriate patient populations. The methods, data and compositions of  
 CC the invention may therefore lead to an increase in the range of  
 CC possible drug targets and decreases in the number of adverse drug  
 CC reactions, failed drug trials, the time taken for a drug to be approved,  
 CC the length of time patients are on medication and the number of different  
 CC medications a patient needs to take before finding an effective therapy  
 XX  
 SQ Sequence 41 BP; 8 A; 12 C; 13 G; 8 T; 0 U; 0 Other;  
 XX  
 Query Match 3.7%; Score 36.2; DB 1; Length 41;  
 Best local similarity 92.7%; Pred. No. 3.1e+02;  
 Matches 38; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 XX  
 QY 643 CCCAGGCTGAGTGCAGTGGCGCAATCTTGCTCATGCGAA 683  
 DB 1 CCCAGGCTGAGTGCAGTGGCGAGATCTTGCTCATGCGAA 41  
 XX  
 RESULT 180  
 ABZ46915  
 ID ABZ46915 standard; DNA; 41 BP.  
 XX  
 AC ABZ46915;  
 XX  
 DT 26-JUN-2003 (first entry)  
 XX  
 DE Human ATP-binding cassette ABCA7 gene polymorphic site, #3699.  
 XX  
 KM Human; drug metabolizing enzyme; gene; drug metabolism; chromosome 19;  
 KM polymorphic site; drug evaluation; drug screening; genotyping;  
 KM genetic profiling; therapeutic customisation; adverse reaction;  
 KM clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FT Key Location/Qualifiers  
 FT variation replace(17,A)  
 FT /\*tag= a  
 FT /standard\_name= "Single nucleotide polymorphism (SNP)"  
 FT FT replace(21,T)  
 FT /\*tag= b  
 FT /standard\_name= "Single nucleotide polymorphism (SNP)"  
 XX  
 PN WO200252044-A2.  
 XX  
 PD 04-JUL-2002.  
 XX  
 PF 27-DEC-2001; 2001WO-JP011592.  
 XX  
 PR 27-DEC-2000; 2000JP-00399443.  
 PR 02-MAY-2001; 2001JP-00135256.  
 PR 27-AUG-2001; 2001JP-00256862.  
 XX  
 PA (RIKE ) RIKEN KK.  
 XX  
 PI Nakamura Y, Sekine A, Iida A, Saito S;  
 XX  
 DR WPI; 2002-583571/62.  
 XX  
 PT Identifying individuals having a polymorphism, useful for determining the  
 PT effectiveness or side effect of a drug or treatment protocol, comprises  
 PT detecting at least one polymorphism in the drug metabolizing enzyme  
 PT nucleic acid.  
 XX  
 PS Claim 23; Page 129; 2785pp; English.  
 XX  
 CC Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes  
 CC encoding enzymes associated with drug metabolism. The invention relates  
 CC to methods and compositions for identifying individuals who have at least  
 CC one polymorphism in such drug metabolizing enzyme-encoding genes. The  
 CC polymorphisms may be identified in a nucleic acid sample using probes or  
 CC primers specific for a sequence selected from ABZ43217-ABZ50887 using a  
 CC variety of detection assays, including hybridisation assays, nucleic acid

arrays and PCR-based methods. The invention also encompasses methods of evaluating and screening drugs using genetic polymorphism data. Genetic polymorphism data, particularly that relating to single nucleotide polymorphisms (SNPs), may be used in studying the relationship between DNA sequence variations and human diseases, conditions, and responses to drugs. SNPs are also useful as polymorphism markers for discovering genes that cause or exacerbate certain diseases. SNPs are particularly useful in the above respects as they are stable in populations, occur frequently, and have lower mutation rates than other genome variations such as repeating sequences. The detection and analysis of polymorphisms in genes encoding drug metabolizing enzymes allows the customization of drug therapies based upon the genetic profile of individual patients. This would not only take the guesswork out of selecting the drug with the greatest therapeutic effect for a particular patient, but would also reduce the likelihood of adverse reactions, thereby increasing safety. Methods of the invention are also useful in the drug discovery and approval processes. For example, individuals could be selected for clinical trials only if their genetic profiles indicate that they are capable of responding to a particular drug or drug class, and previously failed drug candidates could be revived if they were matched with more appropriate patient populations. The methods, data and compositions of the invention may therefore lead to an increase in the range of possible drug targets and decreases in the number of adverse drug reactions, failed drug trials, the time taken for a drug to be approved, the length of time patients are on medication and the number of different medications a patient needs to take before finding an effective therapy

Query Match	3.7%	Score 36.2	DB 1	Length 41
Best Local Similarity	92.7%	Pred No. 3.1e+02		
Matches 38	Conservative 0	Mismatches 3	Indels 0	Gaps 0

```

QY      643  CCCAGGCTGGAGTGCAGTGGCGCAATCTTGCTCACTGCAA 683
          |||||
Db      1  CCCAGGCTGCACTGCAGTGGCGAGATCTTGCTCACTGCAA 41

```

RESULT 181  
ABZ49741/C  
ID ABZ49741 standard; DNA; 41 BP

AC	ABZ49741;	
XX		
DT	26-JUN-2003	(first entry)

AA Human cerebroside transferase CST gene polymorphic site, #6523.  
DE

Human; drug metabolizing enzyme; gene; drug metabolism; chromosome 22;  
polymorphic site; drug evaluation; drug screening; genotyping;  
genetic profiling; therapeutic customization; adverse reaction;  
clinical trial; drug approval; single nucleotide polymorphism; SNP; ds  
Homo sapiens.

Key variation	Location/Qualifiers replace (21,A) /*tag= a	Single nucleotide polymorphism (SNP) " /standard name=
FT		
FT		
FT		

XX  
PN W0200252044-A2.

04-JUL-2002.

PF 27-DEC-2001; 2001WO-JP011592.  
YY

PR	27-DEC-2000; 2000JP-00399443.
PR	02-MAY-2001; 2001JP-00135256.
PR	27-AUG-2001; 2001JP-00256862.

(RIKE ) RIKEN KK.  
 Nakamura Y, Sekine A, Iida A, Salto S;  
 PI

XX  
DR  
WPI; 2002-583571/62.

identifying individuals having a polymorphism, useful for determining the effectiveness or side effect of a drug or treatment protocol, comprises detecting at least one polymorphism in the drug metabolizing enzyme nucleic acid.

XX  
PS Claim 23; Page 197; 2785pp; English

Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes encoding enzymes associated with drug metabolism. The invention relates to methods and compositions for identifying individuals who have at least one polymorphism in such drug metabolizing enzyme-encoding genes. The polymorphisms may be identified in a nucleic acid sample using probes or primers specific for a sequence selected from ABZ43217-ABZ50887 using a variety of detection assays, including hybridization assays, nucleic acid arrays and PCR-based methods. The invention also encompasses methods of evaluating and screening drugs using genetic polymorphism data. Genetic polymorphism data, particularly that relating to single nucleotide polymorphisms (SNPs), may be used in studying the relationship between DNA sequence variations and human diseases, conditions, and responses to drugs. SNPs are also useful as polymorphism markers for discovering genes that cause or exacerbate certain diseases. SNPs are particularly useful in the above respects as they are stable in populations, occur frequently, and have lower mutation rates than other genome variations such as repeating sequences. The detection and analysis of polymorphisms in genes encoding drug metabolizing enzymes allows the customization of drug therapies based upon the genetic profile of individual patients. This would not only take the guesswork out of selecting the drug with the greatest therapeutic effect for a particular patient, but would also reduce the likelihood of adverse reactions, thereby increasing safety. Methods of the invention are also useful in the drug discovery and approval processes. For example, individuals could be selected for clinical trials only if their genetic profiles indicate that they are capable of responding to a particular drug or drug class, and previously failed drug candidates could be revived if they were matched with more appropriate patient populations. The methods, data and compositions of the invention may therefore lead to an increase in the range of possible drug targets and decrease in the number of adverse drug reactions. Failed drug trials, the time taken for a drug to be approved, the length of time patients are on medication and the number of different medications a patient needs to take before finding an effective therapy

Sequence	41 BP; 9 A; 11 C; 13 G; 8 T; 0 U; 0 Other;
Query Match	3.7%; Score 35.2; DB 1; Length 41;
Best Local Similarity	92.7%; Pred. NO. 3.1e+02;
Matches 38; Conservative	0; Mismatches 3; Indels 0; Gaps 0

```

QY      198 CATGTTGGTCAGGCTGGTCTCGAACTCCCGACCTCAGATGA 238
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      41 CATGTTGGCCAGGCTGGTCTCGAACTCCTGACCTCAGACGA 1

```

RESULT 182  
AAH91207/c  
ID AAH91207 standard; DNA; 40 BP.

XX  
AC AAH91207

09-OCT-2001 (first entry)

XX	Human inflammatory bowel disease associated polymorphic site #282.
DE	

Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis  
 KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;  
 KW chromosome 5q31-33; forensic test; gene therapy; ds.

Homo sapiens

XX	Key	Location/Qualifiers
FH		
FT	misc_feature	13

FT /\*tag= a  
FT /note= "SNP, optionally T or C at this position"  
XX  
XX  
XX WO200142511-A2.  
XX  
XX 14-JUN-2001.  
XX  
XX 11-DEC-2000; 2000WO-US033632.  
XX  
XX 10-DEC-1999; 99US-0170257P.  
XX 10-APR-2000; 2000US-0196046P.  
XX  
XX (WHEB) WHITEHEAD INST BIOMEDICAL RES.  
XX (ELI-) ELIPIIS BIOTHERAPEUTICS CORP.  
XX  
XX Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;  
XX WPI; 2001-367874/38.  
XX  
XX Testing for the presence of polymorphisms associated with inflammatory  
XX bowel disease, using a hybridization assay.  
XX  
XX Claim 1; Page 50; 463pp; English.  
XX  
XX The present invention describes a method for detecting the presence of  
XX polymorphisms associated with inflammatory bowel diseases such as  
XX ulcerative colitis and Crohn's disease. The methods can be used to detect  
XX the presence of genetic polymorphisms associated with inflammatory bowel  
XX disease and correlating their occurrence with disease states. They may be  
XX used in this way for phenotypic correlations, forensics, paternity  
XX testing, medicine and genetic analysis. The present sequence is a  
XX polymorphic site described in the exemplification of the invention  
XX  
XX Sequence 40 BP; 13 A; 7 C; 12 G; 7 T; 0 U; 1 Other;  
XX  
XX Query Match 3.6%; Score 35.8; DB 1; Length 40;  
XX Best Local Similarity 92.5%; Pred. No. 3.2e+02;  
XX Matches 37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
XX  
XX 1096 TTTCACCATATTGTCAGGCTGCTCCAAACCTCGACCT 1135  
XX Db 40 TTTCACCATATTGTCAGGCTGCTCCAAACCTCGACCT 1  
XX  
XX RESULT 183  
XX ABZ50133/C  
XX ID ABZ50133 standard; DNA; 41 BP.  
XX  
XX AC ABZ50133;  
XX  
XX 26-JUN-2003 (first entry)  
XX  
XX Human NDUF51 gene polymorphic site, #6915.  
XX  
XX Human; drug metabolising enzyme; gene; drug metabolism; chromosome 2;  
XX polymorphic site; drug evaluation; drug screening; genotyping;  
XX genetic profiling; therapeutic customisation; adverse reaction;  
XX clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX FT replace(21,T)  
XX FT /\*tag= a  
XX FT /standard\_name= "Single nucleotide polymorphism (SNP)"  
XX  
XX WO200252044-A2.  
XX  
XX 04-JUL-2002.  
XX  
XX 27-DEC-2001; 2001WO-JP011592.  
XX  
XX 27-DEC-2000; 2000JP-00399443.  
XX  
XX

PR 02-MAY-2001; 2001JP-00135256.  
PR 27-AUG-2001; 2001JP-00256862.  
XX  
XX (RIKE) RIKEN KK.  
XX  
XX Nakamura Y, Sekine A, Iida A, Saito S;  
XX WPI; 2002-583571/62.  
XX  
XX Identifying individuals having a polymorphism, useful for determining the  
XX effectiveness or side effect of a drug or treatment protocol, comprises  
XX detecting at least one polymorphism in the drug metabolizing enzyme  
XX nucleic acid.  
XX  
XX Claim 23; Page 206; 2785pp; English.  
XX  
XX Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes  
XX encoding enzymes associated with drug metabolism. The invention relates  
XX to methods and compositions for identifying individuals who have at least  
XX one polymorphism in such drug metabolising enzyme-encoding genes. The  
XX polymorphisms may be identified in a nucleic acid sample using probes or  
XX primers specific for a sequence selected from ABZ43217-ABZ50887 using a  
XX variety of detection assays, including hybridisation assays, nucleic acid  
XX arrays and PCR-based methods. The invention also encompasses methods of  
XX evaluating and screening drugs using genetic polymorphism data. Genetic  
XX polymorphism data, particularly that relating to single nucleotide  
XX polymorphisms (SNPs), may be used in studying the relationship between  
XX DNA sequence variations and human diseases, conditions, and responses to  
XX drugs. SNPs are also useful as polymorphism markers for discovering genes  
XX that cause or exacerbate certain diseases. SNPs are particularly useful  
XX in the above respects as they are stable in populations, occur  
XX frequently, and have lower mutation rates than other genome variations  
XX such as repeating sequences. The detection and analysis of polymorphisms  
XX in genes encoding drug metabolising enzymes allows the customisation of  
XX drug therapies based upon the genetic profile of individual patients.  
XX This would not only take the guesswork out of selecting the drug with the  
XX greatest therapeutic effect for a particular patient, but would also  
XX reduce the likelihood of adverse reactions, thereby increasing safety.  
XX Methods of the invention are also useful in the drug discovery and  
XX approval processes. For example, individuals could be selected for  
XX clinical trials only if their genetic profiles indicate that they are  
XX capable of responding to a particular drug or drug class, and previously  
XX failed drug candidates could be revived if they were matched with more  
XX appropriate patient populations. The methods, data and compositions of  
XX the invention may therefore lead to an increase in the range of  
XX possible drug targets and decreases in the number of adverse drug  
XX reactions, failed drug trials, the time taken for a drug to be approved,  
XX the length of time patients are on medication and the number of different  
XX medications a patient needs to take before finding an effective therapy  
XX  
XX Sequence 41 BP; 12 A; 7 C; 12 G; 10 T; 0 U; 0 Other;  
XX  
XX Query Match 3.6%; Score 35.8; DB 1; Length 41;  
XX Best Local Similarity 94.9%; Pred. No. 3.3e+02;  
XX Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
XX  
XX 1045 GGACACCTGCCACACACCCGCTAATTTTGTATTTTCA 1083  
XX Db 40 GGACACCTGCCACACACCCGCTAATTTTGTATTTTCA 2  
XX  
XX RESULT 184  
XX ABZ44123/C  
XX ID ABZ44123 standard; DNA; 41 BP.  
XX  
XX AC ABZ44123;  
XX  
XX 26-JUN-2003 (first entry)  
XX  
XX Human NDUF51 gene polymorphic site, #907.  
XX  
XX Human; drug metabolising enzyme; gene; drug metabolism; chromosome 2;  
XX polymorphic site; drug evaluation; drug screening; genotyping;  
XX  
XX

genetic profiling, therapeutic customisation, adverse reaction;  
 clinical trial, drug approval, single nucleotide polymorphism, SNP, ds.  
 Homo sapiens.  
 Key Location/Qualifiers  
 variation /tag=a  
 /standard\_name="Single nucleotide polymorphism (SNP)"  
 WO200252044-A2.  
 04-JUL-2002.  
 27-DEC-2001; 2001WO-JP011592.  
 27-DEC-2000; 2000JP-00399443.  
 02-MAY-2001; 2001JP-00135256.  
 27-AUG-2001; 2001JP-00256862.  
 (RIKE ) RIKEN KK.  
 Nakamura Y, Sekine A, Iida A, Saito S;  
 WPI; 2002-583571/62.  
 Identifying individuals having a polymorphism, useful for determining the  
 effectiveness or side effect of a drug or treatment protocol, comprises  
 detecting at least one polymorphism in the drug metabolizing enzyme  
 nucleic acid.  
 Claim 23; Page 79; 2785pp; English.  
 Sequences AB243217-AB250887 represent polymorphic sites within genes  
 encoding enzymes associated with drug metabolism. The invention relates  
 to methods and compositions for identifying individuals who have at least  
 one polymorphism in such drug metabolizing enzyme-encoding genes. The  
 polymorphisms may be identified in a nucleic acid sample using probes or  
 primers specific for a sequence selected from AB243217-AB250887 using a  
 variety of detection assays, including hybridisation assays, nucleic acid  
 arrays and PCR-based methods. The invention also encompasses methods of  
 evaluating and screening drugs using genetic polymorphism data. Genetic  
 polymorphism data, particularly that relating to single nucleotide  
 polymorphisms (SNPs), may be used in studying the relationship between  
 DNA sequence variations and human diseases, conditions, and responses to  
 drug. SNPs are also useful as polymorphism markers for discovering genes  
 that cause or exacerbate certain diseases. SNPs are particularly useful  
 in the above respects as they are stable in populations, occur  
 frequently, and have lower mutation rates than other genome variations  
 such as repeating sequences. The detection and analysis of polymorphisms  
 in genes encoding drug metabolizing enzymes allows the customisation of  
 drug therapies based upon the genetic profile of individual patients.  
 This would not only take the guesswork out of selecting the drug with the  
 greatest therapeutic effect for a particular patient, but would also  
 reduce the likelihood of adverse reactions, thereby increasing safety.  
 Methods of the invention are also useful in the drug discovery and  
 approval processes. For example, individuals could be selected for  
 clinical trials only if their genetic profiles indicate that they are  
 capable of responding to a particular drug or drug class, and previously  
 failed drug candidates could be revived if they were matched with more  
 appropriate patient populations. The methods, data and compositions of  
 the invention may therefore lead to an increase in the range of  
 possible drug targets and decreases in the number of adverse drug  
 reactions, failed drug trials, the time taken for a drug to be approved,  
 the length of time patients are on medication and the number of different  
 medications a patient needs to take before finding an effective therapy

Query Match 3.6%; Score 35.8; DB 1; Length 41;  
 Best Local Similarity 94.9%; Pred. No. 3.3e+02;  
 Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1045 GGACCTGCACACACCCGCTAATTTTGTATTTTCA 1083  
 |||||  
 40 GGACATGCCACACACCCGCTAATTTTGTATTTTCA 2  
 |||||  
 RESULT 185  
 AAT97407/C  
 ID AAT97407 standard; DNA; 40 BP.  
 AC AAT97407;  
 DT 14-APR-1998 (first entry)  
 DE Synthetic oligomer D1888 Allele G from WO9722719 Example 2.  
 KW Detection; target site; nucleic acid; fluorophore; labelled; fluorescent;  
 KW inherited disease; tissue typing; PCR; ss.  
 OS Synthetic.  
 XX WO9722719-A1.  
 XX 26-JUN-1997.  
 XX 17-DEC-1996; 96WO-US020379.  
 XX 18-DEC-1995; 95US-0008743P.  
 XX (UNIW ) UNIV WASHINGTON.  
 XX Kwok P, Chen X;  
 PT WPI; 1997-341707/31.  
 XX  
 PT Detecting target site in nucleic acid by forming a fluorophore-labelled  
 oligonucleotide at the site - and detecting fluorescent energy following  
 denaturation, used e.g. to detect inherited diseases, in tissue typing  
 etc.  
 PS Example 2; Page 27; 68pp; English.  
 A method has been developed for detecting the presence of a target site  
 (TS), of at least one nucleotide (nt) in a nucleic acid (NA). The method  
 comprises: (a) forming an oligonucleotide (ON), consisting of two  
 fluorophores (F1, F2) each covalently linked to separate nt, bound to TS;  
 and (b) detecting fluorescence energy transfer (FET) between F1 and F2  
 when ON is released from TS. The present sequence represents a synthetic  
 polynucleotide used in an example of the present invention. The method is  
 used to diagnose hereditary and other diseases; to determine infectious  
 agents; in tissue typing for histocompatibility; in forensic  
 identification and paternity testing, and in monitoring the genetic make  
 up of plants and animals. Specifically it is used to detect single nt  
 polymorphisms. The method provides inexpensive, simple, accurate and  
 automatable nucleic acid analyses

Query Match 3.6%; Score 35.2; DB 1; Length 40;  
 Best Local Similarity 92.5%; Pred. No. 3.4e+02;  
 Matches 37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

675 TCACGTGCAACCTCTGCTCCCGGGTTCAAGTATTTCTCT 714  
 |||||  
 40 TCACGTGCAACCTCTGCTCCCGGGTTCAAGCAATTTCTCT 1  
 |||||

RESULT 186  
 AAV19045/C  
 ID AAV19045 standard; DNA; 40 BP.  
 AC AAV19045;  
 DT 28-JUL-1998 (first entry)

```

XX  Alu PCR primer 2.
DE
XX  PCR; primer; amplification; Alu repeat sequence; vector;
XX  circular yeast artificial chromosome; YAC; ss.
KW
XX  Synthetic.
OS
XX  Saccharomyces sp.
XX  MO9801573-Al.
XX  15-JAN-1998.
XX  09-JUL-1996; 96WO-US011478.
XX  09-JUL-1996; 96WO-US011478.
XX  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA  Resnick MA, Laktionov VL, Kouprina NY, Perkins EL;
PI  WPI; 1998-110234/10.
DR  Preparation of yeast artificial chromosomes - by in vivo recombination
PT  using vector comprising yeast centromere, marker, yeast telomere and
PT  nucleic acid for recombination.
XX  Example 1; Page 45; 117pp; English.
XX  This is the nucleotide sequence for the PCR primer used in the
CC  amplification of the Alu repeat sequence, which is used to demonstrate
CC  the processes described in the invention. It involves the creation and
CC  use of circular yeast artificial chromosome (YAC) to selectively clone
CC  specific nucleic acids from a background of mixed nucleic acids by
CC  introducing the vector(s) into E. coli cells. They can be used to rapidly
CC  isolate human DNA where only a part of the sequence of DNA is known.
CC  Using the methods large fragments of DNA can be easily cloned and
CC  analysed
SQ  Sequence 40 BP; 9 A; 8 C; 19 G; 4 T; 0 U; 0 Other;

Query Match      3.6%; Score 35.2; DB 1; Length 40;
Best Local Similarity 92.5%; Pred. No. 3.4e+02;
Matches 37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY  987 CTGCTCCCGGGCTCAGGATTCTCTGTCTCAGCTCC 1026
DB  40 CCGCTCCCGGGTCAAGGATTCTCTGTCTCAGCTCC 1

RESULT 187
ABL59101/C
ID  ABL59101 standard; DNA; 40 BP.
XX
AC  ABL59101;
XX
DT  27-SEP-2002 (first entry)
XX
DE  Nucleotide sequence of an Alu PCR primer.
XX
KW  Yeast artificial chromosome; YAC; inter-Alu PCR;
XX  transformation-associated recombination; PCR; primer; ss.
OS  Synthetic.
XX
XX  US6391642-B1.
XX  21-MAY-2002.
XX  14-APR-1998; 98US-00060023.
XX  09-JUL-1996; 96WO-US011478.
XX

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PA  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX  Resnick MA, Laktionov VL, Kouprina NY, Perkins EL;
XX  WPI; 2002-498777/53.
XX  Preparing yeast artificial chromosomes, useful e.g. for cloning specific
PT  human nucleic acid, comprises recombination in yeast cells between a
PT  nucleic acid and a yeast vector.
XX  Example 1; Col 27; 50pp; English.
XX  The specification describes a method for making a yeast artificial
CC  chromosome (YAC) that includes an origin of replication (ori). The method
CC  comprises incorporating into yeast cells a population of mammalian
CC  nucleic acid; and a vector that comprises a yeast centromere, selection
CC  marker, yeast telomere and a sequence that recombines with a region of
CC  the nucleic acid, so that in vivo recombination to a YAC occurs. This
CC  method, designated transformation-associated recombination, eliminates
CC  the need for an in vitro ligation step, and makes possible selective
CC  cloning of cDNAs for which only the 3'-sequence is known. The method is
CC  used for making a YAC. The method is also used for selective cloning of
CC  mammalian, specifically human, nucleic acid from a population.
CC  particularly radiation hybrids that contain only a small fragment of a
CC  human chromosome. The present sequence represents an Alu PCR primer. It
CC  was used for inter-Alu PCR, to produce Alu profiles of YACs produced
CC  using the method of the invention
XX  Sequence 40 BP; 9 A; 8 C; 19 G; 4 T; 0 U; 0 Other;

Query Match      3.6%; Score 35.2; DB 1; Length 40;
Best Local Similarity 92.5%; Pred. No. 3.4e+02;
Matches 37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY  987 CTGCTCCCGGGCTCAGGATTCTCTGTCTCAGCTCC 1026
DB  40 CCGCTCCCGGGTCAAGGATTCTCTGTCTCAGCTCC 1

RESULT 188
AAH49727/C
ID  AAH49727 standard; DNA; 41 BP.
XX
AC  AAH49727;
XX
DT  25-SEP-2001 (first entry)
XX
DE  Human DNA mismatch repair protein 11 coding sequence probe #1.
XX
KW  Human; DNA repair mismatch protein 11; cancer; haemopathy; HIV infection;
XX  immunological disease; inflammation; gene therapy; probe; ss.
XX
OS  Homo sapiens.
XX
XX  WO200147988-A1.
XX  05-JUL-2001.
XX  18-DEC-2000; 2000WO-CN000627.
XX  23-DEC-1999; 99CN-00125733.
XX  (YFPU-) UNIV FUDAN.
XX  (SHAN-) SHANGHAI BIO DOOR GENE TECHNOLOGY LTD.
XX  Mao Y, Xie Y;
XX  WPI; 2001-425639/45.
XX  DNA mismatch repair protein 11 and encoded polynucleotide, applicable in
PT  diagnosis and treatment of malignant tumor, hemopathy, HIV infection,
PT  immunological diseases and various inflammation.
XX

```

Db 41 TTCTCCTGCCCTCAACCTCCCGAGTAGCTGGGACTACAGGC 2

## OS Homo sapiens.

```
XX CN1345751-A.
PN
XX 24-APR-2002.
PD
XX 26-SEP-2000; 2000CN-00125456.
PF
XX 26-SEP-2000; 2000CN-00125456.
PR
XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
PA
XX Mao Y, Xie Y;
PI
XX WPI; 2002-675773/73.
DR
XX Novel polypeptide-human G protein subunit 9.01.
PT
XX Example 6; Page 22(Disclosure); 34pp; Chinese.
PS
XX The present invention provides the protein and coding sequences of human
CC G protein subunit 9.02. The sequences can be used in the treatment of
CC cancers, coughs, cardiac asthma, diarrhoea, constipation, colic, psychic
CC disease and morphine analgesic acute poisoning. The present sequence is
CC a probe used to isolate the coding sequence of the invention
XX
SQ Sequence 41 BP; 7 A; 9 C; 16 G; 9 T; 0 U; 0 Other;

Query Match          3.6%; Score 35.2; DB 1; Length 41;
Best Local Similarity 92.5%; Pred. No. 3.5e+02;
Matches 37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 369 TCCACCTGCTCAGCTCCCAAGTCTGGATTACAGGC 408
DB 41 TCCACCTGCTCAGCTCCCAAGTCTGGATTACAGGC 2

RESULT 192
ABQ77547
ID ABQ77547 standard; DNA; 41 BP.
XX
AC ABQ77547;
XX
DT 01-OCT-2002 (first entry)
XX
DE Human red blood cell cytoplasmic protein 15.29 probe, SEQ ID:8.
XX
KM Human; red blood cell cytoplasmic protein 15.29; erythrocyte;
KM recombinant production; gene therapy; cerebral anoxia;
KM respiratory adynamia; arrhythmia; intestinal palsy; anaemia; haemostatic;
KM cardiant; probe; ss.
XX
XX Homo sapiens.
OS
XX CN139497-A.
PN
XX 13-MAR-2002.
PD
XX 23-AUG-2000; 2000CN-00119732.
PF
XX 23-AUG-2000; 2000CN-00119732.
PR
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
PA
XX Mao Y, Xie Y;
PI
XX WPI; 2002-472206/51.
DR
XX New polypeptide-human red blood cell cytoplasmic protein 15.29 for
PT treating anaerobic cerebral disease, respiratory adynamia, arrhythmia,
PT intestinal palsy, and anemia.
XX
PS Example 6; Page 19 (Disclosure); 32pp; Chinese.
```

```
CC The invention relates to human red blood cell cytoplasmic protein 15.29
CC (AAM49384) and nucleic acids encoding it (ABQ77542). The protein has a
CC molecular weight of 15 kD. The invention also relates to a method for the
CC recombinant production of the protein, an antagonist of the protein, and
CC the use of the protein, gene and antagonist in therapeutic applications
CC Red blood cell cytoplasmic protein 15.29 can be used in the treatment of
CC a variety of diseases such as cerebral anoxia, respiratory adynamia,
CC arrhythmia, intestinal palsy and anaemia. The present sequence represents
CC a human red blood cell cytoplasmic protein 15.29 probe used in an
CC exemplification of the invention
XX
SQ Sequence 41 BP; 8 A; 9 C; 11 G; 13 T; 0 U; 0 Other;

Query Match          3.6%; Score 35.2; DB 1; Length 41;
Best Local Similarity 92.5%; Pred. No. 3.5e+02;
Matches 37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1092 GGGGTTCCACCAATTTTGTCAAGCTGCTCAAACTCCTG 1131
DB 2 GAGGTTTACCATATGTGTGTCAGCTGGTCTCAACTGCTG 41

RESULT 193
ABV77328
ID ABV77328 standard; DNA; 41 BP.
XX
AC ABV77328;
XX
DT 07-FEB-2003 (first entry)
XX
DE Human protein 10.01 related probe 1.
XX
KM Human; 10.01; aminolase active site; arrhythmia; diabetes; probe; ss.
XX
XX Homo sapiens.
OS
XX CN1342770-A.
PN
XX 03-APR-2002.
PD
XX 12-SEP-2000; 2000CN-00125186.
PF
XX 12-SEP-2000; 2000CN-00125186.
PR
XX 12-SEP-2000; 2000CN-00125186.
XX
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
PI
XX Mao Y, Xie Y;
XX
XX WPI; 2002-529811/57.
DR
XX New human protein 10.01 containing Phe-His aminolase active site and
XX encoding polynucleotide, useful for treating arrhythmia and diabetes.
XX
XX Example 7; Page 21 (disclosure); 33pp; Chinese.
XX
XX The invention relates to a human protein designated 10.01, containing the
XX Phe-His aminolase active site. Also disclosed are the encoding
XX polynucleotide, and a method for preparing the polypeptide by DNA
XX recombination. The application of the polypeptide is in treating
XX arrhythmia and diabetes. Also disclosed are the antagonist against this
XX polypeptide and its therapeutic action, and the application of the
XX CC polynucleotide. The current sequence represents a human protein 10.01
XX related probe sequence
XX
SQ Sequence 41 BP; 6 A; 16 C; 9 G; 10 T; 0 U; 0 Other;

Query Match          3.6%; Score 35.2; DB 1; Length 41;
Best Local Similarity 92.5%; Pred. No. 3.5e+02;
Matches 37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 655 TGCAGTGGCCGCAATCTTGCTCACTGCAACTCTGCTCC 694
DB 1 TGCAGTGGCCGCAATCTTGCTCACTGCAACTCTGCTCC 40
```





CC dysfunction, psychic disease, endocrinopathy, growth development  
 CC disturbance disease and tumours. The present sequence represents a probe  
 CC for (I), which is used in an example from the present invention  
 XX

SO Sequence 41 BP; 5 A; 10 C; 14 G; 12 T; 0 U; 0 Other;

Query Match 3.5%; Score 34.6; DB 1; Length 41;  
 Best Local Similarity 90.2%; Pred. No. 3.7e+02;  
 Matches 37; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 187 TGGAGTTCTCCATGTGCTGAGCTGCTCGAAGTCCCG 227  
 DB 1 TGGGGTTCCACCATGTGGGAGCTGCTCGAAGTCCCG 41

## RESULT 197

AB083634 standard; DNA; 41 BP.

AB083634;

26-JAN-2003 (first entry)

Human mPer3-10.01 probe 2 SEQ ID NO:9.

XX Human mPer3-10.01; vegetative nervous dysfunction; psychic disease;  
 XX endocrinopathy; growth development disturbance disease; tumour; probe;  
 KW ss.

OS Homo sapiens.

XX CN1345805-A.

XX 24-APR-2002.

XX 26-SEP-2000; 2000CN-00125425.

XX 26-SEP-2000; 2000CN-00125425.

PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.

XX Mao Y, Xie Y;

XX WPI; 2002-539321/58.

PT Novel polypeptide-human mPer 3-10.01 and polynucleotide for encoding the  
 PT polypeptide.

PS Example 6; Page 20 (Disclosure); 33pp; Chinese.

CC The present invention describes human mPer3-10.01 (I). Also described is  
 CC a method for producing (I) using DNA recombination technology. (I) can be  
 CC used in the treatment of several diseases, such as vegetative nervous  
 CC dysfunction, psychic disease, endocrinopathy, growth development  
 CC disturbance disease and tumours. The present sequence represents a probe  
 CC for (I), which is used in an example from the present invention  
 XX

SO Sequence 41 BP; 5 A; 10 C; 14 G; 12 T; 0 U; 0 Other;

Query Match 3.5%; Score 34.6; DB 1; Length 41;  
 Best Local Similarity 90.2%; Pred. No. 3.7e+02;  
 Matches 37; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 187 TGGAGTTCTCCATGTGCTGAGCTGCTCGAAGTCCCG 227  
 DB 1 TGGGGTTCCACCATGTGGGAGCTGCTCGAAGTCCCG 41

## RESULT 198

ABL52955/C

XX ID ABL52955 standard; DNA; 41 BP.  
 XX AC ABL52955;

XX 24-MAY-2002 (first entry)  
 DT Serine proteinase 10 probe #1.  
 DE

XX Serine proteinase 10; enzyme; cancer; HIV infection; anti-HIV;  
 KW cytosolic; probe; ss.

OS Unidentified.

XX CN1325996-A.

XX 12-DEC-2001.

XX 31-MAY-2000; 2000CN-00116278.

XX 31-MAY-2000; 2000CN-00116278.

PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.

XX Mao Y, Xie Y;

XX WPI; 2002-196715/26.

PT Polypeptide-serine proteinase 10 and polynucleotide encoding it.

PS Example 6; Page 19 (Disclosure); 32pp; Chinese.

CC The present invention relates to serine proteinase 10 (AAM48453). Serine  
 CC proteinase 10 and its coding sequence can be used for treating diseases  
 CC such as cancer and HIV infection. The present sequence is a probe, which  
 CC was used in an example from the invention  
 XX

SO Sequence 41 BP; 9 A; 14 C; 13 G; 5 T; 0 U; 0 Other;

Query Match 3.5%; Score 34.6; DB 1; Length 41;  
 Best Local Similarity 90.2%; Pred. No. 3.7e+02;  
 Matches 37; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 637 CTGTACCCAGAGCTGAGTGCAGTGGCGCATCTTGCTCA 677  
 DB 41 CTGTGCCCGAGCTGAGTGCAGTGGCGCATCTTGCTCA 1

## RESULT 199

AB249715 standard; DNA; 41 BP.

AC AB249715;

DT 26-JUN-2003 (first entry)

XX Human sulphotransferase TPST2 gene polymorphic site, #6497.

XX Human; drug metabolising enzyme; gene; drug metabolism; chromosome 22;  
 KW polymorphic site; drug evaluation; drug screening; genotyping;  
 KW genetic profiling; therapeutic customisation; adverse reaction;  
 KW clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.

OS Homo sapiens.

Key Location/Qualifiers  
 FT variation replace(21,A)  
 FT /\*tag= a  
 FT /standard\_name= "Single nucleotide polymorphism (SNP)"

XX WO200252044-A2.

XX 04-JUL-2002.

XX 27-DEC-2001; 2001WO-JP011592.

XX 27-DEC-2000; 2000JP-00399443.

PR 02-MAY-2001; 2001JP-00135256.  
PR 27-AUG-2001; 2001JP-00256862.  
XX  
XX  
PA (RIKE ) RIKEN KK.  
XX  
XX  
PI Nakamura Y, Sekine A, Iida A, Saito S;  
XX  
XX  
DR WPI; 2002-583571/62.  
XX  
XX  
PT Identifying individuals having a polymorphism, useful for determining the  
PT effectiveness or side effect of a drug or treatment protocol, comprises  
PT detecting at least one polymorphism in the drug metabolizing enzyme  
PT nucleic acid.

Claim 23; Page 196; 2785pp; English.

Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes encoding enzymes associated with drug metabolism. The invention relates to methods and compositions for identifying individuals who have at least one polymorphism in such drug metabolising enzyme-encoding genes. The polymorphisms may be identified in a nucleic acid sample using probes or primers specific for a sequence selected from ABZ43217-ABZ50887 using a variety of detection assays, including hybridisation assays, nucleic acid arrays and PCR-based methods. The invention also encompasses methods of evaluating and screening drugs using genetic polymorphism data. Genetic polymorphism data, particularly that relating to single nucleotide polymorphisms (SNPs), may be used in studying the relationship between DNA sequence variations and human diseases, conditions, and responses to drugs. SNPs are also useful as polymorphism markers for discovering genes that cause or exacerbate certain diseases. SNPs are particularly useful in the above respects as they are stable in populations, occur frequently, and have lower mutation rates than other genome variations such as repeating sequences. The detection and analysis of polymorphisms in genes encoding drug metabolising enzymes allows the customisation of drug therapies based upon the genetic profile of individual patients. This would not only take the guesswork out of selecting the drug with the greatest therapeutic effect for a particular patient, but would also reduce the likelihood of adverse reactions, thereby increasing safety. Methods of the invention are also useful in the drug discovery and approval processes. For example, individuals could be selected for clinical trials only if their genetic profiles indicate that they are capable of responding to a particular drug or drug class, and previously failed drug candidates could be revived if they were matched with more appropriate patient populations. The methods, data and compositions of the invention may therefore lead to an increase in the range of possible drug targets and decreases in the number of adverse drug reactions, failed drug trials, the time taken for a drug to be approved, the length of time patients are on medication and the number of different medications a patient needs to take before finding an effective therapy

Sequence 41 BP; 6 A; 17 C; 9 G; 9 T; 0 U; 0 Other;

Query Match	3.5%	Score 34.6	DB 1	Length 41
Best Local Similarity	90.2%	Pred. No. 3.7e+02		
Matches	37	Mismatches	4	Indels 0
				Gaps 0

```

QY      969 CTGGCTCACTGCAACCTTGCCCTCCCCGGGTCAAGCGATT 1003
          |||||
Db      1   CTGGCTCACTGCAACCTCCGCCTCCCGGGTTCAGCAGTT 41

```

RESULT 200	
AB243958	
ID	AB243958 standard; DNA; 41 BP.
XX	
AC	AB243958;
XX	
DT	26-JUN-2003 (first entry)
XX	
DE	Human glutathione-S-transferase MGST2 gene polymorphic site, #742.
XX	
XX	Human; drug metabolising enzyme; gene; drug metabolism; chromosome 4
KW	polymorphic site; drug evaluation; drug screening; genotyping;

KW	Genetic profiling, therapeutic customisation; adverse reaction;
XX	clinical trial; drug approval; single nucleotide polymorphism; SNP; ds
OS	Homo sapiens.

Key	Location/Qualifiers
FT	replace (21,A)
FT	/tag a
FT	/standard name="Single nucleotide polymorphism (SNP)"

PN W0200252044-A2.

PD 04-JUL-2002

PF 27-DEC-2001; 2001WO-JF011592.

PR 27-DEC-2000; 2000JP-00399443.  
 PR 03-MAY-2001; 2001JP-00135256

PR 27-AUG-2001; 2001JP-00256862.

PA (RIKE ) RIKEN KK.

(RIKE ) RIKEN KK

PI Nakamura Y, Sekine A, Iida A, Saito S;

DR WPI; 2002-583571/62.

PT identifying individuals having a polymorphism, useful for determining the  
 PT effectiveness or side effect of a drug or treatment protocol, comprises  
 PT detecting at least one polymorphism in the drug metabolizing enzyme  
 PT nucleic acid.

PS Claim 23; Page 76; 2785pp; English

Sequence ABZ43217-ABZ50887 represent polymorphic sites within genes encoding enzymes associated with drug metabolism. The invention relates to methods and compositions for identifying individuals who have at least one polymorphism in such drug metabolising enzyme-encoding genes. The polymorphisms may be identified in a nucleic acid sample using probes or primers specific for a sequence selected from ABZ43217-ABZ50887 using a variety of detection assays, including hybridisation assays, nucleic acid arrays and PCR-based methods. The invention also encompasses methods of evaluating and screening drugs using genetic polymorphism data. Genetic polymorphism data, particularly that relating to single nucleotide polymorphisms (SNPs), may be used in studying the relationship between DNA sequence variations and human diseases, conditions, and responses to drugs. SNPs are also useful as polymorphism markers for discovering genes that cause or exacerbate certain diseases. SNPs are particularly useful in the above respects as they are stable in populations, occur frequently, and have lower mutation rates than other genome variations such as repeating sequences. The detection and analysis of polymorphisms in genes encoding drug metabolising enzymes allows the customisation of drug therapies based upon the genetic profile of individual patients. This would not only take the guesswork out of selecting the drug with the greatest therapeutic effect for a particular patient, but would also reduce the likelihood of adverse reactions, thereby increasing safety. Methods of the invention are also useful in the drug discovery and approval processes. For example, individuals could be selected for clinical trials only if their genetic profiles indicate that they are capable of responding to a particular drug or drug class, and previously failed drug candidates could be revived if they were matched with more appropriate patient populations. The methods, data and compositions of the invention may therefore lead to an increase in the range of possible drug targets and decreases in the number of adverse drug reactions, failed drug trials, the time taken for a drug to be approved, the length of time patients are on medication and the number of different medications a patient needs to take before finding an effective therapy

Sequence 41 BP; 6 A; 15 C; 10 G; 10 T; 0 U; 0 Other;

Query Match	3.5%;	Score 34.6;	DB 1;	Length 41;
Best Local Similarity	90.2%;	Pred. No. 3.7e+02;		
Matches 37;	Conservative	4;	Indels	0;
			Gaps	0

[illegible]

CC	approval processes. For example, individuals could be selected for
CC	clinical trials only if their genetic profiles indicate that they are
CC	capable of responding to a particular drug or drug class, and previously
CC	failed drug candidates could be revived if they were matched with more
CC	appropriate patient populations. The methods, data and compositions of
CC	the invention may therefore lead to an increase in the range of
CC	possible drug targets and decreases in the number of adverse drug
CC	reactions, failed drug trials, the time taken for a drug to be approved,
CC	the length of time patients are on medication and the number of different
CC	medications a patient needs to take before finding an effective therapy
XX	
SQ	Sequence 41 BP; 6 A; 15 C; 10 G; 10 T; 0 U; 0 Other;
Query Match	3.5%; Score 34.6; DB 1; Length 41;
Best Local Similarity	90.2%; Pred. No. 3.7e+02;
Matches 37; Conservative	0; Mismatches 4; Indels 0; Gaps 0;
Gy	831 CCTGTGATCTGCAGCGTGGGCGCTCCCAGAAGTGCTGGGAT 871 
Dd	1 CCTGCTATTGTCACCTCGGCGCTCCCAAGTGCTGGGAT 41 
RESULT 202	
ABZ49230	
ID	ABZ49230 standard; DNA; 41 BP.
XX	
AC	ABZ49230;
XX	
DT	26-JUN-2003 (first entry)
XX	
DE	Human aldehyde dehydrogenase ALDH6A1 gene polymorphic site, #6013.
XX	
KM	Human; drug metabolising enzyme; gene; drug metabolism; polymorphic site;
KW	drug evaluation; drug screening; genotyping; genetic profiling;
KX	therapeutic customisation; adverse reaction; clinical trial;
XX	drug approval; single nucleotide polymorphism; SNP; de.
OS	Homo sapiens.
XX	
PH	Key Location/Qualifiers
FT	Variation replace(21..A)
FT	/tag= g
FT	/standard_name= "Single nucleotide polymorphism (SNP)"
PN	WO200252044-A2.
PD	04-JUL-2002.
XX	
Pf	27-DEC-2001; 2001WO-JP011592.
XX	
PR	27-DEC-2000; 2000JP--00399443.
PR	02-MAY-2001; 2001JP--00135256.
PR	27-AUG-2001; 2001JP--00256862.
XX	
PA	(RIKE ) RIKEN KK.
PI	Nakamura Y, Sekine A, Iida A, Saito S;
XX	
DR	WPI, 2002-583571/62.
XX	
PT	Identifying individuals having a polymorphism, useful for determining the
PT	effectiveness or side effect of a drug or treatment protocol, comprises
PT	detecting at least one polymorphism in the drug metabolizing enzyme
XX	nucleic acid.
PS	Claim 23; Page 184; 2785pp; English.
XX	
CC	Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes
CC	encoding enzymes associated with drug metabolism. The invention relates
CC	to methods and compositions for identifying individuals who have at least
CC	one polymorphism in such drug metabolising enzyme-encoding genes. The
CC	polymorphisms may be identified in a nucleic acid sample using probes or
CC	primers specific for a sequence selected from ABZ43217-ABZ50887 using a

CC variety of detection assays, including hybridisation assays, nucleic acid  
CC arrays and PCR-based methods. The invention also encompasses methods of  
CC evaluating and screening drugs using genetic polymorphism data. Genetic  
CC polymorphism data, particularly that relating to single nucleotide  
CC polymorphisms (SNPs), may be used in studying the relationship between  
CC DNA sequence variations and human diseases, conditions, and responses to  
CC drugs. SNPs are also useful as polymorphism markers for discovering genes  
CC that cause or exacerbate certain diseases. SNPs are particularly useful  
CC in the above respects as they are stable in populations, occur  
CC frequently, and have lower mutation rates than other genome variations  
CC such as repeating sequences. The detection and analysis of polymorphisms  
CC in genes encoding drug metabolising enzymes allows the customisation of  
CC drug therapies based upon the genetic profile of individual patients.  
CC This would not only take the guesswork out of selecting the drug with the  
CC greatest therapeutic effect for a particular patient, but would also  
CC reduce the likelihood of adverse reactions, thereby increasing safety.  
CC Methods of the invention are also useful in the drug discovery and  
CC approval processes. For example, individuals could be selected for  
CC clinical trials only if their genetic profiles indicate that they are  
CC capable of responding to a particular drug or drug class, and previously  
CC failed drug candidates could be revived if they were matched with more  
CC appropriate patient populations. The methods, data and compositions of  
CC the invention may therefore lead to an increase in the range of  
CC possible drug targets and decreases in the number of adverse drug  
CC reactions, failed drug trials, the time taken for a drug to be approved,  
CC the length of time patients are on medication and the number of different  
CC medications a patient needs to take before finding an effective therapy

Sequence 41 BP; 6 A; 16 C; 9 G; 10 T; 0 U; 0 Other;

Query Match 3.5%; Score 34.6; DB 1; Length 41;  
Best Local Similarity 90.2%; Pred. No. 3.7e+02;  
Matches 37; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 992 TCCCGGGCTCAGCGATTCTCTGTCTCAGCTCCCAAGCA 1032  
DB 1 TCCCGGGCTCAGCGATTCTCTCTCGCTCAGCTCCCAAGCA 41

RESULT 203

ABZ49236

XX ABZ49236 standard; DNA; 41 BP.

XX AC ABZ49236;

XX 26-JUN-2003 (first entry)

XX Human aldehyde dehydrogenase ALDH6A1 gene polymorphic site, #6019.

XX Human; drug metabolising enzyme; gene; drug metabolism; polymorphic site;  
XX drug evaluation; drug screening; genotyping; genetic profiling;  
XX therapeutic customisation; adverse reaction; clinical trial;  
XX drug approval; single nucleotide polymorphism; SNP; ds.

XX Homo sapiens.

XX Key Location/Qualifiers  
XX replace(21,C)  
XX /tag= a  
XX /standard\_name= "Single nucleotide polymorphism (SNP) "

XX WO200252044-A2.

XX 04-JUL-2002.

XX 27-DEC-2001; 2001WO-JP011592.

XX 27-DEC-2000; 2000JP-00399443.

XX 02-MAY-2001; 2001JP-00135256.

XX 27-AUG-2001; 2001JP-00256862.

XX (RIKE ) RIKEN KK.

PI Nakamura Y, Sekine A, Iida A, Saito S;  
XX WPI; 2002-583571/62.  
XX  
XX Identifying individuals having a polymorphism, useful for determining the  
XX effectiveness or side effect of a drug or treatment protocol, comprises  
XX detecting at least one polymorphism in the drug metabolizing enzyme  
XX nucleic acid.

PS Claim 23; Page 184; 27855P; English.

XX Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes  
XX encoding enzymes associated with drug metabolism. The invention relates  
XX to methods and compositions for identifying individuals who have at least  
XX one polymorphism in such drug metabolising enzyme-encoding genes. The  
XX polymorphisms may be identified in a nucleic acid sample using probes or  
XX primers specific for a sequence selected from ABZ43217-ABZ50887 using a  
XX variety of detection assays, including hybridisation assays, nucleic acid  
XX arrays and PCR-based methods. The invention also encompasses methods of  
XX evaluating and screening drugs using genetic polymorphism data. Genetic  
XX polymorphism data, particularly that relating to single nucleotide  
XX polymorphisms (SNPs), may be used in studying the relationship between  
XX DNA sequence variations and human diseases, conditions, and responses to  
XX drugs. SNPs are also useful as polymorphism markers for discovering genes  
XX that cause or exacerbate certain diseases. SNPs are particularly useful  
XX in the above respects as they are stable in populations, occur  
XX frequently, and have lower mutation rates than other genome variations  
XX such as repeating sequences. The detection and analysis of polymorphisms  
XX in genes encoding drug metabolising enzymes allows the customisation of  
XX drug therapies based upon the genetic profile of individual patients.  
XX This would not only take the guesswork out of selecting the drug with the  
XX greatest therapeutic effect for a particular patient, but would also  
XX reduce the likelihood of adverse reactions, thereby increasing safety.  
XX Methods of the invention are also useful in the drug discovery and  
XX approval processes. For example, individuals could be selected for  
XX clinical trials only if their genetic profiles indicate that they are  
XX capable of responding to a particular drug or drug class, and previously  
XX failed drug candidates could be revived if they were matched with more  
XX appropriate patient populations. The methods, data and compositions of  
XX the invention may therefore lead to an increase in the range of  
XX possible drug targets and decreases in the number of adverse drug  
XX reactions, failed drug trials, the time taken for a drug to be approved,  
XX the length of time patients are on medication and the number of different  
XX medications a patient needs to take before finding an effective therapy

Sequence 41 BP; 6 A; 10 C; 13 G; 12 T; 0 U; 0 Other;

Query Match 3.5%; Score 34.6; DB 1; Length 41;  
Best Local Similarity 90.2%; Pred. No. 3.7e+02;  
Matches 37; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 198 CATGTTGTCAGGCTGCTCGAAGTCCGACCTCAGATGA 238  
DB 1 CGTTGTCAGGCTGCTCTTGAACCTCGACCTCAGATGA 41

RESULT 204

ABZ43562

XX ABZ43562 standard; DNA; 41 BP.

XX AC ABZ43562;

XX 26-JUN-2003 (first entry)

XX Human sulphotransferase TPST2 gene polymorphic site, #346.

XX Human; drug metabolising enzyme; gene; drug metabolism; chromosome 22;  
XX polymorphic site; drug evaluation; drug screening; genotyping;  
XX genetic profiling; therapeutic customisation; adverse reaction;  
XX clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.

XX Homo sapiens.

```

FH Key Location/Qualifiers
FT variation replace(21,A)
FT /*tag= a
FT /standard_name= "Single nucleotide polymorphism (SNP)"
XX
XX WO200252044-A2.
XX
XX 04-JUL-2002.
XX
XX 27-DEC-2001; 2001WO-0P011592.
XX
XX 27-DEC-2000; 2000JP-00399443.
XX
XX 02-MAY-2001; 2001JP-00135256.
XX
XX 27-AUG-2001; 2001JP-00256862.
XX
XX (RIKEN ) RIKEN KK.
XX
XX Nakamura Y, Sekine A, Iida A, Satto S;
XX
XX WPI, 2002-583571/62.
XX
XX Identifying individuals having a polymorphism, useful for determining the
XX effectiveness or side effect of a drug or treatment protocol, comprises
XX detecting at least one polymorphism in the drug metabolizing enzyme
XX nucleic acid.
XX
XX Claim 23; Page 69; 2785pp; English.
XX
XX Sequences AB243217-AB250887 represent polymorphic sites within genes
XX encoding enzymes associated with drug metabolism. The invention relates
XX to methods and compositions for identifying individuals who have at least
XX one polymorphism in such drug metabolizing enzyme-encoding genes. The
XX polymorphisms may be identified in a nucleic acid sample using probes or
XX primers specific for a sequence selected from AB243217-AB250887 using a
XX variety of detection assays, including hybridisation assays, nucleic acid
XX arrays and PCR-based methods. The invention also encompasses methods of
XX evaluating and screening drugs using genetic polymorphism data. Genetic
XX polymorphisms (SNPs), may be used in studying the relationship between
XX DNA sequence variations and human diseases, conditions, and responses to
XX drugs. SNPs are also useful as polymorphism markers for discovering genes
XX that cause or exacerbate certain diseases. SNPs are particularly useful
XX in the above respects as they are stable in populations, occur
XX frequently, and have lower mutation rates than other genome variations
XX such as repeating sequences. The detection and analysis of polymorphisms
XX in genes encoding drug metabolising enzymes allows the customisation of
XX drug therapies based upon the genetic profile of individual patients.
XX This would not only take the guesswork out of selecting the drug with the
XX greatest therapeutic effect for a particular patient, but would also
XX reduce the likelihood of adverse reactions, thereby increasing safety.
XX Methods of the invention are also useful in the drug discovery and
XX approval processes. For example, individuals could be selected for
XX clinical trials only if their genetic profiles indicate that they are
XX capable of responding to a particular drug or drug class, and previously
XX failed drug candidates could be revived if they were matched with more
XX appropriate patient populations. The methods, data and compositions of
XX the invention may therefore lead to an increase in the range of
XX possible drug targets and decreases in the number of adverse drug
XX reactions, failed drug trials, the time taken for a drug to be approved,
XX the length of time patients are on medication and the number of different
XX medications a patient needs to take before finding an effective therapy
XX
XX Sequence 41 BP; 6 A; 17 C; 9 G; 9 T; 0 U; 0 Other:
XX
XX Query Match 3.5%; Score 34.6; DB 1; Length 41;
XX Best Local Similarity 90.2%; Pred. No. 3.7e+02;
XX Matches 37; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 969 CTCGGCTCAGTCAACCTCTGCTCCCGGGCTCAGGCATT 1009
XX 1 CTCGGCTCAGTCAACCTCTGCTCCCGGGCTCAGGCATT 41

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```

RESULT 205
ADP75520/C
ID ADP75520 standard; DNA; 41 BP.
XX
XX ADP75520;
XX
XX 12-AUG-2004 (first entry)
XX
XX Human ADAM19 gene, sequence surrounding SNP 16.
XX
XX DE
XX
XX Human; de; ADAM19; Endophilin 1; Endophilin 2; NRG2; ADAMTS2;
XX a disintegrin and metalloprotease; neuroregulin 2; SNP;
XX single nucleotide polymorphism;
XX a disintegrin and metalloprotease with thrombospondin type1 motif 2;
XX asthma; atopy; obesity; inflammatory bowel disease; respiratory disorder.
XX
XX OS
XX Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT variation replace(21,G)
XX FT /*tag= a
XX FT /standard_name= "Single nucleotide polymorphism"
XX
XX WO2003031594-A2.
XX
XX 17-APR-2003.
XX
XX 11-OCT-2002; 2002WO-US032700.
XX
XX 11-OCT-2001; 2001US-0328424P.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
XX
XX Keith T, Little RD, Van Berdewegh P, Dupuis J, Del Mastro RG;
XX Allen K;
XX WPI, 2003-381712/36.
XX
XX New isolated nucleic acid or alternate splice variant, useful for
XX diagnosing and treating a disintegrin and metalloprotease (ADAM) or
XX interactor gene-associated disorder, e.g. asthma, atopy, obesity or
XX inflammatory bowel disease.
XX
XX Claim 2; Page 135; 338pp; English.
XX
XX The invention relates to an isolated nucleic acid or alternate splice
XX variant comprising a nucleotide sequence containing at least one of the
XX single nucleotide polymorphisms given in the specification, a nucleotide
XX sequence having at least 15 contiguous nucleotides of them, or
XX complements of them. The genes are ADAM19 (a disintegrin and
XX metalloprotease 19, also known as gene 845), NRG2 (neuroregulin 2, also
XX known as gene 847), endophilin 1 (also known as gene 874), endophilin 2
XX (also known as gene 803) and ADAMTS2 (a disintegrin and metalloprotease
XX with thrombospondin type1 motif 2, also known as gene 962). Also included
XX are a vector comprising the isolated nucleic acid (or alternate splice
XX variant), a host cell containing the vector, an isolated polypeptide
XX encoded by the novel nucleic acid (or alternate splice variant), an
XX antibody or antibody fragment that binds to the polypeptide,
XX pharmaceutical compositions (comprising the nucleic acid or alternate
XX splice variant, vector, polypeptide or antibody, and a carrier,
XX excipient or diluent), a kit for detecting a disintegrin and
XX metalloprotease (ADAM) gene nucleotide sequence (comprising the isolated
XX nucleic acid or alternate splice variant, antibody or antibody fragment,
XX and at least one component to detect the hybridisation of the variant or
XX the binding of the antibody to an ADAM gene amino acid sequence), a kit
XX for detecting an interactor gene amino acid sequence (comprising the
XX antibody or antibody fragment, and at least one component to detect the
XX binding of the antibody to the interactor gene amino acid sequence),
XX diagnosing an ADAM or interactor gene-associated disorder or a
XX respiratory disorder in a human subject, determining an ADAM or
XX interactor gene pharmacogenetic profile in a human subject, identifying
XX an orthologue of a human ADAM or interactor gene, treating an ADAM or
XX interactor gene-associated disorder (or a respiratory disorder) by

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CC administering the pharmaceutical composition, a transgenic mouse (whose  
CC genome comprises an introduced null mutation in an endogenous gene that  
CC is orthologous to a human ADAM gene), making a homozygous transgenic  
CC knockout mouse, forming a crystal of the isolated polypeptide, a cell  
CC line comprising the isolated nucleic acid or alternate splice variant, a  
CC biochip comprising the isolated nucleic acid or alternate splice variant,  
CC an isolated nucleic acid probe or primer comprising at least 8 contiguous  
CC nucleotides of the nucleic acid, an isolated antisense nucleic acid,  
CC identifying an ADAM or interactor gene ligand and an isolated nucleic  
CC acid variant of Gene 803, 845, 847, 874 or 962. The nucleic acid or  
CC alternate splice variants, methods, kits and antibody/antibody fragment  
CC are useful for diagnosing and treating an ADAM or interactor gene-  
CC associated disorder, e.g. asthma, atopy, obesity or inflammatory bowel  
CC disease. The present sequence is a SNP (single nucleotide polymorphism)  
CC containing region from one of the above mentioned genes.

SQ Sequence 41 BP; 7 A; 12 C; 14 G; 8 T; 0 U; 0 Other;

Query Match 3.5%; Score 34.6; DB 1; Length 41;

Best Local Similarity 90.2%; Pred. No. 3.7e+02; Mismatches 4; Indels 0; Gaps 0;

Matches 37; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

844 CTGCTCGGCTCCCAAGTCTGGATTACAGGCGCTGAGC 884

41 CCGCTTGGCCACCCAAAGTCTGGATTACAGGCGCTGAGC 1

RESULT 206 ADL64137/C

ID ADL64137 standard; DNA; 41 BP.

AC ADL64137;

DT 20-MAY-2004 (first entry)

DE Human single nucleotide polymorphism (SNP) #60.

XX ss; human; single nucleotide polymorphism; SNP;  
XX C1 S subcomponent protein; C1S; alanyl aminopeptidase protein; ANPEP;  
XX meprin A beta protein; aminopeptidase P-like protein; XPN-PEP1;  
XX tissue kallikrein protein; KLK1; aminopeptidase P protein; MEPRB;  
XX soluble guanylate cyclase 1 alpha-2 subunit protein; GUCY1A2; haplotype;  
XX angioedema; angioedema-like disorder; paternity testing;  
XX cardiovascular diseases; angina pectoris; hypertension; heart failure;  
XX myocardial infarction; aneurysm; stroke; embolism; thrombosis;  
XX coronary artery disease; arteriosclerosis; hypersensitivity;  
XX haemodialysis; sepsis; inflammatory disease; inflammatory arthritis;  
XX asthma; chronic obstructive pulmonary disease; cough reflex; allergy;  
XX cancer; ANPEP.

OS Homo sapiens.

PN US2004033582-A1.

PD 19-FEB-2004.

PF 03-JUN-2003; 2003US-00453827.

PR 03-JUN-2002; 2002US-0384980P.

XX (EDMO/) EDMONDS M.

XX (HUI/) HUI L.

XX (PERR/) PERRONE M.

XX (POWE/) POWELL J R.

XX (RAMA/) RAMANATHAN C S.

XX (SWAN/) SWANSON B.

XX (TSUC/) TSUCHIHASHI Z.

XX (ZERB/) ZERBA K.

PI Edmonds M, Hui L, Perrone M, Powell JR, Ramanathan CS, Swanson B;  
PI Tsuchihashi Z, Zerba K;  
XX WPI; 2004-180052/17.

XX New nucleic acid comprising a single nucleotide polymorphism at a  
PT specific location, useful in paternity testing, genetic analysis or  
PT diagnosing, preventing or treating cardiovascular diseases e.g.  
PT angioedema or angina pectoris.

PS Claim 3; SEQ ID NO 60; 376pp; English.

XX The invention relates to an isolated nucleic acid (I) derived from a  
XX human gene encoding a protein, such as the C1 S subcomponent protein  
XX (C1S), the alanyl aminopeptidase protein (ANPEP), the meprin A, beta  
XX protein (MEPRB), the aminopeptidase P-like protein (XPN-PEP1), the tissue  
XX kallikrein protein (KLK1), the membrane bound aminopeptidase P protein  
XX (XPNPEP2), or the soluble guanylate cyclase 1, alpha-2 subunit protein  
XX (GUCY1A2). The nucleic acid comprises at least one polymorphic position,  
XX including the alleles, reference alleles and alternate alleles of the  
XX single nucleotide polymorphisms, listed in the specification. The  
XX polymorphic position resides in a (non) coding position within the genomic  
XX sequence of the gene. The polymorphic position residing in a coding  
XX position results in a missense or silent mutation of the translated  
XX product of the gene. The polymorphic position residing in a non-coding  
XX position resides within the untranslated region or an intronic region of  
XX the gene. Constructing haplotypes using the nucleic acids above further  
XX comprises using the haplotypes to identify an individual for the presence  
XX of a disease phenotype. The disease phenotype is angioedema or an  
XX phenotype with the haplotype. The disease phenotype is angioedema or an  
XX angioedema-like disorder. The nucleic acids, primers and probes are  
XX useful in phenotype correlations, paternity testing, medicine and genetic  
XX analysis. The nucleic acids and polypeptides can be used in diagnosing,  
XX preventing or treating cardiovascular diseases, e.g. angioedema, angina  
XX pectoris, hypertension, heart failure, myocardial infarction, aneurysm,  
XX stroke, embolism, thrombosis, coronary artery disease or  
XX arteriosclerosis, hypersensitivity reactions during haemodialysis,  
XX sepsis, inflammatory diseases, inflammatory arthritis, asthma, chronic  
XX obstructive pulmonary disease, cough reflex, allergies, or cancer. The  
XX present sequence represents a human single nucleotide polymorphism (SNP)  
XX of the invention.

SQ Sequence 41 BP; 8 A; 13 C; 12 G; 8 T; 0 U; 0 Other;

Query Match 3.5%; Score 34.6; DB 1; Length 41;

Best Local Similarity 90.2%; Pred. No. 3.7e+02; Mismatches 4; Indels 0; Gaps 0;

Matches 37; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

643 CCCAGGCTGAGTGCAGTGCAGTCTTGGCTCACTGCA 683

41 CCCAGGCTGAGTGCAGTGCAGTCTTGGCTCACTGCA 1

RESULT 207 ADL64139

ID ADL64139 standard; DNA; 41 BP.

AC ADL64139;

DT 20-MAY-2004 (first entry)

DE Human single nucleotide polymorphism (SNP) #62.

XX ss; human; single nucleotide polymorphism; SNP;  
XX C1 S subcomponent protein; C1S; alanyl aminopeptidase protein; ANPEP;  
XX meprin A beta protein; aminopeptidase P-like protein; XPN-PEP1;  
XX tissue kallikrein protein; KLK1; aminopeptidase P protein; MEPRB;  
XX soluble guanylate cyclase 1 alpha-2 subunit protein; GUCY1A2; haplotype;  
XX angioedema; angioedema-like disorder; paternity testing;  
XX cardiovascular diseases; angina pectoris; hypertension; heart failure;  
XX myocardial infarction; aneurysm; stroke; embolism; thrombosis;  
XX coronary artery disease; arteriosclerosis; hypersensitivity;  
XX haemodialysis; sepsis; inflammatory disease; inflammatory arthritis;  
XX asthma; chronic obstructive pulmonary disease; cough reflex; allergy;  
XX cancer; ANPEP.

OS Homo sapiens.







CC preventing or treating cardiovascular diseases, e.g. angioedema, angina  
 CC pectoris, hypertension, heart failure, myocardial infarction, aneurysm,  
 CC stroke, embolism, thrombosis, coronary artery disease or  
 CC arteriosclerosis, hypersensitivity reactions during haemodialysis,  
 CC sepsis, inflammatory diseases, inflammatory arthritis, asthma, chronic  
 CC obstructive pulmonary disease, cough reflex, allergies, or cancer. The  
 CC present sequence represents a human single nucleotide polymorphism (SNP)  
 CC of the invention.

XX Sequence 41 BP; 7 A; 14 C; 12 G; 8 T; 0 U; 0 Other;

XX Query Match 3.5%; Score 34.6; DB 1; Length 41;

XX Best Local Similarity 90.2%; Pred. No. 3.7e+02;

XX Matches 37; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 643 CCAGGCTGAGTGCAGTGGCGCATCTGGCTCACTGCA 683

DB 41 CCAGGCTGAGTGCAGTGGCGCATCTGGCTCACTGCA 1

RESULT 209

XX AAT97406/C

XX ID AAT97406 standard; DNA; 40 BP.

XX AAT97406;

XX 14-APR-1998 (first entry)

XX Synthetic oligomer D188 Allele A from WO9722719 Example 2.

XX Detection; target site; nucleic acid; fluorophore; labelled; fluorescent;

XX inherited disease; tissue typing; PCR; ss.

XX Synthetic.

XX WO9722719-A1.

XX 26-JUN-1997.

XX 17-DEC-1996; 96WO-US020379.

XX 18-DEC-1995; 95US-0008743P.

XX (UNIW) UNIV WASHINGTON.

XX Kwok P, Chen X;

XX WPI; 1997-341707/31.

XX Detecting target site in nucleic acid by forming a fluorophore-labelled  
 PT oligonucleotide at the site - and detecting fluorescent energy following  
 PT denaturation, used e.g. to detect inherited diseases, in tissue typing  
 PT etc.

XX Example 2; Page 27; 68pp; English.

XX A method has been developed for detecting the presence of a target site  
 CC (TS), of at least one nucleotide (nt) in a nucleic acid (NA). The method  
 CC comprises: (a) forming an oligonucleotide (ON), consisting of two  
 CC fluorophores (F1, F2) each covalently linked to separate nt, bound to TS;  
 CC and (b) detecting fluorescence energy transfer (FET) between F1 and F2  
 CC when ON is released from TS. The present sequence represents a synthetic  
 CC polynucleotide used in an example of the present invention. The method is  
 CC used to diagnose hereditary and other diseases; to determine infectious  
 CC agents; in tissue typing for histocompatibility; in forensic  
 CC identification and paternity testing, and in monitoring the genetic make  
 CC up of plants and animals. Specifically it is used to detect single nt  
 CC polymorphisms. The method provides inexpensive, simple, accurate and  
 CC automatable nucleic acid analyses

XX Sequence 40 BP; 12 A; 7 C; 14 G; 7 T; 0 U; 0 Other;

XX Query Match 3.4%; Score 33.6; DB 1; Length 40;

Best Local Similarity 90.0%; Pred. No. 4.1e+02;

XX Matches 36; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 675 TCACGCAACCTCTGCTCCCGGGTTCAAGTATCTCT 714

DB 40 TCACGCAACCTCTGCTCCCGGGTTCAAGCAATCTCT 1

RESULT 210

XX ADK41334/C

XX ID ADK41334 standard; DNA; 40 BP.

XX ADK41334;

XX 06-MAY-2004 (first entry)

XX Human chromosome 19 single nucleotide polymorphism detecting probe #22.

XX sequence polymorphism analysis; human; chromosome 19q; cancer; RAI; ss;

XX single nucleotide polymorphism; SNP; probe.

XX Homo sapiens.

XX Synthetic.

XX Key

XX variation

XX Location/Qualifiers

XX replace(20,G)

XX /\*tag= a

XX /standard\_name= "single nucleotide polymorphism"

XX MO2004003229-A2.

XX 08-JAN-2004.

XX 27-JUN-2003; 2003WO-DK000448.

XX 27-OCT-2002; 2002DK-00001005.

XX 25-FEB-2003; 2003DK-00001500.

XX 29-APR-2003; 2003DK-00000639.

XX (UYAA-) UNIV AARHUS.

XX (ARBE-) ARBEJDSMILJO INST NAT INST OCCUPA.

XX Nexo BA, Vogel U, Rockenbauer E, Bukowy ZK;

XX WPI; 2004-142878/14.

XX Estimating the disease risk or prognosis of an individual by sequence

XX polymorphism analysis.

XX Claim 18; SEQ ID NO 92; 145pp; English.

XX The invention relates to a novel method of estimating disease risk or  
 CC prognosis of an individual by sequence polymorphism analysis, especially  
 CC polymorphisms in the human chromosome 19q. The invention further relates  
 CC to: estimating a treatment response of an individual suffering from  
 CC cancer to a disease treatment; a primer or probe for use in the method of  
 CC estimating the disease risk or prognosis of an individual or for  
 CC estimating a treatment response of an individual suffering from cancer to  
 CC a disease treatment; an antibody directed to an epitope of a RAI gene  
 CC product; and a kit for use in the method of estimating the disease risk  
 CC or prognosis of an individual or for estimating a treatment response of  
 CC an individual suffering from cancer to a disease treatment, comprising at  
 CC least one primer or probe and optionally amplifying means for nucleic  
 CC acid amplification. The novel method is useful for estimating the disease  
 CC risk or prognosis of an individual or for estimating a treatment response  
 CC of an individual suffering from cancer to a disease treatment. This  
 CC polynucleotide sequence represents a probe used for detecting single  
 CC nucleotide polymorphisms in the DNA of human chromosome 19 of the  
 CC invention.

XX Sequence 40 BP; 8 A; 13 C; 12 G; 7 T; 0 U; 0 Other;



XX PS Example 6; Page 19 (Disclosure); 32pp; Chinese.  
 XX CC The present invention describes human tyrosinase 10.34 (I). The present  
 CC invention also described a method for preparing (I) using DNA  
 CC recombination techniques. (I) and the polynucleotide encoding it can be  
 CC used in the treatment of diseases such as cancer and human  
 CC immunodeficiency virus (HIV) infection. The present sequence represents a  
 CC probe for human tyrosinase 10.34, which is used in an example from the  
 CC present invention  
 XX CC  
 SQ Sequence 41 BP; 5 A; 12 C; 13 G; 11 T; 0 U; 0 Other;  
 Query Match 3.4%; Score 33.6; DB 1; Length 41;  
 Best Local Similarity 90.0%; Pred. No. 4.2e+02;  
 Matches 36; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 187 TGGAGTTTCCATGTTGTCAGGCTGGTCTCGAATCTCC 226  
 DB 1 TGGGGTTTCACCATGTTGGCGGCTGCTCTCGAATCTCC 40  
 RESULT 214  
 ABZ20667/c  
 ID ABZ20667 standard; DNA; 41 BP.  
 XX AC ABZ20667;  
 XX DT 03-MAR-2003 (first entry)  
 XX DE Human G protein subunit 9-02 coding sequence probe #2.  
 XX KW Human; G protein subunit 9.02; cancer; constipation; diarrhoea; cough;  
 KW cardiac asthma; colic; psychic disease; probe;  
 KW morphinic analgesic acute poisoning; ss.  
 XX OS Homo sapiens.  
 XX PS CN1345751-A.  
 XX PD 24-APR-2002.  
 XX PF 26-SEP-2000; 2000CN-00125456.  
 XX PR 26-SEP-2000; 2000CN-00125456.  
 XX PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.  
 XX PI Mao Y, Xie Y;  
 XX DR WPI; 2002-675773/73.  
 XX PS Novel polypeptide-human G protein subunit 9.01.  
 XX PS Example 6; Page 22(Disclosure); 34pp; Chinese.  
 CC The present invention provides the protein and coding sequences of human  
 CC G protein subunit 9.02. The sequences can be used in the treatment of  
 CC cancers, coughs, cardiac asthma, diarrhoea, constipation, colic, psychic  
 CC disease and morphinic analgesic acute poisoning. The present sequence is  
 CC a probe used to isolate the coding sequence of the invention  
 XX CC  
 SQ Sequence 41 BP; 7 A; 10 C; 16 G; 8 T; 0 U; 0 Other;  
 Query Match 3.4%; Score 33.6; DB 1; Length 41;  
 Best Local Similarity 90.0%; Pred. No. 4.2e+02;  
 Matches 36; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 369 TCCACGCTCCTCAGCTCCCAAGTGGCTGGATTACAGGC 408  
 DB 41 TCCACCCACCTCGGCTCCCAAGTGGCTGGATTACAGGC 2

RESULT 215  
 ABA94091/c  
 ID ABA94091 standard; DNA; 41 BP.  
 XX AC ABA94091;  
 XX DT 08-MAY-2002 (first entry)  
 XX DE Human tumour suppressor factor 11.77 probe 1 SEQ ID NO:8.  
 XX KW Human; tumour suppressor factor 11.77; cytostatic; haemostatic; virucide;  
 KW immunomodulatory; antiinflammatory; gene therapy; malignant tumour;  
 KW haemopathy; human immunodeficiency virus infection; HIV infection;  
 KW immunological disease; inflammation; probe; ss.  
 XX OS Homo sapiens.  
 XX PN MO200196526-A2.  
 XX PD 20-DEC-2001.  
 XX PF 04-JUN-2001; 2001WO-CN000906.  
 XX PR 07-JUN-2000; 2000CN-00116365.  
 XX PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.  
 XX PI Mao Y, Xie Y;  
 XX DR WPI; 2002-075588/10.  
 XX PS Human tumor suppressor factor 11.77 and encoding polynucleotide, used in  
 XX PT diagnosis and treatment of malignant tumors, hemopathy, human  
 XX PT immunodeficiency virus infection, immunological diseases and  
 XX PT inflammation.  
 XX OS Homo sapiens.  
 XX PS Example 6; Page 20; 33pp; Chinese.  
 CC The present invention describes human tumour suppressor factor 11.77 (I).  
 CC (I) has cytostatic, haemostatic, virucide, immunomodulatory and  
 CC antiinflammatory activities. The polynucleotide (II) encoding (I) can be  
 CC used in gene therapy. (I) and (II) can be used in the diagnosis and  
 CC treatment of malignant tumour, haemopathy, human immunodeficiency virus  
 CC (HIV) infection, immunological diseases and various inflammations. The  
 CC present sequence represents a probe for human tumour suppressor factor  
 CC 11.77, which is used in an example from the present invention  
 XX CC  
 SQ Sequence 41 BP; 9 A; 11 C; 14 G; 7 T; 0 U; 0 Other;  
 Query Match 3.4%; Score 33.6; DB 1; Length 41;  
 Best Local Similarity 90.0%; Pred. No. 4.2e+02;  
 Matches 36; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 839 TCTGCTGCTCGGCTCCCAAGTCTGGGATTACAGGC 878  
 DB 41 TCCGCCGCTCTGCTCCCAAGTCTGGGATTACAGGC 2  
 RESULT 216  
 AAL43826  
 ID AAL43826 standard; DNA; 41 BP.  
 XX AC AAL43826;  
 XX DT 19-SEP-2002 (first entry)  
 XX DE Human oncogene protein 11-66 nucleotide probe 1.  
 XX KW Human; ss; gene therapy; oncogene protein 11.66; malignant tumour;  
 KW haemopathy; development disturbance; HIV; immunological disease;  
 KW inflammation; probe.  
 XX OS Homo sapiens.

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XX CN1333235-A.
PN 30-JAN-2002.
XX 07-JUL-2000; 2000CN-00119427.
XX 07-JUL-2000; 2000CN-00119427.
XX 07-JUL-2000; 2000CN-00119427.
XX (SHAN-) SHANGHAI BIODOR GENE DEV CO LTD.
XX Mao Y, Xie Y;
XX WPI; 2002-305565/35.
XX Novel polypeptide-oncoprotein 11.66 and polynucleotide for encoding said
XX polypeptide.
PT Example 6; Page 21 (Disclosure); 33pp; Chinese.
PS
CC The invention comprises the amino acid and coding sequence of the human
CC oncoprotein 11.66. The oncoprotein 11.66 DNA and protein
CC sequences are useful for treating malignant tumour, haemopathy,
CC development disturbance, HIV infection, immunological disease and various
CC inflammations. The present DNA sequence represents a probe that is
CC specific for the gene sequence of the human oncoprotein 11.66
SQ Sequence 41 BP; 6 A; 13 C; 12 G; 10 T; 0 U; 0 Other;
Query Match 3.4%; Score 33.6; DB 1; Length 41;
Best Local Similarity 90.0%; Pred. No. 4.2e+02;
Matches 36; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 187 TGGAGTTTCATGTTGTCAGGCTGTCGTAACCTCCC 226
DB 1 TGGAGTTTCACCGTGTGGCCAGGCTGTCGTAACCTCCC 40
RESULT 217
AAL43827
ID AAL43827 standard; DNA; 41 BP.
XX
AC AAL43827;
XX
DT 19-SEP-2002 (first entry)
XX
DE Human oncogene protein 11-66 nucleotide probe 2.
XX
KW Human; ss; gene therapy; oncogene protein 11.66; malignant tumour;
KW haemopathy; development disturbance; HIV; immunological disease;
KW inflammation; probe.
XX
OS Homo sapiens.
XX
XX CN1333235-A.
XX
XX 30-JAN-2002.
XX
XX 07-JUL-2000; 2000CN-00119427.
XX
XX 07-JUL-2000; 2000CN-00119427.
XX
XX (SHAN-) SHANGHAI BIODOR GENE DEV CO LTD.
XX
XX Mao Y, Xie Y;
XX
XX WPI; 2002-305565/35.
XX
XX Novel polypeptide-oncoprotein 11.66 and polynucleotide for encoding said
XX polypeptide.
XX
XX Example 6; Page 21 (Disclosure); 33pp; Chinese.
XX
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CC The invention comprises the amino acid and coding sequence of the human
CC oncoprotein 11.66. The oncoprotein 11.66 DNA and protein
CC sequences are useful for treating malignant tumour, haemopathy,
CC development disturbance, HIV infection, immunological disease and various
CC inflammations. The present DNA sequence represents a probe that is
CC specific for the gene sequence of the human oncoprotein 11.66
SQ Sequence 41 BP; 6 A; 13 C; 12 G; 10 T; 0 U; 0 Other;
Query Match 3.4%; Score 33.6; DB 1; Length 41;
Best Local Similarity 90.0%; Pred. No. 4.2e+02;
Matches 36; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 187 TGGAGTTTCATGTTGTCAGGCTGTCGTAACCTCCC 226
DB 1 TGGAGTTTCACCGTGTGGCCAGGCTGTCGTAACCTCCC 40
RESULT 218
ABZ44551/C
ID ABZ44551 standard; DNA; 41 BP.
XX
AC ABZ44551;
XX
DT 26-JUN-2003 (first entry)
XX
DE Human glycosyltransferase DDOST gene polymorphic site, #1335.
XX
XX Human; drug metabolising enzyme; gene; drug metabolism; chromosome 1;
XX polymorphic site; drug evaluation; drug screening; genotyping;
XX genetic profiling; therapeutic customisation; adverse reaction;
XX clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH variation replace(21,A)
FT /*tag= a
FT /standard_name= "Single nucleotide polymorphism (SNP)"
XX
PN WO200252044-A2.
XX
XX 04-JUL-2002.
XX
XX 27-DEC-2001; 2001WO-JP011592.
XX
XX 27-DEC-2000; 2000JP-00399443.
XX
XX 02-MAY-2001; 2001JP-00135256.
XX
XX 27-AUG-2001; 2001JP-00256862.
XX
XX (RIKE ) RIKEN KK.
XX
XX Nakamura Y, Sekine A, Iida A, Saito S;
XX
XX WPI; 2002-583571/62.
XX
XX Identifying individuals having a polymorphism, useful for determining the
XX effectiveness or side effect of a drug or treatment protocol, comprises
XX detecting at least one polymorphism in the drug metabolising enzyme
XX nucleic acid.
XX
XX Claim 23; Page 86; 2785pp; English.
XX
XX Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes
XX encoding enzymes associated with drug metabolism. The invention relates
XX to methods and compositions for identifying individuals who have at least
XX one polymorphism in such drug metabolising enzyme-encoding genes. The
XX polymorphisms may be identified in a nucleic acid sample using probes or
XX primers specific for a sequence selected from ABZ43217-ABZ50887 using a
XX variety of detection assays, including hybridisation assays, nucleic acid
XX arrays and PCR-based methods. The invention also encompasses methods of
XX evaluating and screening drugs using genetic polymorphism data. Genetic
XX polymorphism data, particularly that relating to single nucleotide
```

CC polymorphisms (SNPs), may be used in studying the relationship between  
 CC DNA sequence variations and human diseases, conditions, and responses to  
 CC drugs. SNPs are also useful as polymorphism markers for discovering genes  
 CC that cause or exacerbate certain diseases. SNPs are particularly useful  
 CC in the above respects as they are stable in populations, occur  
 CC frequently, and have lower mutation rates than other genome variations  
 CC such as repeating sequences. The detection and analysis of polymorphisms  
 CC in genes encoding drug metabolising enzymes allows the customisation of  
 CC drug therapies based upon the genetic profile of individual patients.  
 CC This would not only take the guesswork out of selecting the drug with the  
 CC greatest therapeutic effect for a particular patient, but would also  
 CC reduce the likelihood of adverse reactions, thereby increasing safety.  
 CC Methods of the invention are also useful in the drug discovery and  
 CC approval processes. For example, individuals could be selected for  
 CC clinical trials only if their genetic profiles indicate that they are  
 CC capable of responding to a particular drug or drug class, and previously  
 CC failed drug candidates could be revived if they were matched with more  
 CC appropriate patient populations. The methods, data and compositions of  
 CC the invention may therefore lead to an increase in the range of  
 CC possible drug targets and decreases in the number of adverse drug  
 CC reactions, failed drug trials, the time taken for a drug to be approved,  
 CC the length of time patients are on medication and the number of different  
 CC medications a patient needs to take before finding an effective therapy

XX SQ Sequence 41 BP, 10 A; 8 C; 16 G; 7 T; 0 U; 0 Other;

XX Query Match 3.4%; Score 33.6; DB 1; Length 41;  
 XX Best Local Similarity 90.0%; Pred. No. 4.2e+02;  
 XX Matches 36; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

XX 669 CTTGGCTCAGTCAACCTCTGCTCCCGGGTTCAAGTTAT 708  
 XX Db 40 CTTGGCTCAGTCAACCTCTGCTCCCGGGTTCAAGCAAT 1

XX RESULT 219  
 XX ABZ50761/C  
 XX ID ABZ50761 standard; DNA; 41 BP.  
 XX AC ABZ50761;  
 XX 26-JUN-2003 (first entry)  
 XX Human glycosyltransferase DOST gene polymorphic site, #7543.  
 XX DE Human; drug metabolising enzyme; gene; drug metabolism; chromosome 1;  
 XX KW polymorphic site; drug evaluation; drug screening; genotyping;  
 XX KW genetic profiling; therapeutic customisation; adverse reaction;  
 XX KW clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.  
 XX OS Homo sapiens.  
 XX XX  
 XX Key Location/Qualifiers  
 XX FH replace(21,A)  
 XX FT /\*tag= a  
 XX FT /standard\_name= "Single nucleotide polymorphism (SNP)"  
 XX PN WO200252044-A2.  
 XX 04-JUL-2002.  
 XX PD 27-DEC-2001; 2001WO-JP011592.  
 XX PF 27-DEC-2000; 2000JP-00399443.  
 XX PR 02-MAY-2001; 2001JP-00135256.  
 XX PR 27-AUG-2001; 2001JP-00256862.  
 XX XX  
 XX PA (RIKEN ) RIKEN KK.  
 XX XX  
 XX PI Nakamura Y, Sekine A, Iida A, Saito S;  
 XX DR WPI; 2002-583571/62.

PT Identifying individuals having a polymorphism, useful for determining the  
 PT effectiveness or side effect of a drug or treatment protocol, comprises  
 PT detecting at least one polymorphism in the drug metabolising enzyme  
 PT nucleic acid.

XX Claim 23; Page 221; 27855pp; English.

XX Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes  
 CC encoding enzymes associated with drug metabolism. The invention relates  
 CC to methods and compositions for identifying individuals who have at least  
 CC one polymorphism in such drug metabolising enzyme-encoding genes. The  
 CC polymorphisms may be identified in a nucleic acid sample using probes or  
 CC primers specific for a sequence selected from ABZ43217-ABZ50887 using a  
 CC variety of detection assays, including hybridisation assays, nucleic acid  
 CC arrays and PCR-based methods. The invention also encompasses methods of  
 CC evaluating and screening drugs using genetic polymorphism data. Genetic  
 CC polymorphism data, particularly that relating to single nucleotide  
 CC polymorphisms (SNPs), may be used in studying the relationship between  
 CC DNA sequence variations and human diseases, conditions, and responses to  
 CC drugs. SNPs are also useful as polymorphism markers for discovering genes  
 CC that cause or exacerbate certain diseases. SNPs are particularly useful  
 CC in the above respects as they are stable in populations, occur  
 CC frequently, and have lower mutation rates than other genome variations  
 CC such as repeating sequences. The detection and analysis of polymorphisms  
 CC in genes encoding drug metabolising enzymes allows the customisation of  
 CC drug therapies based upon the genetic profile of individual patients.  
 CC This would not only take the guesswork out of selecting the drug with the  
 CC greatest therapeutic effect for a particular patient, but would also  
 CC reduce the likelihood of adverse reactions, thereby increasing safety.  
 CC Methods of the invention are also useful in the drug discovery and  
 CC approval processes. For example, individuals could be selected for  
 CC clinical trials only if their genetic profiles indicate that they are  
 CC capable of responding to a particular drug or drug class, and previously  
 CC failed drug candidates could be revived if they were matched with more  
 CC appropriate patient populations. The methods, data and compositions of  
 CC the invention may therefore lead to an increase in the range of  
 CC possible drug targets and decreases in the number of adverse drug  
 CC reactions, failed drug trials, the time taken for a drug to be approved,  
 CC the length of time patients are on medication and the number of different  
 CC medications a patient needs to take before finding an effective therapy

XX SQ Sequence 41 BP, 10 A; 8 C; 16 G; 7 T; 0 U; 0 Other;

XX Query Match 3.4%; Score 33.6; DB 1; Length 41;  
 XX Best Local Similarity 90.0%; Pred. No. 4.2e+02;  
 XX Matches 36; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

XX 669 CTTGGCTCAGTCAACCTCTGCTCCCGGGTTCAAGTTAT 708  
 XX Db 40 CTTGGCTCAGTCAACCTCTGCTCCCGGGTTCAAGCAAT 1

XX RESULT 220  
 XX ABV77329  
 XX ID ABV77329 standard; DNA; 41 BP.  
 XX AC ABV77329;  
 XX 07-FEB-2003 (first entry)  
 XX Human protein 10.01 related probe 2.  
 XX DE Human protein 10.01 related probe 2.  
 XX KW Human; 10.01; aminolysase active site; arrhythmia; diabetes; probe; ss.  
 XX OS Homo sapiens.  
 XX OS CN1342770-A.  
 XX PN 03-APR-2002.  
 XX PD 12-SEP-2000; 2000CN-00125186.  
 XX PF 12-SEP-2000; 2000CN-00125186.  
 XX PR 12-SEP-2000; 2000CN-00125186.

XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
PA  
XX Mao Y, Xie Y;  
PI  
XX WPI; 2002-529811/57.  
XX  
XX New human protein 10.01 containing Phe-His aminolysase active site and  
PT encoding polynucleotide, useful for treating arrhythmia and diabetes.  
XX  
XX Example 7; Page 22 (disclosure); 33pp; Chinese.  
PS  
XX The invention relates to a human protein designated 10.01, containing the  
CC Phe-His aminolysase active site. Also disclosed are the encoding  
CC polynucleotide, and a method for preparing the polypeptide by DNA  
CC recombination. The application of the polypeptide is in treating  
CC arrhythmia and diabetes. Also disclosed are the antagonist against this  
CC polypeptide and its therapeutic action, and the application of the  
CC polynucleotide. The current sequence represents a human protein 10.01  
CC related probe sequence  
XX  
SQ Sequence 41 BP; 6 A; 17 C; 9 G; 9 T; 0 U; 0 Other;  
Query Match 3.4%; Score 33.6; DB 1; Length 41;  
Best Local Similarity 90.0%; Pred. No. 4.2e+02;  
Matches 36; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
OY 655 TGCAGTGGCGCAATCTTGGCTCACTGCAACCTTGCTCC 694  
DB 1 TGCAGTGGCGCAATCTTGGCTCACTGCAACCTTGCTCC 40  
RESULT 221  
ACCG00157  
ID ACC00157 standard; DNA; 41 BP.  
XX  
XX ACC00157;  
AC  
XX  
XX 14-JUL-2003 (first entry)  
DT  
XX  
XX Probe #2 for guanosine triphosphate activator 10.01.  
DE  
XX Guanosine triphosphatase activator 10.01; squamobasal cell;  
XX carcinoma of skin; osteosarcoma; leukemia; teratoma; probe; ss.  
KW  
XX Unidentified.  
OS  
XX CN1380320-A.  
PN  
XX 20-NOV-2002.  
PD  
XX 10-APR-2001; 2001CN-00105912.  
PF  
XX 10-APR-2001; 2001CN-00105912.  
PR  
XX 10-APR-2001; 2001CN-00105912.  
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.  
XX  
XX Mao Y, Xie Y;  
PI  
XX WPI; 2003-222552/22.  
DR  
XX A polypeptide-guanosine triphosphatase activator protein -10.01 and  
PT polynucleotide for coding this polypeptide.  
XX  
XX Example 7; Page 23; 33pp; Chinese.  
PS  
XX The present invention discloses a polypeptide-guanosine triphosphatase  
CC activator protein-10.01. The invention also discloses the method for  
CC curing several diseases, such as squamobasal cell carcinoma of skin,  
CC osteosarcoma, leukemia and teratoma by using said polypeptide. The  
CC present sequence represents a probe for guanosine triphosphatase activator  
CC protein 10.01  
XX

SQ Sequence 41 BP; 6 A; 16 C; 11 G; 8 T; 0 U; 0 Other;  
Query Match 3.4%; Score 33.6; DB 1; Length 41;  
Best Local Similarity 90.0%; Pred. No. 4.2e+02;  
Matches 36; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
OY 655 TGCAGTGGCGCAATCTTGGCTCACTGCAACCTTGCTCC 694  
DB 1 TGCAGTGGCGCAATCTTGGCTCACTGCAACCTTGCTCC 40  
RESULT 222  
ABZ57114  
ID ABZ57114 standard; DNA; 41 BP.  
XX  
XX ABZ57114;  
AC  
XX 24-MAR-2003 (first entry)  
DT  
XX  
XX Human KIAA0608 protein 10.12 probe, SEQ ID NO:9.  
DE  
XX  
XX Human; KIAA0608 protein 10.12; recombinant production; gene therapy;  
KW peptic ulcer; diabetes; probe; ss.  
KM  
XX Homo sapiens.  
OS  
XX CN1355220-A.  
PN  
XX 26-JUN-2002.  
PD  
XX 24-NOV-2000; 2000CN-00127565.  
PF  
XX 24-NOV-2000; 2000CN-00127565.  
PR  
XX 24-NOV-2000; 2000CN-00127565.  
PA (UYFU-) UNIV FUDAN.  
XX  
XX Mao Y, Xie Y;  
PI  
XX WPI; 2003-000145/01.  
DR  
XX  
XX Polypeptide-human KIAA0608 protein 10.12 and polynucleotide encoding it.  
PT  
XX  
XX Example 6; Page 22 (Disclosure); 35pp; Chinese.  
PS  
XX The invention relates to human KIAA0608 protein 10.12 (ABP58674) and  
CC nucleic acids encoding it (ABZ57108). The protein has a molecular weight  
CC of 10 KD. The invention also relates to a method for the recombinant  
CC production of the protein, an antagonist in therapeutic applications. KIAA0608  
CC the protein, gene and antagonist in the treatment of a variety of diseases such  
CC as peptic ulcers and diabetes. Sequences ABZ57113-ABZ57114 represent  
CC human KIAA0608 protein 10.12 probes used in an exemplification of the  
CC invention  
XX  
SQ Sequence 41 BP; 6 A; 11 C; 14 G; 10 T; 0 U; 0 Other;  
Query Match 3.4%; Score 33.6; DB 1; Length 41;  
Best Local Similarity 90.0%; Pred. No. 4.2e+02;  
Matches 36; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
OY 648 GCTGAGTGCAGTGGCGCAATCTTGGCTCACTGCAACCTC 687  
DB 2 GCTGAGTGCAGTGGCGCAATCTTGGCTCACTGCAACCTC 41  
RESULT 223  
ADL64136/C  
ID ADL64136 standard; DNA; 41 BP.  
XX  
XX ADL64136;  
AC  
XX 20-MAY-2004 (first entry)  
DT  
XX

DE Human single nucleotide polymorphism (SNP) #59.  
 XX  
 KW ss; human: single nucleotide polymorphism; SNP;  
 KW C1 S subcomponent protein; C1S; alanyl aminopeptidase protein; ANPEP;  
 KW mepirin A beta protein; aminopeptidase P-like protein; XPN-PEP;  
 KW tissue kallikrein protein; KLK1; aminopeptidase P protein; MEPIB;  
 KW soluble guanylate cyclase 1 alpha-2 subunit protein; GUCY1A2; haplotype;  
 KW angioedema; angioedema-like disorder; paternity testing;  
 KW cardiovascular diseases; angina pectoris; hypertension; heart failure;  
 KW myocardial infarction; aneurysm; stroke; embolism; thrombosis;  
 KW coronary artery disease; arteriosclerosis; hypersensitivity;  
 KW haemodialysis; sepsis; inflammatory disease; inflammatory arthritis;  
 KW asthma; chronic obstructive pulmonary disease; cough reflex; allergy;  
 KW cancer; ANPEP.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US200403582-A1.  
 XX  
 PD 19-FEB-2004.  
 XX  
 PF 03-JUN-2003; 2003US-00453827.  
 XX  
 PR 03-JUN-2002; 2002US-0384980P.  
 XX  
 PA (EDMO/) EDMONDS M.  
 PA (HUI/) HUI L.  
 PA (PERR/) PERRON M.  
 PA (POWE/) POWELL J R.  
 PA (RAMA/) RAMANATHAN C S.  
 PA (SWAN/) SWANSON B.  
 PA (TSUC/) TSUCHIHASHI Z.  
 PA (ZERR/) ZERBA K.  
 XX  
 PI Edmonds M, Hui L, Perrone M, Powell JR, Ramanathan CS, Swanson B;  
 PI Tsuchihashi Z, Zerba K;  
 XX  
 DR WPI; 2004-180052/17.  
 XX  
 PT New nucleic acid comprising a single nucleotide polymorphism at a  
 PT specific location, useful in paternity testing, genetic analysis or  
 PT diagnosing, preventing or treating cardiovascular diseases e.g.  
 PT angioedema or angina pectoris.  
 XX  
 PS Claim 3; SEQ ID NO 59; 376bp; English.  
 XX  
 CC The invention relates to an isolated nucleic acid (1) derived from a  
 CC human gene encoding a protein, such as the C1 S subcomponent protein  
 CC (C1S), the alanyl aminopeptidase protein (ANPEP), the mepirin A, beta  
 CC protein (MEPIB), the aminopeptidase P-like protein (XPN-PEP), the tissue  
 CC kallikrein protein (KLK1), the membrane bound aminopeptidase P protein  
 CC (XPNPEP2), or the soluble guanylate cyclase 1, alpha-2 subunit protein  
 CC (GUCY1A2). The nucleic acid comprises at least one polymorphic position,  
 CC including the alleles, reference alleles and alternate alleles of the  
 CC single nucleotide polymorphisms, listed in the specification. The  
 CC polymorphic position resides in a (non)coding position within the genomic  
 CC sequence of the gene. The polymorphic position residing in a coding  
 CC position results in a missense or silent mutation of the translated  
 CC product of the gene. The polymorphic position residing in a non-coding  
 CC position resides within the untranslated region or an intronic region of  
 CC the gene. Constructing haplotypes using the nucleic acids above further  
 CC comprises using the haplotypes to identify an individual for the presence  
 CC of a disease phenotype, and correlating the presence of the disease  
 CC phenotype with the haplotype. The disease phenotype is angioedema or an  
 CC angioedema-like disorder. The nucleic acids, primers and probes are  
 CC useful in phenotype correlations, paternity testing, medicine and genetic  
 CC analysis. The nucleic acids and polypeptides can be used in diagnosing,  
 CC preventing or treating cardiovascular diseases, e.g. angioedema, angina  
 CC pectoris, hypertension, heart failure, myocardial infarction, aneurysm,  
 CC stroke, embolism, thrombosis, coronary artery disease or  
 CC arteriosclerosis, hypersensitivity reactions during haemodialysis,  
 CC sepsis, inflammatory diseases, inflammatory arthritis, asthma, chronic  
 CC obstructive pulmonary disease, cough reflex, allergies, or cancer. The

CC present sequence represents a human single nucleotide polymorphism (SNP)  
 CC of the invention.  
 XX  
 XX Sequence 41 BP; 9 A; 13 C; 11 G; 8 T; 0 U; 0 Other;  
 SQ  
 Query Match 3.4%; Score 33.6; DB 1; Length 41;  
 Best Local Similarity 90.0%; Pred No. 4.2e+02;  
 Matches 36; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 644 CCAGGCTGAGTGCAGTGGCCGCAATCTTGCTCACTGCA 683  
 DB 41 CCAGGCTGAGTGCAGTGGTGCATCTCACTGCACTGCA 2  
 RESULT 224  
 ABZ45510  
 ID ABZ45510 strand; DNA; 41 BP.  
 XX  
 AC ABZ45510;  
 XX  
 DT 26-JUN-2003 (first entry)  
 XX  
 DE Human ATP-binding cassette ABCA7 gene polymorphic site, #2294.  
 XX  
 KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 19;  
 KW polymorphic site; drug evaluation; drug screening; genotyping;  
 KW genetic profiling; therapeutic customisation; adverse reaction;  
 KW clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT replace(21,T)  
 FT /tag= a  
 FT /strand\_name= "Single nucleotide polymorphism (SNP)"  
 XX  
 PN WO200252044-A2.  
 XX  
 PD 04-JUL-2002.  
 XX  
 PP 27-DEC-2001; 2001WO-JP011592.  
 XX  
 PR 27-DEC-2000; 2000JP-00399443.  
 PR 02-MAY-2001; 2001JP-00135256.  
 PR 27-AUG-2001; 2001JP-00256862.  
 XX  
 PA (RIKE ) RIKEN KK.  
 XX  
 PI Nakamura Y, Sekine A, Iida A, Saito S;  
 PI  
 XX  
 DR WPI; 2002-583571/62.  
 XX  
 PT Identifying individuals having a polymorphism, useful for determining the  
 PT effectiveness or side effect of a drug or treatment protocol, comprises  
 PT detecting at least one polymorphism in the drug metabolizing enzyme  
 PT nucleic acid.  
 XX  
 PS Claim 23; Page 102; 2785bp; English.  
 XX  
 CC Sequences ABZ4217-ABZ50887 represent polymorphic sites within genes  
 CC encoding enzymes associated with drug metabolism. The invention relates  
 CC to methods and compositions for identifying individuals who have at least  
 CC one polymorphism in such drug metabolising enzyme-encoding genes. The  
 CC polymorphisms may be identified in a nucleic acid sample using probes or  
 CC primers specific for a sequence selected from ABZ4217-ABZ50887 using a  
 CC variety of detection assays, including hybridisation assays, nucleic acid  
 CC arrays and PCR-based methods. The invention also encompasses methods of  
 CC evaluating and screening drugs using genetic polymorphism data. Genetic  
 CC polymorphism data, particularly that relating to single nucleotide  
 CC polymorphisms (SNPs), may be used in studying the relationship between  
 CC DNA sequence variations and human diseases, conditions, and responses to  
 CC drugs. SNPs are also useful as polymorphism markers for discovering genes  
 CC that cause or exacerbate certain diseases. SNPs are particularly useful

in the above respects as they are stable in populations, occur frequently, and have lower mutation rates than other genome variations such as repeating sequences. The detection and analysis of polymorphisms in genes encoding drug metabolising enzymes allows the customisation of drug therapies based upon the genetic profile of individual patients. This would not only take the guesswork out of selecting the drug with the greatest therapeutic effect for a particular patient, but would also reduce the likelihood of adverse reactions, thereby increasing safety. Methods of the invention are also useful in the drug discovery and approval processes. For example, individuals could be selected for clinical trials only if their genetic profiles indicate that they are capable of responding to a particular drug or drug class, and previously failed drug candidates could be revived if they were matched with more appropriate patient populations. The methods, data and compositions of the invention may therefore lead to an increase in the range of possible drug targets and decreases in the number of adverse drug reactions, failed drug trials, the time taken for a drug to be approved, the length of time patients are on medication and the number of different medications a patient needs to take before finding an effective therapy

Query Match	3.4%	Score	33.2	DB	1	Length	41
Best Local Similarity	92.1%	Pred.	No. 4.3e+02				
Matches	35	Conservative	0	Mismatches	3	Indels	0
						Gaps	0

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Oy      667 ATCTGGCTACTGCAACCTCTGCCCTCCCGGTTCAAG 704
          |||||
Db      4 ATCTGGCTACTGCAACCTCCGCCCTCTGGATTCAAG 41

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RESULT 225  
ABZ46916  
ID ABZ46916 standard; DNA; 41 BP.

AC	ABZ46916;
XX	
DT	26-JUN-2003 (first entry)

DE Human ATP-binding cassette ABCA7 gene polymorphic site, #3700.

KM Human, drug metabolising enzyme; gene; drug metabolism; chromosome 19;  
 KM polymorphic site; drug evaluation; drug screening; genotyping;  
 KM genetic profiling; therapeutic customisation; adverse reaction;  
 KM clinical trial; drug approval; single nucleotide polymorphism; SNP; ds

OS Homo sapiens.

Key	Location/Qualifiers
EH	replace(21,T)
FT	/*tag= a
FT	/standard name= "Single nucleotide polymorphism (SNP) "

PN WO200252044-A2

PD 04-JUL-2002

PF 27-DEC-2001; 2001WO-JP011592.  
VY

PR 27-DEC-2000; 2000JP-00399443.  
PR 02-MAY-2001; 2001JP-00135256.

2/-AUG-2001; 2001JUF-002568862.

[illegible]

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8

PT effectiveness or side effects at 1 year

PT nucleic acid.

XX  
PS Claim 23; Page 129; 2785pp; English.

CC Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes  
CC encoding enzymes associated with drug metabolism. The invention relates  
CC to methods and compositions for identifying individuals who have at least  
CC one polymorphism in such drug metabolizing enzyme-encoding genes. The  
CC polymorphisms may be identified in a nucleic acid sample using probes or  
CC primers specific for a sequence selected from ABZ43217-ABZ50887 using a  
CC variety of detection assays, including hybridization assays, nucleic acid  
CC arrays and PCR-based methods. The invention also encompasses methods of  
CC evaluating and screening drugs using genetic polymorphism data. Genetic  
CC polymorphism data, particularly that relating to single nucleotide  
CC polymorphisms (SNPs), may be used in studying the relationship between  
CC DNA sequence variations and human diseases, conditions, and responses to  
CC drugs. SNPs are also useful as polymorphism markers for discovering genes  
CC that cause or exacerbate certain diseases. SNPs are particularly useful  
CC in the above respects as they are stable in populations, occur  
CC frequently, and have lower mutation rates than other genome variations  
CC such as repeating sequences. The detection and analysis of polymorphisms  
CC in genes encoding drug metabolizing enzymes allows the customization of  
CC drug therapies based upon the genetic profile of individual patients.  
CC This would not only take the guesswork out of selecting the drug with the  
CC greatest therapeutic effect for a particular patient, but would also  
CC reduce the likelihood of adverse reactions, thereby increasing safety.  
CC Methods of the invention are also useful in the drug discovery and  
CC approval processes. For example, individuals could be selected for  
CC clinical trials only if their genetic profiles indicate that they are  
CC capable of responding to a particular drug or drug class, and previously  
CC failed drug candidates could be revived if they were matched with more  
CC appropriate patient populations. The methods, data and compositions of  
CC the invention may therefore lead to an increase in the range of  
CC possible drug targets and decreases in the number of adverse drug  
CC reactions, failed drug trials, the time taken for a drug to be approved,  
CC the length of time patients are on medication and the number of different  
CC medications a patient needs to take before finding an effective therapy.

Query Match	3.4%	Score 33.2;	DB 1;	Length 41;
Best Local Similarity	92.1%;	Pred. No. 4.3e+02;		
Matches 35; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

QY 667 ATCTGGCTACTGCACCTCTGCTCCCGGTTCAAG 704  
|||||  
Db 4 ATCTGGCTACTGCACCTCCGCTCTGGATTCAAG 41

RESULT 226  
ACC84461  
ID ACC84461 standard: DNA: 33 BP.

AC ACC84461;

DT 28-AUG-2003 (first entry)

DE NTP peptide encoding sequence #8.

KW Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;  
KW neutral thread protein; NMD; tumour; de

XX  
OS  
identified

XX  
PN WO2003008443-A2.

PD 30-JAN-2003.

PF 19-JUL-2002; 2002WO-CA001105.

PR 19-JUL-2001; 2001US-0306150P.

PR 16-NOV-2001; 2001US-0331477P.  
YY



PA (NTMO-) NYMOX CORP.  
 XX  
 PS  
 PI Averbach PA;  
 XX  
 DR WPI; 2003-247999/24.  
 DR P-PSDB; ABR63256.  
 XX  
 PT Novel neural thread protein peptide, referred as cell death peptide,  
 PT useful for treating prostatic hyperplasia, psoriasis, eczema, dermatosis,  
 PT atherosclerosis, cosmetic modification to skin, throat, mouth, muscle.  
 PS  
 XX Disclosure; Page 17, 77pp; English.  
 XX  
 CC The present invention relates to a neural thread protein (NTP) peptide  
 CC referred to as cell death peptide. Thought to be cytostatic,  
 CC antibacterial, immunosuppressive and antiinflammatory. It is useful for  
 CC treating a condition in a patient requiring removal or destruction of  
 CC cells, for treating a condition such as benign or malignant tumor,  
 CC inflammatory disease, autoimmune disease and infectious disease. The  
 CC peptide useful for treatment is derived from the amino acid sequence for  
 CC a pancreatic thread protein. The peptide is conjugated, linked or bound  
 CC to a molecule chosen from antibody or its fragment, antibody-like binding  
 CC molecule, where the molecule has a higher affinity for binding to a tumor  
 CC or other target than binding to other cells. Treatment using NTP peptides  
 CC can remove benign tumors with less risk and fewer of the undesirable side  
 CC effects of surgery. The present sequence is an NTP encoding sequence  
 XX  
 SQ Sequence 33 BP; 7 A; 10 C; 9 G; 7 T; 0 U; 0 Other;  
 Query Match 3.3%; Score 33; DB 1; Length 33;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 378 CTCAGCCTCCCAAGTCGTGATTAACAGGCGT 410  
 Db 1 CTCAGCCTCCCAAGTCGTGATTAACAGGCGT 33  
 RESULT 227  
 AA199796  
 ID AA199796 standard; DNA; 41 BP.  
 XX  
 AC AA199796;  
 XX  
 DT 24-JAN-2002 (first entry)  
 XX  
 DE Human eukaryotic acetyl transferase 10 probe SEQ ID NO 8.  
 XX  
 KW Human; eukaryotic acetyl transferase 10; cytosolic; virucidal;  
 KW immunomodulatory; antiinflammatory; haemostatic; malignant tumour;  
 KW human immunodeficiency virus; HIV; infection; immunological disease;  
 KW gene therapy; probe; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200175026-A2.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PF 19-MAR-2001; 2001MO-CN000378.  
 XX  
 PR 22-MAR-2000; 2000CN-00115031.  
 XX  
 PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.  
 XX  
 PI Mao Y, Xie Y;  
 XX  
 DR WPI; 2002-025848/03.  
 XX  
 PT Human eucaryotic acetyl transferase 10 and encoded polynucleotide, used  
 PT in diagnosis and treatment of malignant tumors, hemopathy, human  
 PT immunodeficiency virus infection, immunological diseases and  
 PT inflammation.

XX  
 PS Example 6; Page 15; 33pp; Chinese.  
 XX  
 CC The invention relates to human eukaryotic acetyl transferase 10 with  
 CC cytosolic, virucidal, immunomodulatory, antiinflammatory and haemostatic  
 CC activity. The protein and encoding polynucleotide are used in diagnosis  
 CC and treatment of malignant tumour, haemopathy, human immunodeficiency  
 CC virus (HIV) infection, immunological diseases and various inflammations.  
 CC The polynucleotide is useful in gene therapy. The present sequence is  
 CC that of a probe, useful to the invention  
 XX  
 SQ Sequence 41 BP; 9 A; 10 C; 8 G; 14 T; 0 U; 0 Other;  
 Query Match 3.3%; Score 33; DB 1; Length 41;  
 Best Local Similarity 87.8%; Pred. No. 4.4e+02;  
 Matches 36; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 1051 TGGCACACACCGCGCTAATTTGTATTTTCATTAGAGGC 1091  
 Db 1 TGGCACACACCGCGCTAATTTGTATTTTCATTAGAGGC 41  
 RESULT 228  
 AB152956/c  
 ID AB152956 standard; DNA; 41 BP.  
 XX  
 AC AB152956;  
 XX  
 DT 24-MAY-2002 (first entry)  
 XX  
 DE Serine proteinase 10 probe #2.  
 XX  
 KW Serine proteinase 10; enzyme; cancer; HIV infection; anti-HIV;  
 KW cytosolic; probe; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN CN1325996-A.  
 XX  
 PD 12-DEC-2001.  
 XX  
 PF 31-MAY-2000; 2000CN-00116278.  
 XX  
 PR 31-MAY-2000; 2000CN-00116278.  
 XX  
 PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
 XX  
 PI Mao Y, Xie Y;  
 XX  
 DR WPI; 2002-196715/26.  
 XX  
 PT Polypeptide-serine proteinase 10 and polynucleotide encoding it.  
 XX  
 PS Example 6; Page 19 (Disclosure); 32pp; Chinese.  
 XX  
 CC The present invention relates to serine proteinase 10 (AAM48453). Serine  
 CC proteinase 10 and its coding sequence can be used for treating diseases  
 CC such as cancer and HIV infection. The present sequence is a probe, which  
 CC was used in an example from the invention  
 XX  
 SQ Sequence 41 BP; 9 A; 15 C; 12 G; 5 T; 0 U; 0 Other;  
 Query Match 3.3%; Score 33; DB 1; Length 41;  
 Best Local Similarity 87.8%; Pred. No. 4.4e+02;  
 Matches 36; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 637 CTGTACACGAGGCTGAGTGGCGGCAATCTGGCTCA 677  
 Db 41 CTGTACACGAGGCTGAGTGGCGGCAATCTGGCTCA 1  
 RESULT 229  
 ABZ4124/c

ID AB244124 standard; DNA; 41 BP.  
XX  
AC AB244124;  
XX  
DT 26-JUN-2003 (first entry)  
XX  
DE Human NDUF51 gene polymorphic site, #908.  
XX  
DE Human; drug metabolising enzyme; gene; drug metabolism; chromosome 2;  
KW polymorphic site; drug evaluation; drug screening; genotyping;  
KW genetic profiling; therapeutic customisation; adverse reaction;  
KW clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key location/Qualifiers  
FT variation /tag=a  
FT /standard\_name="Single nucleotide polymorphism (SNP)"  
XX  
PN MO200252044-A2.  
XX  
PD 04-JUL-2002.  
XX  
PF 27-DEC-2001; 2001WO-JP011592.  
XX  
PR 27-DEC-2000; 2000JP-00399443.  
PR 02-MAY-2001; 2001JP-00135256.  
PR 27-AUG-2001; 2001JP-00256862.  
XX  
PA (RIKEN ) RIKEN KK.  
XX  
PI Nakamura Y, Sekine A, Iida A, Satto S;  
XX  
DR WPI; 2002-583571/62.  
XX  
PT Identifying individuals having a polymorphism, useful for determining the  
PT effectiveness or side effect of a drug or treatment protocol, comprises  
PT detecting at least one polymorphism in the drug metabolizing enzyme  
PT nucleic acid.  
XX  
PS Claim 23; Page 79; 2785pp; English.  
XX  
CC Sequences AB243217-AB250887 represent polymorphic sites within genes  
CC encoding enzymes associated with drug metabolism. The invention relates  
CC to methods and compositions for identifying individuals who have at least  
CC one polymorphism in such drug metabolising enzyme-encoding genes. The  
CC polymorphisms may be identified in a nucleic acid sample using probes or  
CC primers specific for a sequence selected from AB243217-AB250887 using a  
CC variety of detection assays, including hybridisation assays, nucleic acid  
CC arrays and PCR-based methods. The invention also encompasses methods of  
CC evaluating and screening drugs using genetic polymorphism data. Genetic  
CC polymorphisms (SNPs), may be used in studying the relationship between  
CC DNA sequence variations and human diseases, conditions, and responses to  
CC drugs. SNPs are also useful as polymorphism markers for discovering genes  
CC that cause or exacerbate certain diseases. SNPs are particularly useful  
CC in the above respects as they are stable in populations, occur  
CC frequently, and have lower mutation rates than other genome variations  
CC such as repeating sequences. The detection and analysis of polymorphisms  
CC in genes encoding drug metabolising enzymes allows the customisation of  
CC drug therapies based upon the genetic profile of individual patients.  
CC This would not only take the guesswork out of selecting the drug with the  
CC greatest therapeutic effect for a particular patient, but would also  
CC reduce the likelihood of adverse reactions, thereby increasing safety.  
CC Methods of the invention are also useful in the drug discovery and  
CC approval processes. For example, individuals could be selected for  
CC clinical trials only if their genetic profiles indicate that they are  
CC capable of responding to a particular drug or drug class, and previously  
CC failed drug candidates could be revived if they were matched with more  
CC appropriate patient populations. The methods, data and compositions of  
CC the invention may therefore lead to an increase in the range of  
CC possible drug targets and decreases in the number of adverse drug

CC reactions, failed drug trials, the time taken for a drug to be approved,  
CC the length of time patients are on medication and the number of different  
CC medications a patient needs to take before finding an effective therapy  
XX  
SO Sequence 41 BP; 8 A; 14 C; 12 G; 7 T; 0 U; 0 Other;  
XX  
Query Match 3.3%; Score 33; DB 1; Length 41;  
Best Local Similarity 87.8%; Pred. No. 4,4e+02;  
Matches 36; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
XX  
QY 643 CCCAGGCTGAGTCAGTGGCGCAATCTTGCTCAGTCGCA 683  
DB 41 CCCAGGCTGAGTCAGTGGCGCAATCTTGCTCAGTCGCA 1  
XX  
RESULT 230  
AB245508  
ID AB245508 standard; DNA; 41 BP.  
XX  
AC AB245508;  
XX  
DT 26-JUN-2003 (first entry)  
XX  
DE Human ATP-binding cassette ABCA7 gene polymorphic site, #2292.  
XX  
DE Human; drug metabolising enzyme; gene; drug metabolism; chromosome 19;  
KW polymorphic site; drug evaluation; drug screening; genotyping;  
KW genetic profiling; therapeutic customisation; adverse reaction;  
KW clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key location/Qualifiers  
FT variation /tag=a  
FT /standard\_name="Single nucleotide polymorphism (SNP)"  
XX  
PN MO200252044-A2.  
XX  
PD 04-JUL-2002.  
XX  
PF 27-DEC-2001; 2001WO-JP011592.  
XX  
PR 27-DEC-2000; 2000JP-00399443.  
PR 02-MAY-2001; 2001JP-00135256.  
PR 27-AUG-2001; 2001JP-00256862.  
XX  
PA (RIKEN ) RIKEN KK.  
XX  
PI Nakamura Y, Sekine A, Iida A, Satto S;  
XX  
DR WPI; 2002-583571/62.  
XX  
PT Identifying individuals having a polymorphism, useful for determining the  
PT effectiveness or side effect of a drug or treatment protocol, comprises  
PT detecting at least one polymorphism in the drug metabolizing enzyme  
PT nucleic acid.  
XX  
PS Claim 23; Page 102; 2785pp; English.  
XX  
CC Sequences AB243217-AB250887 represent polymorphic sites within genes  
CC encoding enzymes associated with drug metabolism. The invention relates  
CC to methods and compositions for identifying individuals who have at least  
CC one polymorphism in such drug metabolising enzyme-encoding genes. The  
CC polymorphisms may be identified in a nucleic acid sample using probes or  
CC primers specific for a sequence selected from AB243217-AB250887 using a  
CC variety of detection assays, including hybridisation assays, nucleic acid  
CC arrays and PCR-based methods. The invention also encompasses methods of  
CC evaluating and screening drugs using genetic polymorphism data. Genetic  
CC polymorphisms (SNPs), may be used in studying the relationship between  
CC DNA sequence variations and human diseases, conditions, and responses to  
CC drugs. SNPs are also useful as polymorphism markers for discovering genes

CC that cause or exacerbate certain diseases. SNPs are particularly useful  
CC in the above respects as they are stable in populations, occur  
CC frequently, and have lower mutation rates than other genome variations  
CC such as repeating sequences. The detection and analysis of polymorphisms  
CC in genes encoding drug metabolising enzymes allows the customisation of  
CC drug therapies based upon the genetic profile of individual patients.  
CC This would not only take the guesswork out of selecting the drug with the  
CC greatest therapeutic effect for a particular patient, but would also  
CC reduce the likelihood of adverse reactions, thereby increasing safety.  
CC Methods of the invention are also useful in the drug discovery and  
CC approval processes. For example, individuals could be selected for  
CC clinical trials only if their genetic profiles indicate that they are  
CC capable of responding to a particular drug or drug class, and previously  
CC failed drug candidates could be revived if they were matched with more  
CC appropriate patient populations. The methods, data and compositions of  
CC the invention may therefore lead to an increase in the range of  
CC possible drug targets and decreases in the number of adverse drug  
CC reactions, failed drug trials, the time taken for a drug to be approved,  
CC the length of time patients are on medication and the number of different  
CC medications a patient needs to take before finding an effective therapy  
CC  
SQ Sequence 41 BP; 6 A; 11 C; 14 G; 10 T; 0 U; 0 Other;  
Query Match 3.3%; Score 33; DB 1; Length 41;  
Best Local Similarity 87.8%; Pred. No. 4.4e+02;  
Matches 36; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 639 CTCACCCAGGCTGAGTGCAGTGGCGCCATCTTGCTCACT 679  
DB 1 GTTGCCAGGCTGACTGCAGTGGCGAGATCTTGCTCACT 41  
RESULT 231  
AB249572/C  
ID AB249572 strand; DNA; 41 BP.  
XX AB249572;  
AC  
XX  
XX  
DT 26-JUN-2003 (first entry)  
DE Human glutathione-S-transferase MGST3 gene polymorphic site, #6355.  
XX  
XX  
KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 1;  
KW polymorphic site; drug evaluation; drug screening; genotyping;  
KW genetic profiling; therapeutic customisation; adverse reaction;  
KW clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT variation replace(21,C)  
FT /\*tag= a  
FT /standard\_name= "Single nucleotide polymorphism (SNP)"  
PN WO200252044-A2.  
XX  
XX  
PD 04-JUL-2002.  
XX  
XX  
PF 27-DEC-2001; 2001WO-DP011592.  
XX  
XX  
PR 27-DEC-2000; 2000JP-00399443.  
XX  
PR 02-MAY-2001; 2001JP-00135256.  
XX  
PR 27-AUG-2001; 2001JP-00256862.  
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XX  
PA (RIKE ) RIKEN KK.  
XX  
XX  
PI Nakamura Y, Sekine A, Iida A, Saito S;  
XX  
DR WPI; 2002-583571/62.  
XX  
XX  
PT Identifying individuals having a polymorphism, useful for determining the  
PT effectiveness or side effect of a drug or treatment protocol, comprises  
PT detecting at least one polymorphism in the drug metabolizing enzyme

PT nucleic acid.  
XX  
XX  
PS Claim 23; Page 192; 27855bp; English.  
XX  
XX  
XX Sequences AB243217-AB250887 represent polymorphic sites within genes  
XX encoding enzymes associated with drug metabolism. The invention relates  
XX to methods and compositions for identifying individuals who have at least  
XX one polymorphism in such drug metabolising enzyme-encoding genes. The  
XX polymorphisms may be identified in a nucleic acid sample using probes or  
XX primers specific for a sequence selected from AB243217-AB250887 using a  
XX variety of detection assays, including hybridisation assays, nucleic acid  
XX arrays and PCR-based methods. The invention also encompasses methods of  
XX evaluating and screening drugs using genetic polymorphism data. Genetic  
XX polymorphism data, particularly that relating to single nucleotide  
XX polymorphisms (SNPs), may be used in studying the relationship between  
XX DNA sequence variations and human diseases, conditions, and responses to  
XX drugs. SNPs are also useful as polymorphism markers for discovering genes  
XX that cause or exacerbate certain diseases. SNPs are particularly useful  
XX in the above respects as they are stable in populations, occur  
XX frequently, and have lower mutation rates than other genome variations  
XX such as repeating sequences. The detection and analysis of polymorphisms  
XX in genes encoding drug metabolising enzymes allows the customisation of  
XX drug therapies based upon the genetic profile of individual patients.  
XX This would not only take the guesswork out of selecting the drug with the  
XX greatest therapeutic effect for a particular patient, but would also  
XX reduce the likelihood of adverse reactions, thereby increasing safety.  
XX Methods of the invention are also useful in the drug discovery and  
XX approval processes. For example, individuals could be selected for  
XX clinical trials only if their genetic profiles indicate that they are  
XX capable of responding to a particular drug or drug class, and previously  
XX failed drug candidates could be revived if they were matched with more  
XX appropriate patient populations. The methods, data and compositions of  
XX the invention may therefore lead to an increase in the range of  
XX possible drug targets and decreases in the number of adverse drug  
XX reactions, failed drug trials, the time taken for a drug to be approved,  
XX the length of time patients are on medication and the number of different  
XX medications a patient needs to take before finding an effective therapy  
XX  
SQ Sequence 41 BP; 10 A; 9 C; 14 G; 8 T; 0 U; 0 Other;  
Query Match 3.3%; Score 33; DB 1; Length 41;  
Best Local Similarity 87.8%; Pred. No. 4.4e+02;  
Matches 36; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 361 TCAGCAGTCCACCTGCTGCACCTCCCAAGTCTGGGAT 401  
DB 41 TCAGCATCTGCTGCTGCTGCTGCCCTCCCAAGTGTGGAT 1  
RESULT 232  
AB249713  
ID AB249713 strand; DNA; 41 BP.  
XX AB249713;  
AC  
XX  
XX  
DT 26-JUN-2003 (first entry)  
DE Human sulphotransferase TPST2 gene polymorphic site, #6495.  
XX  
XX  
KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 22;  
KW polymorphic site; drug evaluation; drug screening; genotyping;  
KW genetic profiling; therapeutic customisation; adverse reaction;  
KW clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.  
XX  
XX  
OS Homo sapiens.  
XX  
XX  
FH Key Location/Qualifiers  
FT variation replace(21,C)  
FT /\*tag= a  
FT /standard\_name= "Single nucleotide polymorphism (SNP)"  
FT variation replace(25,T)  
FT /\*tag= b  
FT /standard\_name= "Single nucleotide polymorphism (SNP)"

XX WO200252044-A2.  
 PN 04-JUL-2002.  
 XX  
 XX 27-DEC-2001; 2001WO-JP011592.  
 PF  
 XX 27-DEC-2000; 2000JP-00399443.  
 XX 02-MAY-2001; 2001JP-00135256.  
 PR 27-AUG-2001; 2001JP-00256862.  
 XX  
 XX (RIKE ) RIKEN KK.  
 XX  
 PI Nakamura Y, Sekine A, Iida A, Saito S;  
 DR WPI; 2002-583571/62.  
 PT  
 PT Identifying individuals having a polymorphism, useful for determining the  
 PT effectiveness or side effect of a drug or treatment protocol, comprises  
 PT detecting at least one polymorphism in the drug metabolizing enzyme  
 PT nucleic acid.  
 PS  
 PS Claim 23; Page 196; 2785pp; English.  
 XX  
 XX Sequences AB243217-AB250887 represent polymorphic sites within genes  
 CC encoding enzymes associated with drug metabolism. The invention relates  
 CC to methods and compositions for identifying individuals who have at least  
 CC one polymorphism in such drug metabolizing enzyme-encoding genes. The  
 CC polymorphisms may be identified in a nucleic acid sample using probes or  
 CC primers specific for a sequence selected from AB243217-AB250887 using a  
 CC variety of detection assays, including hybridisation assays, nucleic acid  
 CC arrays and PCR-based methods. The invention also encompasses methods of  
 CC evaluating and screening drugs using genetic polymorphism data. Genetic  
 CC polymorphisms (SNPs), particularly that relating to single nucleotide  
 CC polymorphisms (SNPs), may be used in studying the relationship between  
 CC DNA sequence variations and human diseases, conditions, and responses to  
 CC drugs. SNPs are also useful as polymorphism markers for discovering genes  
 CC that cause or exacerbate certain diseases. SNPs are particularly useful  
 CC in the above respects as they are stable in populations, occur  
 CC frequently, and have lower mutation rates than other genome variations  
 CC such as repeating sequences. The detection and analysis of polymorphisms  
 CC in genes encoding drug metabolizing enzymes allows the customisation of  
 CC drug therapies based upon the genetic profile of individual patients.  
 CC This would not only take the guesswork out of selecting the drug with the  
 CC greatest therapeutic effect for a particular patient, but would also  
 CC reduce the likelihood of adverse reactions, thereby increasing safety.  
 CC Methods of the invention are also useful in the drug discovery and  
 CC approval processes. For example, individuals could be selected for  
 CC clinical trials only if their genetic profiles indicate that they are  
 CC capable of responding to a particular drug or drug class, and previously  
 CC failed drug candidates could be revived if they were matched with more  
 CC appropriate patient populations. The methods, data and compositions of  
 CC the invention may therefore lead to an increase in the range of  
 CC possible drug targets and decreases in the number of adverse drug  
 CC reactions, failed drug trials, the time taken for a drug to be approved,  
 CC the length of time patients are on medication and the number of different  
 CC medications a patient needs to take before finding an effective therapy  
 XX  
 XX Sequence 41 BP; 7 A; 10 C; 14 G; 10 T; 0 U; 0 Other;  
 SQ  
 Query Match 3.3%; Score 33; DB 1; Length 41;  
 Best Local Similarity 87.8%; Pred. No. 4.4e-02;  
 Matches 36; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 643 CCCAGGCTGAGTGCAGTGGCGCAATCTTGCTCACTGCA 683  
 DB 1 CCCAGGCTGAGTGCAGTGGCTGATCTCGGCTCACTGCA 41

AC AB250134;  
 XX 26-JUN-2003 (first entry)  
 DT  
 XX Human NDUF51 gene polymorphic site, #6916.  
 DE  
 XX Human, drug metabolising enzyme; gene; drug metabolism; chromosome 2;  
 KW polymorphic site; drug evaluation; drug screening; genotyping;  
 KW genetic profiling; therapeutic customisation; adverse reaction;  
 KM clinical trial; drug approval; single nucleotide polymorphism; SNP, ds.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX Key location/Qualifiers  
 FH replace(21,T)  
 FT variation /\*tag= a  
 FT /standard\_name= "Single nucleotide polymorphism (SNP)"  
 XX  
 XX WO200252044-A2.  
 XX  
 XX 04-JUL-2002.  
 PD  
 XX 27-DEC-2001; 2001WO-JP011592.  
 XX  
 XX 27-DEC-2000; 2000JP-00399443.  
 XX 02-MAY-2001; 2001JP-00135256.  
 PR 27-AUG-2001; 2001JP-00256862.  
 XX  
 XX (RIKE ) RIKEN KK.  
 XX  
 PI Nakamura Y, Sekine A, Iida A, Saito S;  
 DR WPI; 2002-583571/62.  
 PT  
 PT Identifying individuals having a polymorphism, useful for determining the  
 PT effectiveness or side effect of a drug or treatment protocol, comprises  
 PT detecting at least one polymorphism in the drug metabolizing enzyme  
 PT nucleic acid.  
 PS  
 PS Claim 23; Page 206; 2785pp; English.  
 XX  
 XX Sequences AB243217-AB250887 represent polymorphic sites within genes  
 CC encoding enzymes associated with drug metabolism. The invention relates  
 CC to methods and compositions for identifying individuals who have at least  
 CC one polymorphism in such drug metabolizing enzyme-encoding genes. The  
 CC polymorphisms may be identified in a nucleic acid sample using probes or  
 CC primers specific for a sequence selected from AB243217-AB250887 using a  
 CC variety of detection assays, including hybridisation assays, nucleic acid  
 CC arrays and PCR-based methods. The invention also encompasses methods of  
 CC evaluating and screening drugs using genetic polymorphism data. Genetic  
 CC polymorphism data, particularly that relating to single nucleotide  
 CC polymorphisms (SNPs), may be used in studying the relationship between  
 CC DNA sequence variations and human diseases, conditions, and responses to  
 CC drugs. SNPs are also useful as polymorphism markers for discovering genes  
 CC that cause or exacerbate certain diseases. SNPs are particularly useful  
 CC in the above respects as they are stable in populations, occur  
 CC frequently, and have lower mutation rates than other genome variations  
 CC such as repeating sequences. The detection and analysis of polymorphisms  
 CC in genes encoding drug metabolizing enzymes allows the customisation of  
 CC drug therapies based upon the genetic profile of individual patients.  
 CC This would not only take the guesswork out of selecting the drug with the  
 CC greatest therapeutic effect for a particular patient, but would also  
 CC reduce the likelihood of adverse reactions, thereby increasing safety.  
 CC Methods of the invention are also useful in the drug discovery and  
 CC approval processes. For example, individuals could be selected for  
 CC clinical trials only if their genetic profiles indicate that they are  
 CC capable of responding to a particular drug or drug class, and previously  
 CC failed drug candidates could be revived if they were matched with more  
 CC appropriate patient populations. The methods, data and compositions of  
 CC the invention may therefore lead to an increase in the range of  
 CC possible drug targets and decreases in the number of adverse drug  
 CC reactions, failed drug trials, the time taken for a drug to be approved,  
 CC the length of time patients are on medication and the number of different

```
CC medications a patient needs to take before finding an effective therapy
XX
XX Sequence 41 BP; 8 A; 14 C; 12 G; 7 T; 0 U; 0 Other;
SQ
Query Match 3.3%; Score 33; DB 1; Length 41;
Best Local Similarity 87.8%; Pred. No. 4.4e+02;
Matches 36; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

643 CCCAGGCTGAGTGCAGTGGCCCATCTTGCTCACTGCA 683
DB 41 CCCAGGCTGAGTGCAGTGGCCCATCTTGCTCACTGCA 1

RESULT 234
AB243560
ID AB243560 standard; DNA; 41 BP.
XX
XX AB243560;
AC
XX
XX 26-JUN-2003 (first entry)
XX
XX Human sulphotransferase TPST2 gene polymorphic site, #344.
XX
XX Human; drug metabolising enzyme; gene; drug metabolism; chromosome 22;
XX
XX polymorphic site; drug evaluation; drug screening; genotyping;
XX
XX genetic profiling; therapeutic customisation; adverse reaction;
XX
XX clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX variation replace(21,C)
XX /tag= a
XX /standard_name= "Single nucleotide polymorphism (SNP)"
XX
XX WO200252044-A2.
XX
XX 04-JUL-2002.
XX
XX 27-DEC-2001; 2001WO-JP011592.
XX
XX 27-DEC-2000; 2000JP-00399443.
XX
XX 02-MAY-2001; 2001JP-00135256.
XX
XX 27-AUG-2001; 2001JP-00256862.
XX
XX (RIKE ) RIKEN KK.
XX
XX Nakamura Y, Sekine A, Iida A, Salto S;
XX
XX WPI; 2002-583571/62.
XX
XX Identifying individuals having a polymorphism, useful for determining the
XX effectiveness or side effect of a drug or treatment protocol, comprises
XX detecting at least one polymorphism in the drug metabolizing enzyme
XX nucleic acid.
XX
XX Claim 23; Page 69; 2785pp; English.
XX
XX Sequences AB243217-AB250887 represent polymorphic sites within genes
XX encoding enzymes associated with drug metabolism. The invention relates
XX to methods and compositions for identifying individuals who have at least
XX one polymorphism in such drug metabolising enzyme-encoding genes. The
XX polymorphisms may be identified in a nucleic acid sample using probes or
XX primers specific for a sequence selected from AB243217-AB250887 using a
XX variety of detection assays, including hybridisation assays, nucleic acid
XX arrays and PCR-based methods. The invention also encompasses methods of
XX evaluating and screening drugs using genetic polymorphism data. Genetic
XX polymorphism data, particularly that relating to single nucleotide
XX polymorphisms (SNPs), may be used in studying the relationship between
XX DNA sequence variations and human diseases, conditions, and responses to
XX drugs. SNPs are also useful as polymorphism markers for discovering genes
XX that cause or exacerbate certain diseases. SNPs are particularly useful
XX in the above respects as they are stable in populations, occur
```

```
CC frequently, and have lower mutation rates than other genome variations
CC such as repeating sequences. The detection and analysis of polymorphisms
CC in genes encoding drug metabolising enzymes allows the customisation of
CC drug therapies based upon the genetic profile of individual patients.
CC This would not only take the guesswork out of selecting the drug with the
CC greatest therapeutic effect for a particular patient, but would also
CC reduce the likelihood of adverse reactions, thereby increasing safety.
CC Methods of the invention are also useful in the drug discovery and
CC approval processes. For example, individuals could be selected for
CC clinical trials only if their genetic profiles indicate that they are
CC capable of responding to a particular drug or drug class, and previously
CC failed drug candidates could be revived if they were matched with more
CC appropriate patient populations. The methods, data and compositions of
CC the invention may therefore lead to an increase in the range of
CC possible drug targets and decreases in the number of adverse drug
CC reactions, failed drug trials, the time taken for a drug to be approved,
CC the length of time patients are on medication and the number of different
CC medications a patient needs to take before finding an effective therapy
XX
XX Sequence 41 BP; 7 A; 10 C; 14 G; 10 T; 0 U; 0 Other;
SQ
Query Match 3.3%; Score 33; DB 1; Length 41;
Best Local Similarity 87.8%; Pred. No. 4.4e+02;
Matches 36; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

643 CCCAGGCTGAGTGCAGTGGCCCATCTTGCTCACTGCA 683
DB 1 CCCAGGCTGAGTGCAGTGGCCCATCTTGCTCACTGCA 41

RESULT 235
AB243980/C
ID AB243980 standard; DNA; 41 BP.
XX
XX AB243980;
AC
XX
XX 26-JUN-2003 (first entry)
XX
XX Human glutathione-S-transferase MGST3 gene polymorphic site, #764.
XX
XX Human; drug metabolising enzyme; gene; drug metabolism; chromosome 1;
XX
XX polymorphic site; drug evaluation; drug screening; genotyping;
XX
XX genetic profiling; therapeutic customisation; adverse reaction;
XX
XX clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX variation replace(21,C)
XX /tag= a
XX /standard_name= "Single nucleotide polymorphism (SNP)"
XX
XX WO200252044-A2.
XX
XX 04-JUL-2002.
XX
XX 27-DEC-2001; 2001WO-JP011592.
XX
XX 27-DEC-2000; 2000JP-00399443.
XX
XX 02-MAY-2001; 2001JP-00135256.
XX
XX 27-AUG-2001; 2001JP-00256862.
XX
XX (RIKE ) RIKEN KK.
XX
XX Nakamura Y, Sekine A, Iida A, Salto S;
XX
XX WPI; 2002-583571/62.
XX
XX Identifying individuals having a polymorphism, useful for determining the
XX effectiveness or side effect of a drug or treatment protocol, comprises
XX detecting at least one polymorphism in the drug metabolizing enzyme
XX nucleic acid.
XX
```

PS Claim 23; Page 76; 2785pp; English.

XX Sequences AB243217-AB250887 represent polymorphic sites within genes  
XX encoding enzymes associated with drug metabolism. The invention relates  
XX to methods and compositions for identifying individuals who have at least  
XX one polymorphism in such drug metabolizing enzyme-encoding genes. The  
XX polymorphisms may be identified in a nucleic acid sample using probes or  
XX primers specific for a sequence selected from AB243217-AB250887 using a  
XX variety of detection assays, including hybridisation assays, nucleic acid  
XX arrays and PCR-based methods. The invention also encompasses methods of  
XX evaluating and screening drugs using genetic polymorphism data. Genetic  
XX polymorphisms (SNPs), may be used in studying the relationship between  
XX DNA sequence variations and human diseases, conditions, and responses to  
XX drugs. SNPs are also useful as polymorphism markers for discovering genes  
XX that cause or exacerbate certain diseases. SNPs are particularly useful  
XX in the above respects as they are stable in populations, occur  
XX frequently, and have lower mutation rates than other genome variations  
XX such as repeating sequences. The detection and analysis of polymorphisms  
XX in genes encoding drug metabolizing enzymes allows the customisation of  
XX drug therapies based upon the genetic profile of individual patients.  
XX This would not only take the guesswork out of selecting the drug with the  
XX greatest therapeutic effect for a particular patient, but would also  
XX reduce the likelihood of adverse reactions, thereby increasing safety.  
XX Methods of the invention are also useful in the drug discovery and  
XX approval processes. For example, individuals could be selected for  
XX clinical trials only if their genetic profiles indicate that they are  
XX capable of responding to a particular drug or drug class, and previously  
XX failed drug candidates could be revived if they were matched with more  
XX appropriate patient populations. The methods, data and compositions of  
XX the invention may therefore lead to an increase in the range of  
XX possible drug targets and decreases in the number of adverse drug  
XX reactions, failed drug trials, the time taken for a drug to be approved,  
XX the length of time patients are on medication and the number of different  
XX medications a patient needs to take before finding an effective therapy

XX Sequence 41 BP; 10 A; 9 C; 14 G; 8 T; 0 U; 0 Other;  
SQ  
Query Match 3.3%; Score 33; DB 1; Length 41;  
Best Local Similarity 87.8%; Pred. No. 4.4e+02;  
Matches 36; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 361 TCAGCAGTCCAGCTGCTCAGCTCCCAAGTCTGGCAT 401  
DB 41 TCAGCAGTCCAGCTGCTCAGCTCCCAAGTCTGGCAT 1

RESULT 236  
AB246914  
ID AB246914 standard; DNA; 41 BP.

XX AC AB246914;  
XX 26-JUN-2003 (first entry)  
XX Human ATP-binding cassette ABCA7 gene polymorphic site, #3698.

XX Human; drug metabolising enzyme; gene; drug metabolism; chromosome 19;  
XX polymorphic site; drug evaluation; drug screening; genotyping;  
XX genetic profiling; therapeutic customisation; adverse reaction;  
XX clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.

XX OS Homo sapiens.

XX Key Location/Qualifiers  
FH variation replace(21,A)

FT /tag= a  
FT /standard\_name= "Single nucleotide polymorphism (SNP)"  
FT replace(25,T)  
FT /tag= b

FT /standard\_name= "Single nucleotide polymorphism (SNP)"

XX WO200252044-A2.

XX 04-JUL-2002.

XX 27-DEC-2001; 2001WO-JP011592.

XX 27-DEC-2000; 2000JP-00399443.

XX 02-MAY-2001; 2001JP-00135256.

XX 27-AUG-2001; 2001JP-00256862.

XX (RIKE ) RIKEN KK.

XX Nakamura Y, Sekine A, Iida A, Saito S;  
XX WPI; 2002-583571/62.

XX Identifying individuals having a polymorphism, useful for determining the  
XX effectiveness or side effect of a drug or treatment protocol, comprises  
XX detecting at least one polymorphism in the drug metabolizing enzyme  
XX nucleic acid.

PS Claim 23; Page 129; 2785pp; English.

XX Sequences AB243217-AB250887 represent polymorphic sites within genes  
XX encoding enzymes associated with drug metabolism. The invention relates  
XX to methods and compositions for identifying individuals who have at least  
XX one polymorphism in such drug metabolizing enzyme-encoding genes. The  
XX polymorphisms may be identified in a nucleic acid sample using probes or  
XX primers specific for a sequence selected from AB243217-AB250887 using a  
XX variety of detection assays, including hybridisation assays, nucleic acid  
XX arrays and PCR-based methods. The invention also encompasses methods of  
XX evaluating and screening drugs using genetic polymorphism data. Genetic  
XX polymorphism data, particularly that relating to single nucleotide  
XX polymorphisms (SNPs), may be used in studying the relationship between  
XX DNA sequence variations and human diseases, conditions, and responses to  
XX drugs. SNPs are also useful as polymorphism markers for discovering genes  
XX that cause or exacerbate certain diseases. SNPs are particularly useful  
XX in the above respects as they are stable in populations, occur  
XX frequently, and have lower mutation rates than other genome variations  
XX such as repeating sequences. The detection and analysis of polymorphisms  
XX in genes encoding drug metabolizing enzymes allows the customisation of  
XX drug therapies based upon the genetic profile of individual patients.  
XX This would not only take the guesswork out of selecting the drug with the  
XX greatest therapeutic effect for a particular patient, but would also  
XX reduce the likelihood of adverse reactions, thereby increasing safety.  
XX Methods of the invention are also useful in the drug discovery and  
XX approval processes. For example, individuals could be selected for  
XX clinical trials only if their genetic profiles indicate that they are  
XX capable of responding to a particular drug or drug class, and previously  
XX failed drug candidates could be revived if they were matched with more  
XX appropriate patient populations. The methods, data and compositions of  
XX the invention may therefore lead to an increase in the range of  
XX possible drug targets and decreases in the number of adverse drug  
XX reactions, failed drug trials, the time taken for a drug to be approved,  
XX the length of time patients are on medication and the number of different  
XX medications a patient needs to take before finding an effective therapy

XX Sequence 41 BP; 6 A; 11 C; 14 G; 10 T; 0 U; 0 Other;  
SQ  
Query Match 3.3%; Score 33; DB 1; Length 41;  
Best Local Similarity 87.8%; Pred. No. 4.4e+02;  
Matches 36; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 639 GTCACCCAGGCTGAGTGCAGTGCAGCATCTTGGCTCACT 679  
DB 1 GTTCCCAAGGCTGAGTGCAGTGCAGCATCTTGGCTCACT 41

RESULT 237

AB247296/C  
ID AB247296 standard; DNA; 41 BP.

XX AC AB247296;  
XX

DT 26-JUN-2003 (first entry)  
XX Human ATP-binding cassette ABC1 gene polymorphic site, #4080.  
DE  
XX Human; drug metabolising enzyme; gene; drug metabolism; polymorphic site;  
KM drug evaluation; drug screening; genotyping; genetic profiling;  
KM therapeutic customisation; adverse reaction; clinical trial;  
KW drug approval; single nucleotide polymorphism; SNP; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT variation replace(21, G)  
FT /\*tag= a  
FT /standard\_name= "Single nucleotide polymorphism (SNP)"  
XX  
PN WO200252044-A2.  
XX  
PD 04-JUL-2002.  
XX  
PF 27-DEC-2001; 2001WO-JP011592.  
XX  
PR 27-DEC-2000; 2000JP-00399443.  
XX 02-MAY-2001; 2001JP-00135256.  
PR 27-AUG-2001; 2001JP-00256862.  
XX  
XX (RIKE ) RIKEN KK.  
XX  
PI Nakamura Y, Sekine A, Iida A, Saito S;  
XX  
DR WPI; 2002-583571/62.  
XX  
PT Identifying individuals having a polymorphism, useful for determining the  
PT effectiveness or side effect of a drug or treatment protocol, comprises  
PT detecting at least one polymorphism in the drug metabolizing enzyme  
PT nucleic acid.  
XX  
PS Claim 23; Page 138; 2785pp; English.  
XX  
XX Sequences AB243217-AB250887 represent polymorphic sites within genes  
XX encoding enzymes associated with drug metabolism. The invention relates  
XX to methods and compositions for identifying individuals who have at least  
XX one polymorphism in such drug metabolising enzyme-encoding genes. The  
XX polymorphisms may be identified in a nucleic acid sample using probes or  
XX primers specific for a sequence selected from AB243217-AB250887 using a  
XX variety of detection assays, including hybridisation assays, nucleic acid  
XX arrays and PCR-based methods. The invention also encompasses methods of  
XX evaluating and screening drugs using genetic polymorphism data. Genetic  
XX polymorphisms (SNPs), may be used in studying the relationship between  
XX DNA sequence variations and human diseases, conditions, and responses to  
XX drugs. SNPs are also useful as polymorphism markers for discovering genes  
XX that cause or exacerbate certain diseases. SNPs are particularly useful  
XX in the above respects as they are stable in populations, occur  
XX frequently, and have lower mutation rates than other genome variations  
XX such as repeating sequences. The detection and analysis of polymorphisms  
XX in genes encoding drug metabolising enzymes allows the customisation of  
XX drug therapies based upon the genetic profile of individual patients.  
XX This would not only take the guesswork out of selecting the drug with the  
XX greatest therapeutic effect for a particular patient, but would also  
XX reduce the likelihood of adverse reactions, thereby increasing safety.  
XX Methods of the invention are also useful in the drug discovery and  
XX approval processes. For example, individuals could be selected for  
XX clinical trials only if their genetic profiles indicate that they are  
XX capable of responding to a particular drug or drug class, and previously  
XX failed drug candidates could be revived if they were matched with more  
XX appropriate patient populations. The methods, data and compositions of  
XX the invention may therefore lead to an increase in the range of  
XX possible drug targets and decreases in the number of adverse drug  
XX reactions, failed drug trials, the time taken for a drug to be approved,  
XX the length of time patients are on medication and the number of different  
XX medications a patient needs to take before finding an effective therapy

SEQ Sequence 41 BP; 11 A; 12 C; 12 G; 6 T; 0 U; 0 Other;  
Query Match 3.3%; Score 33; DB 1; Length 41;  
Best Local Similarity 87.8%; Pred. No. 4.4e+02;  
Matches 36; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 369 TCCACCTGCTGAGCTCCCAAGCTGCTGATTCACAGCG 409  
DB 41 TCCACTGCTGCTGAGCTCCCAAGCTGCTGATTCACAGCT 1  
RESULT 238  
ABA94080  
ID ABA94080 standard; DNA; 41 BP.  
AC ABA94080;  
XX  
DT 08-MAY-2002 (first entry)  
XX  
DE Human multi-copper oxidase 12 probe 1 SEQ ID NO:8.  
XX  
XX Human; multi-copper oxidase 12; enzyme; cytosolic; haemostatic;  
XX virucide; immunomodulatory; antiinflammatory; gene therapy;  
XX malignant tumour; haemopathy; human immunodeficiency virus infection;  
XX HIV infection; immunological disease; inflammation; probe; ss.  
XX  
OS Homo sapiens.  
XX  
XX WO200196572-A1.  
XX  
PN 20-DEC-2001.  
XX  
PF 14-MAY-2001; 2001WO-CN000786.  
XX  
PR 19-MAY-2000; 2000CN-00115756.  
XX  
XX (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.  
XX  
PI Mao Y, Xie Y;  
XX  
DR WPI; 2002-075593/10.  
XX  
PT Multi-copper oxidase 12 and encoding polynucleotide, used in diagnosis  
PT and treatment of malignant tumors, hemopathy, human immunodeficiency  
PT virus infection, immunological diseases and inflammation.  
XX  
XX Example 7; Page 14; 31pp; Chinese.  
XX  
XX The present invention describes human multi-copper oxidase 12 (I). (I)  
XX has cytosolic, haemostatic, virucide, immunomodulatory and  
XX antiinflammatory activities. The polynucleotide (II) encoding (I) can be  
XX used in gene therapy. (I) and (II) can be used in the diagnosis and  
XX treatment of malignant tumour, haemopathy, human immunodeficiency virus  
XX (HIV) infection, immunological diseases and various inflammations. The  
XX present sequence represents a probe which is used in an example from the  
XX present invention  
XX  
SQ Sequence 41 BP; 6 A; 6 C; 14 G; 15 T; 0 U; 0 Other;  
Query Match 3.3%; Score 33; DB 1; Length 41;  
Best Local Similarity 87.8%; Pred. No. 4.4e+02;  
Matches 36; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 172 TTTTATAGTAGAGATGAGTTTCTCAGTTGTGAGGCT 212  
DB 1 TGTTTTATAGTAGAGGCGGTTTCCACCATGTTGTGAGGCT 41  
RESULT 239  
AAS15590  
ID AAS15590 standard; DNA; 41 BP.  
XX  
AC AAS15590;



```
XX 14-FEB-2002 (first entry)
XX
XX Human DNA mismatch repair protein 10, probe #1.
DE
XX Human; DNA mismatch repair protein 10; cytostatic; virucidal;
KW immunomodulatory; antiinflammatory; haemostatic; anti-HIV; inflammation;
KW human immunodeficiency virus; malignancy; haemopathy; infection;
KW immunological disease; probe; ss.
XX
OS Homo sapiens.
XX
XX MO200175100-A1.
XX
XX 11-OCT-2001.
XX
XX 19-MAR-2001; 2001WO-CN000337.
XX
XX 22-MAR-2000; 2000CN-00115057.
XX
XX (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
XX Mao Y, Xie Y;
XX
XX WPI; 2002-025860/03.
XX
XX New human DNA mismatch repair protein 10 for diagnosing and treating
PT malignancy, hemopathy, human immunodeficiency virus infection,
PT immunological diseases and inflammation.
XX
XX Example 6; Page 15; 36pp; Chinese.
XX
XX The invention relates to an isolated polypeptide of human DNA mismatch
CC repair protein 10. The polypeptide can be used for screening mimics,
CC agonists, antagonists or inhibitors, or in peptide fingerprinting
CC identification. The polynucleotide can be used as primers for nucleic
CC acid amplification reactions, as probes for hybridisation reactions, or
CC in producing gene chips or microarrays. Drug compositions, which contain
CC the polypeptide, polynucleotide, mimics, agonists, antagonists,
CC inhibitors and their preparations, can be used treatment and diagnosis of
CC diseases relating to the polypeptide. In particular, the polypeptide and
CC encoded polynucleotide are applicable in diagnosis and treatment of
CC malignancy, haemopathy, human immunodeficiency virus (HIV) infection,
CC immunological diseases and various inflammations. The present sequence
CC represents probe #1 used in Northern blot analysis of human DNA mismatch
CC repair protein 10
XX
XX Sequence 41 BP; 8 A; 10 C; 11 G; 12 T; 0 U; 0 Other;
SQ
Query Match 3.3%; Score 33; DB 1; Length 41;
Best Local Similarity 87.8%; Pred. No. 4.4e+02;
Matches 36; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Oy 200 TGTGGTCAGGCTGCTCGAAGCTCCGACCTCAGATGATC 240
Db 1 TGTGGTCAGACTGCTCTTGAACCTCCCAACGTCAGGTATC 41
RESULT 240
ADL64285
ID ADL64285 standard; DNA; 41 BP.
XX
XX ADL64285;
XX
XX 20-MAY-2004 (first entry)
DE Human single nucleotide polymorphism (SNP) #208.
XX
XX ss: human; single nucleotide polymorphism; SNP;
KW C1 S subcomponent protein; C1S; alanyl aminopeptidase protein; ANPEP;
KW meprin A beta protein; aminopeptidase P-like protein; XPN-PEPL;
KW tissue kallikrein protein; KKL1; aminopeptidase P protein; MEPLB;
KW soluble guanylate cyclase 1 alpha-2 subunit protein; GUCY1A2; haplotype;
```

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KW angiodema; angiodema-like disorder; paternity testing;
KW cardiovascular diseases; angina pectoris; hypertension; heart failure;
KW myocardial infarction; aneurysm; stroke; embolism; thrombosis;
KW coronary artery disease; arteriosclerosis; hypersensitivity;
KW haemodialysis; sepsis; inflammatory disease; inflammatory arthritis;
KW asthma; chronic obstructive pulmonary disease; cough reflex; allergy;
KW cancer; ANPEP.
XX
OS Homo sapiens.
XX
XX US2004033582-A1.
XX
XX 19-FEB-2004.
XX
XX 03-JUN-2003; 2003US-00453827.
XX
XX 03-JUN-2002; 2002US-0384980P.
XX
XX (EDMO/) EDMONDS M.
XX (HUI/) HUI L.
XX (PERR/) PERRONE M.
XX (POWE/) POWELL J R.
XX (RAMA/) RAMANATHAN C S.
XX (SWAN/) SWANSON B.
XX (TSUC/) TSUCHIHASHI Z.
XX (ZERR/) ZERRA K.
XX
XX Edmonds M, Hui L, Perrone M, Powell JR, Ramanathan CS, Swanson B;
XX Tsuchihashi Z, Zerba K;
XX
XX WPI; 2004-180052/17.
XX
XX New nucleic acid comprising a single nucleotide polymorphism at a
PT specific location, useful in paternity testing, genetic analysis or
PT diagnosing, preventing or treating cardiovascular diseases e.g.
PT angiodema or angina pectoris.
XX
XX Claim 3; SEQ ID NO 208; 376pp; English.
XX
XX The invention relates to an isolated nucleic acid (I) derived from a
CC human gene encoding a protein, such as the C1 S subcomponent protein
CC (C1S), the alanyl aminopeptidase protein (ANPEP), the meprin A, beta
CC kallikrein (MEPLB), the aminopeptidase P-like protein (XPN-PEPL), the tissue
CC kallikrein protein (KKL1), the membrane bound aminopeptidase P protein
CC (XNPEP2), or the soluble guanylate cyclase 1, alpha-2 subunit protein
CC (GUCY1A2). The nucleic acid comprises at least one polymorphic position,
CC including the alleles, reference alleles and alternate alleles of the
CC single nucleotide polymorphisms, listed in the specification. The
CC polymorphic position resides in a (non)coding position within the genomic
CC sequence of the gene. The polymorphic position residing in the translated
CC position results in a missense or silent mutation of the translated
CC product of the gene. The polymorphic position residing in a non-coding
CC position resides within the untranslated region or an intronic region of
CC the gene. Constructing haplotypes using the nucleic acids above further
CC comprises using the haplotypes to identify an individual for the presence
CC of a disease phenotype, and correlating the presence of the disease
CC phenotype with the haplotype. The disease phenotype is angiodema or an
CC angiodema-like disorder. The nucleic acids, primers and probes are
CC useful in phenotype correlations, paternity testing, medicine and genetic
CC analysis. The nucleic acids and polypeptides can be used in diagnosing,
CC preventing or treating cardiovascular diseases, e.g. angiodema, angina
CC pectoris, hypertension, heart failure, myocardial infarction, aneurysm,
CC stroke, embolism, thrombosis, coronary artery disease or
CC arteriosclerosis, hypersensitivity reactions during haemodialysis,
CC sepsis, inflammatory diseases, inflammatory arthritis, asthma, chronic
CC obstructive pulmonary disease, cough reflex, allergies, or cancer. The
CC present sequence represents a human single nucleotide polymorphism (SNP)
CC of the invention.
XX
XX Sequence 41 BP; 5 A; 14 C; 11 G; 11 T; 0 U; 0 Other;
SQ
Query Match 3.3%; Score 33; DB 1; Length 41;
Best Local Similarity 87.8%; Pred. No. 4.4e+02;
```



Matches 36; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 659 GGGGCAATCTGGCTCACTGCAACCTCTGCTCCGGAT 699  
DB 1 GTGGTGTATCTCGGCTCACTGCAACCTCTGCTCCAGAT 41

## RESULT 241

ADL64286

ID ADL64286 strand; DNA; 41 BP.

XX ADL64286;

XX 20-MAY-2004 (first entry)

DE Human single nucleotide polymorphism (SNP) #209.

XX ss; human; single nucleotide polymorphism; SNP;  
KW C1 S subcomponent protein; C1S; alanyl aminopeptidase protein; ANPEP;  
KW mepirin A beta protein; aminopeptidase P-like protein; XPN-PEP;  
KW tissue kallikrein protein; KLK1; aminopeptidase P protein; MEPIB;  
KW soluble guanylate cyclase 1 alpha-2 subunit protein; GUCY1A2; haploctype;  
KW angioedema; angioedema-like disorder; paternity testing; heart failure;  
KW cardiovascular diseases; angina pectoris; hypertension; stroke; embo-  
KW myocardial infarction; aneurysm; stroke; embolism; thrombosis;  
KW coronary artery disease; arteriosclerosis; hypersensitivity;  
KW haemodialysis; sepsis; inflammatory disease; inflammatory arthritis;  
KW asthma; chronic obstructive pulmonary disease; cough reflex; allergy;  
KW cancer; ANPEP.

XX Homo sapiens.

XX US2004033582-A1.

XX 19-FEB-2004.

XX 03-JUN-2003; 2003US-00453827.

XX 03-JUN-2002; 2002US-0384980P.

XX (EDMC/) EDMONDS M.

XX (HUI/) HUI L.

XX (PERR/) PERRONE M.

XX (POWE/) POWELL J R.

XX (RAMA/) RAMANATHAN C S.

XX (SWAN/) SWANSON B.

XX (TSUC/) TSUCHIHASHI Z.

XX (ZERR/) ZERBA K.

XX Edmonds M, Hui L, Perrone M, Powell JR, Ramanathan CS, Swanson B;

XX Tsuchihashi Z, Zerba K;

XX WPI; 2004-180052/17.

XX New nucleic acid comprising a single nucleotide polymorphism at a

XX PT specific location, useful in paternity testing, genetic analysis or

XX PT diagnosing, preventing or treating cardiovascular diseases e.g.

XX angioedema or angina pectoris.

XX Claim 3; SEQ ID NO 209; 376pp; English.

XX The invention relates to an isolated nucleic acid (I) derived from a

XX human gene encoding a protein, such as the C1 S subcomponent protein

XX (C1S), the alanyl aminopeptidase protein (ANPEP), the mepirin A, beta

XX protein (MEPIB), the aminopeptidase P-like protein (XPN-PEP), the tissue

XX kallikrein protein (KLK1), the membrane bound aminopeptidase P protein

XX (XPNPEP2), or the soluble guanylate cyclase 1, alpha-2 subunit protein

XX (GUCY1A2). The nucleic acid comprises at least one polymorphic position,

XX including the alleles, reference alleles and alternate alleles of the

XX single nucleotide polymorphisms, listed in the specification. The

XX polymorphic position resides in a (non) coding position within the genomic

XX sequence of the gene. The polymorphic position residing in a coding

XX position results in a missense or silent mutation of the translated

CC product of the gene. The polymorphic position residing in a non-coding  
CC position resides within the untranslated region or an intronic region of  
CC the gene. Constructing haplotypes using the nucleic acids above further  
CC comprises using the haplotypes to identify an individual for the presence  
CC of a disease phenotype, and correlating the presence of the disease  
CC phenotype with the haplotype. The disease phenotype is angioedema or an  
CC angioedema-like disorder. The nucleic acids, primers and probes are  
CC useful in phenotype correlations, paternity testing, medicine and genetic  
CC analysis. The nucleic acids and polypeptides can be used in diagnosing,  
CC preventing or treating cardiovascular diseases, e.g. angioedema, angina  
CC pectoris, hypertension, heart failure, myocardial infarction, aneurysm,  
CC stroke, embolism, thrombosis, coronary artery disease or  
CC arteriosclerosis, hypersensitivity reactions during haemodialysis,  
CC sepsis, inflammatory diseases, inflammatory arthritis, asthma, chronic  
CC obstructive pulmonary disease, cough reflex, allergies, or cancer. The  
CC present sequence represents a human single nucleotide polymorphism (SNP)  
CC of the invention.

SQ Sequence 41 BP; 11 A; 13 C; 8 G; 9 T; 0 U; 0 Other;

Query Match 3.3%; Score 33; DB 1; Length 41;

Best Local Similarity 87.8%; Pred. No. 4.4e+02;

Matches 36; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 557 AGCTGGACCAAGACATGACCACTACACCTGGCTAATT 597

DB 1 AGCTGGATTACAGACATGCCCCACACACCTGGCTAATT 41

## RESULT 242

ABZ48532

ID ABZ48532 strand; DNA; 40 BP.

XX ABZ48532;

XX 26-JUN-2003 (first entry)

XX Human oligopeptide transporter PEPT1 gene polymorphic site, #5315.

XX Human; drug metabolizing enzyme; gene; drug metabolism; polymorphic site;

XX drug evaluation; drug screening; genotyping; genetic profiling;

XX therapeutic customisation; adverse reaction; clinical trial;

XX drug approval; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

XX FT variation /\*tag= a

XX FT MO200252044-A2.

XX PD 04-JUL-2002.

XX 27-DEC-2001; 2001WO-DP011592.

XX 27-DEC-2000; 2000JP-00399443;

XX PR 02-MAY-2001; 2001JP-00135256.

XX PR 27-AUG-2001; 2001JP-00256862.

XX (RIKE ) RIKEN KK.

XX Nakamura Y, Sekine A, Iida A, Saito S;

XX WPI; 2002-583571/62.

XX Identifying individuals having a polymorphism, useful for determining the

XX effectiveness or side effect of a drug or treatment protocol, comprises

XX PT detecting at least one polymorphism in the drug metabolizing enzyme

XX PT nucleic acid.

XX Claim 23; Page 168; 2785pp; English.

CC Sequences AB243217-AB250887 represent polymorphic sites within genes  
 CC encoding enzymes associated with drug metabolism. The invention relates  
 CC to methods and compositions for identifying individuals who have at least  
 CC one polymorphism in such drug metabolizing enzyme-encoding genes. The  
 CC polymorphisms may be identified in a nucleic acid sample using probes or  
 CC primers specific for a sequence selected from AB243217-AB250887 using a  
 CC variety of detection assays, including hybridization assays, nucleic acid  
 CC arrays and PCR-based methods. The invention also encompasses methods of  
 CC evaluating and screening drugs using genetic polymorphism data. Genetic  
 CC polymorphism data, particularly that relating to single nucleotide  
 CC polymorphisms (SNPs), may be used in studying the relationship between  
 CC DNA sequence variations and human diseases, conditions, and responses to  
 CC drugs. SNPs are also useful as polymorphism markers for discovering genes  
 CC that cause or exacerbate certain diseases. SNPs are particularly useful  
 CC in the above respects as they are stable in populations, occur  
 CC frequently, and have lower mutation rates than other genome variations  
 CC such as repeating sequences. The detection and analysis of polymorphisms  
 CC in genes encoding drug metabolizing enzymes allows the customization of  
 CC drug therapies based upon the genetic profile of individual patients.  
 CC This would not only take the guesswork out of selecting the drug with the  
 CC greatest therapeutic effect for a particular patient, but would also  
 CC reduce the likelihood of adverse reactions, thereby increasing safety.  
 CC Methods of the invention are also useful in the drug discovery and  
 CC approval processes. For example, individuals could be selected for  
 CC clinical trials only if their genetic profiles indicate that they are  
 CC capable of responding to a particular drug or drug class, and previously  
 CC failed drug candidates could be revived if they were matched with more  
 CC appropriate patient populations. The methods, data and compositions of  
 CC the invention may therefore lead to an increase in the range of  
 CC possible drug targets and decreases in the number of adverse drug  
 CC reactions, failed drug trials, the time taken for a drug to be approved,  
 CC the length of time patients are on medication and the number of different  
 CC medications a patient needs to take before finding an effective therapy

SQ Sequence 40 BP; 9 A; 7 C; 11 G; 13 T; 0 U; 0 Other;

Query Match 3.2%; Score 32; DB 1; Length 40;  
 Best Local Similarity 87.5%; Pred. No. 4.9e+02;  
 Matches 35; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1076 TATTTTCATTAGAGCGGGGTTTCACCATATTTGTCAGGC 1115  
 DB 1 TATTTTATAGTAGAGCGGGGTTTCACCATATTTGTCAGGC 40

RESULT 243

AAQ45257/c  
 ID AAQ45257 standard; DNA; 35 BP.

AC AAQ45257;

DT 25-MAR-2003 (revised)

DT 28-OCT-1994 (first entry)

XX Alu primer PDJ34 to amplify Yeast Artificial Chromosome DNA.

XX Yeast Artificial Chromosome; YAC; polymerase chain reaction; PCR;

XX sequence tagged site; genetic disorder; diagnosis; abnormality;

XX Prader-Willi; Angelman; Beckwith-Wiedemann; syndrome; ss.

XX Synthetic.

XX WO9406936-A1.

XX 31-MAR-1994.

XX 10-SEP-1993; 93WO-US008501.

XX 11-SEP-1992; 92US-00943639.

XX (BAYU ) BAYLOR COLLEGE MEDICINE.

XX Althart SD, Multirangura A, Ledbetter DH;

XX WPI; 1994-118484/14.  
 XX Diagnosis of genetic disorders associated with chromosomal abnormalities  
 XX and uniparental disomy, e.g. Prader-Willi/Angelman syndrome - using in  
 XX situ hybridization using probes spanning the IR4-3R or GABRB3 regions.  
 XX Example 5; Page 32; 91pp; English.

XX The Alu primers PDJ34 and 2484 (AAQ45257 and AAQ45258) were used to  
 CC amplify DNA from yeast artificial chromosomes as part of a cloning  
 CC procedure to isolate probes for specific chromosomal abnormalities. In  
 CC particular, probes to diagnose Prader-Willi/Angelman Syndrome were  
 CC identified. The majority of PWS/Angelman patients are deleted for a  
 CC common set of markers including MU34, IR4-3R, TD189-1 and TD3-21.  
 CC (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 35 BP; 5 A; 9 C; 8 G; 5 T; 0 U; 8 Other;

Query Match 3.2%; Score 31.8; DB 1; Length 35;  
 Best Local Similarity 77.1%; Pred. No. 4.5e+02;  
 Matches 27; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

OY 643 CCCAGCTGAGTGTGAGTGGCGCAATCTTGCTCA 677  
 DB 35 CCCAGCTGAGTGTGAGTGTGAGTGGCGCAATCTTGCTCA 1

RESULT 244

ABA93847/c  
 ID ABA93847 standard; DNA; 35 BP.

AC ABA93847;

DT 02-MAY-2002 (first entry)

XX Human GASCL PCR primer SEQ ID NO:5.

XX Human; GASCL; gene amplified in squamous cell carcinoma 1; cancer;

XX chromosome 9; Chromosome 9p23-24; cell differentiation; gene therapy;

XX cell proliferation; PCR primer; ss.

XX Homo sapiens.

XX WO200196566-A1.

XX 20-DEC-2001.

XX 12-JUN-2001; 2001WO-JP004959.

XX 12-JUN-2000; 2000JP-00174946.

XX (SAKA ) OTSUKA PHARM CO LTD.

XX Inazawa J, Imoto I;

XX WPI; 2002-090209/12.

XX Gene GASCL amplified in squamous cell carcinoma and its expression

XX product for diagnosis investigation and treatment of disorders involving

XX cell proliferation such as cancer.

XX Example 1; Page 77; 82pp; Japanese.

XX The present invention describes human GASCL (gene amplified in squamous  
 CC cell carcinoma 1). GASCL has been located to the p23-24 region of human  
 CC chromosome 9. GASCL can be used in the diagnosis and investigation of  
 CC diseases with which cell differentiation and proliferation are  
 CC associated, such as cancer. It can also be used in gene therapy of these  
 CC diseases, and screening substances for their ability to modify the  
 CC expression of GASCL and for use as drugs. The present sequence represents  
 CC a PCR primer for human GASCL, which is used in an example from the  
 CC present invention

XX Sequence 35 BP; 5 A; 9 C; 8 G; 5 T; 0 U; 8 Other;  
SQ

Query Match 3.2%; Score 31.8; DB 1; Length 35;  
Best Local Similarity 77.1%; Pred. No. 4.5e+02;  
Matches 27; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 643 CCCAGGCTGAGTGCAGTGGCCCAATCTTGCTCA 677  
DB 35 CCCAGGCTGAGTGCAGTGGCCCAATCTTGCTCA 1

RESULT 245  
AAQ27392/C  
ID AAQ27392 standard; DNA; 35 BP.  
XX  
XX AAQ27392;  
AC  
XX 25-MAR-2003 (revised)  
DT 27-JAN-1993 (first entry)  
XX  
XX Inter-Alu specific primer PDU34.  
DE  
XX Polymerase chain reaction; PCR; repetitive element; ss.  
XX  
XX Synthetic.  
OS  
XX MO9213101-A1.  
PN  
XX 06-AUG-1992.  
PD  
XX  
XX 24-JAN-1992; 92MO-NL000018.  
PF  
XX  
XX 25-JAN-1991; 91NL-00000132.  
PR  
XX (INGE-) INGENY BV.  
PA  
XX Uiterlinden AG, Vrijg J;  
PI  
XX MPI; 1992-284683/34.  
DR  
XX  
XX Detection of genetic variation by 2-D electrophoresis of fragments - and  
PT hybridisation with labelled probes, carried out on fragments consisting  
PT of inter-repeat sequences generated by PCR.  
XX  
XX  
PS Claim 6; Page 6; 3pp; English.  
XX  
XX Primer PDU34 is one of several primers which are preferred for use in  
CC amplifying inter-Alu regions of DNA. The amplified fragments are then  
CC subjected to 2-D electrophoresis on the basis of length and differences  
CC in base sequence. The resulting separation pattern is transferred to a  
CC filter for screening with a probe. The method can be used to detect  
CC genetic variation. See AAQ27389-Q27404 and AAQ33141-Q33144. (Updated on  
CC 25-MAR-2003 to correct FN field.)  
XX  
XX  
SQ Sequence 35 BP; 6 A; 12 C; 11 G; 5 T; 0 U; 1 Other;  
XX

Query Match 3.2%; Score 31.4; DB 1; Length 35;  
Best Local Similarity 91.4%; Pred. No. 4.7e+02;  
Matches 32; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 643 CCCAGGCTGAGTGCAGTGGCCCAATCTTGCTCA 677  
DB 35 CCCAGGCTGAGTGCAGTGGCCCAATCTTGCTCA 1

RESULT 246  
ADE14248/C  
ID ADE14248 standard; DNA; 32 BP.  
XX  
XX ADE14248;  
AC  
XX 29-JAN-2004 (first entry)  
DT

XX Optineurin promoter motif, repeat element or regulatory region #357.  
DE  
XX Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;  
XX SNP; glaucoma; progressive ocular hypertensive disorder;  
KW glaucoma related disorder; motif; repeat element; regulatory region.  
XX  
XX Homo sapiens.  
OS  
XX US2003190617-A1.  
PN  
XX 09-OCT-2003.  
PD  
XX 06-MAR-2002; 2002US-00091281.  
PF  
XX 06-MAR-2002; 2002US-00091281.  
PR  
XX (SIEE/) SI E.  
PA (RAYM/) RAYMOND V.  
PA (MORI/) MORISSETTE J.  
XX  
XX Raymond V, Morissette J, Si E;  
PI  
XX MPI; 2003-864168/80.  
DR  
XX  
XX New nucleic acid sequences of the optineurin gene are useful to detect  
PT polymorphisms particularly single nucleotide polymorphisms in the  
PT optineurin promoter to diagnose, prognose and treat glaucoma and related  
PT disorders.  
XX  
XX  
PS Claim 11; SEQ ID NO 359; 159pp; English.  
XX  
XX The invention relates to an isolated nucleic acid (NI) comprising at  
CC least 20 but not more than 1500 consecutive nucleotides of the optineurin  
CC promoter appearing as ADE13890. Also included are the optineurin promoter  
CC operably linked to a heterologous nucleic acid, a nucleic acid capable of  
CC detecting a single nucleotide polymorphism (SNP) in the optineurin  
CC promoter, a host cell comprising the promoter operably linked to a  
CC heterologous sequence, diagnosing or prognosing glaucoma in a sample  
CC obtained from a cell or bodily fluid (comprising detecting a polymorphism  
CC in a promoter region of the optineurin gene, associated with a glaucoma  
CC phenotype), detecting a SNP sequence variation in a sample containing  
CC DNA, detecting the presence of an optineurin promoter sequence variation  
CC in a sample containing DNA, determining the presence or increased  
CC susceptibility to glaucoma or to a progressive ocular hypertensive  
CC disorder resulting in loss of visual field in a patient (or the severity  
CC or progression of glaucoma in a patient, comprising providing  
CC amplification reaction primers that direct amplification of a selected  
CC nucleic acid region containing the variation within the optineurin  
CC promoter and amplifying the DNA) and detecting a polymorphism (comprising  
CC obtaining a sample containing human genomic DNA, providing a nucleic acid  
CC capable of detecting a SNP located within an optineurin promoter, and  
CC detecting the polymorphism). The invention is used to diagnose and  
CC prognose glaucoma and also to treat glaucoma related disorders. The  
CC present sequence is an optineurin promoter motif, repeat element or  
CC putative regulatory region.  
XX  
XX  
SQ Sequence 32 BP; 5 A; 12 C; 8 G; 7 T; 0 U; 0 Other;  
XX

Query Match 3.1%; Score 30.4; DB 1; Length 32;  
Best Local Similarity 96.9%; Pred. No. 5e+02;  
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 860 AAGTGTGGGATTACAGGCGTGAGCCAGCAGC 891  
DB 32 AAGTGTGGGATTACAGGCGTGAGCCAGCAGC 1

RESULT 247  
AAH91142/C  
ID AAH91142 standard; DNA; 36 BP.  
XX  
XX AAH91142;  
AC

```
XX 09-OCT-2001 (first entry)
DT
XX
DE Human inflammatory bowel disease associated polymorphic site #217.
XX
XX Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
XX single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
XX chromosome 5q31-33; forensic test; gene therapy; ds.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX misc_feature 19
XX /tag= a
XX /note= "SNP, optionally G or T at this position"
XX
XX WO200142511-A2.
XX
XX 14-JUN-2001.
XX
XX 11-DEC-2000; 2000WO-US033632.
XX
XX 10-DEC-1999; 99US-0170257P.
XX 10-APR-2000; 2000US-0196046P.
XX
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.
XX
XX Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;
XX WPI; 2001-367874/38.
XX
XX Testing for the presence of polymorphisms associated with inflammatory
XX bowel disease, using a hybridization assay.
XX
XX Claim 1; Page 48; 463pp; English.
XX
XX The present invention describes a method for detecting the presence of
XX polymorphisms associated with inflammatory bowel diseases such as
XX ulcerative colitis and Crohn's disease. The methods can be used to detect
XX the presence of genetic polymorphisms associated with inflammatory bowel
XX disease and correlating their occurrence with disease states. They may be
XX used in this way for phenotypic correlations, forensics, paternity
XX testing, medicine and genetic analysis. The present sequence is a
XX polymorphic site described in the exemplification of the invention.
XX
XX Sequence 36 BP; 5 A; 10 C; 13 G; 7 T; 0 U; 1 Other;
SQ
XX
XX Query Match 3.1%; Score 30.2; DB 1; Length 36;
XX Best Local Similarity 88.9%; Pred. No. 5.5e+02;
XX Matches 32; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1032 AGCTGGATTACGGGACCTGCCACACACCCCGCT 1067
DB 36 AGCTGGATTACAGGCANCTGCCACCACGCCCGGCT 1
XX
XX RESULT 248
XX AC084462
XX ID AC084462 standard; DNA; 30 BP.
XX
XX AC084462;
XX
XX 28-AUG-2003 (first entry)
XX
XX NTP peptide encoding sequence #9.
XX
XX Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;
XX neural thread protein; NTP; tumour; ds.
XX
XX Unidentified.
XX
XX WO2003008443-A2.
XX
XX
```

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XX 30-JAN-2003.
PD
XX 19-JUN-2002; 2002WO-CA001105.
XX
XX 19-JUN-2001; 2001US-0306150P.
XX 19-JUN-2001; 2001US-0306151P.
XX 16-NOV-2001; 2001US-0331477P.
XX
XX (NYMO-) NYMOX CORP.
XX
XX Averbach PA;
XX
XX WPI; 2003-247999/24.
XX P-PSDB; ABR63257.
XX
XX Novel neural thread protein peptide, referred as cell death peptide,
XX useful for treating prostatic hyperplasia, psoriasis, eczema, dermatosis,
XX atherosclerosis, cosmetic modification to skin, throat, mouth, muscle.
XX
XX Disclosure; Page 17; 77pp; English.
XX
XX The present invention relates to a neural thread protein (NTP) peptide
XX referred to as cell death peptide. Thought to be cytostatic,
XX antibacterial, immunosuppressive and antiinflammatory. It is useful for
XX treating a condition in a patient requiring removal or destruction of
XX cells, for treating a condition such as benign or malignant tumor,
XX inflammatory disease, autoimmune disease and infectious disease. The
XX peptide useful for treatment is derived from the amino acid sequence for
XX a pancreatic thread protein. The peptide is conjugated, linked or bound
XX to a molecule chosen from antibody or its fragment, antibody-like binding
XX molecule, where the molecule has a higher affinity for binding to a tumor
XX or other target than binding to other cells. Treatment using NTP peptides
XX can remove benign tumors with less risk and fewer of the undesirable side
XX effects of surgery. The present sequence is an NTP encoding sequence
XX
XX Sequence 30 BP; 6 A; 9 C; 10 G; 5 T; 0 U; 0 Other;
SQ
XX
XX Query Match 3.0%; Score 30; DB 1; Length 30;
XX Best Local Similarity 100.0%; Pred. No. 5e+02;
XX Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 720 AGCTCTCTAGTACTGGGACTACAGGCGC 749
DB 1 AGCTCTCTAGTACTGGGACTACAGGCGC 30
XX
XX RESULT 249
XX ADE14029/C
XX ID ADE14029 standard; DNA; 32 BP.
XX
XX ADE14029;
XX
XX 29-JAN-2004 (first entry)
XX
XX Optineurin promoter motif, repeat element or regulatory region #138.
XX
XX Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;
XX SNP; glaucoma; progressive ocular hypertensive disorder;
XX glaucoma related disorder; motif; repeat element; regulatory region.
XX
XX Homo sapiens.
XX
XX US2003190617-A1.
XX
XX 09-OCT-2003.
XX
XX 06-MAR-2002; 2002US-00091281.
XX 06-MAR-2002; 2002US-00091281.
XX
XX (SIEE/) SI E.
XX (RAYM/) RAYMOND V.
XX
XX
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PA (MORI/) MORISSETTE J.  
XX  
PI Raymond V, Morissette J, Si E;  
XX  
XX WPI; 2003-864168/80.  
DR  
XX New nucleic acid sequences of the optineurin gene are useful to detect  
PT polymorphisms particularly single nucleotide polymorphisms in the  
PT optineurin promoter to diagnose, prognose and treat glaucoma and related  
PT disorders.  
XX  
PS Claim 11; SEQ ID NO 140; 159pp; English.  
XX  
XX The invention relates to an isolated nucleic acid (NI) comprising at  
CC least 20 but not more than 1500 consecutive nucleotides of the optineurin  
CC promoter appearing as ABE13890. Also included are the optineurin promoter  
CC operably linked to a heterologous nucleic acid, a nucleic acid capable of  
CC detecting a single nucleotide polymorphism (SNP) in the optineurin  
CC promoter, a host cell comprising the promoter operably linked to a  
CC heterologous sequence, diagnosing or prognosing glaucoma in a sample  
CC obtained from a cell or bodily fluid (comprising detecting a polymorphism  
CC in a promoter region of the optineurin gene, associated with a glaucoma  
CC phenotype), detecting the presence of a SNP sequence variation in a sample containing  
CC DNA, detecting the presence of an optineurin promoter sequence variation  
CC in a sample containing DNA, determining the presence or increased  
CC susceptibility to glaucoma or to a progressive ocular hypertensive  
CC disorder resulting in loss of visual field in a patient (or the severity  
CC or progression of glaucoma in a patient, comprising providing  
CC amplification reaction primers that direct amplification of a selected  
CC nucleic acid region containing the variation within the optineurin  
CC promoter and amplifying the DNA) and detecting a polymorphism (comprising  
CC obtaining a sample containing human genomic DNA, providing a nucleic acid  
CC capable of detecting a SNP located within an optineurin promoter, and  
CC detecting the polymorphism). The invention is used to diagnose and  
CC prognose glaucoma and also to treat glaucoma related disorders. The  
CC present sequence is an optineurin promoter motif, repeat element or  
CC putative regulatory region.  
XX  
SQ Sequence 32 BP; 5 A; 11 C; 9 G; 7 T; 0 U; 0 Other;  
XX  
Query Match 3.0%; Score 29.4; DB 1; Length 32;  
Best Local Similarity 96.8%; Pred. No. 5.5e+02;  
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
QY 860 AAGTCTGGATTACAGCGGTGAGCCACGAC 890  
DB 32 AAGTCTGGATTACAGCGGTGAGCCACGAC 2  
XX  
RESULT 250  
AAQ73572  
ID AAQ73572 standard; DNA; 31 BP.  
XX  
XX AAQ73572;  
AC  
XX 25-MAR-2003 (revised)  
DT 25-JUN-1995 (first entry)  
XX  
XX Enhancer element er-4 conserved basepair sequence.  
XX  
XX Enhancer element; carcinoma; tumor; cancer; SLP1 gene;  
KW secretory leukoprotease-inhibitor gene; cytokeratin gene-8; ss.  
XX  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH misc\_difference 14  
FT /\*tag= a  
FT /\*tag= purine  
FT misc\_difference 24  
FT /\*tag= b  
FT /\*tag= pyrimidine  
XX

PN M09421118-A1.  
XX  
XX 29-SEP-1994.  
PD  
XX 24-MAR-1994; 94WO-US003197.  
XX  
XX 24-MAR-1993; 93US-00035435.  
XX  
XX (UABR-) UAB RES FOUND.  
PA  
XX Garver RI, Sorscher EJ;  
PI  
XX WPI; 1994-316537/39.  
DR  
XX DNA construct for treating human carcinoma - includes a cancer-  
PT therapeutic gene under the control of a promoter and a gp. of enhancer  
PT sequences.  
XX  
PS Claim 1; Fig 6; 54pp; English.  
XX  
XX This enhancer element is part of a DNA construct used for treating human  
CC carcinoma which contains a cancer therapeutic protein under the control  
CC of a promoter and 3 enhancer sequences in a specific 5'-3' order. This  
CC enhancer element is derived from the flanking region of the human  
CC epithelial cell cytokeratin-8 gene. (Updated on 25-MAR-2003 to correct PN  
CC field.)  
XX  
SQ Sequence 31 BP; 6 A; 10 C; 8 G; 5 T; 0 U; 2 Other;  
XX  
Query Match 2.9%; Score 29; DB 1; Length 31;  
Best Local Similarity 93.5%; Pred. No. 5.7e+02;  
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
XX  
QY 378 CTCAGCTCCCAAGTCTGGATTACAGGC 408  
DB 1 CTCAGCTCCCAAGTCTGGATTACAGGC 31  
XX  
RESULT 251  
AAA04659  
ID AAA04659 standard; DNA; 29 BP.  
XX  
XX AAA04659;  
AC  
XX 22-MAY-2000 (first entry)  
DT  
XX Polymorphic fragment of hypertension associated gene TBXA2R.  
DB  
XX  
XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;  
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;  
KW Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;  
KW polycystic kidney disease; von Willebrand's disease; forensic; human;  
KW tuberosus sclerosis; hereditary hemorrhagica telangiectasia;  
KW familial colonic polyposis; osteogenesis imperfecta; porphyria;  
KW Ehlers-Danlos syndrome; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX EP955382-A2.  
PN  
XX 10-NOV-1999.  
PD  
XX 07-MAY-1999; 99EP-00250150.  
XX  
XX 07-MAY-1998; 98US-0084641P.  
PR  
XX 03-MAY-1999; 99US-00304232.  
XX  
XX (AFRY-) AFFYMETRIX INC.  
PA (UYCA-) UNIV CASE WESTERN RESERVE.  
XX  
XX Fan JB, Chakravarti A, Haisuka MK;  
PI  
XX WPI; 2000-107928/10.  
DR

XX Novel nucleic acids containing polymorphisms used in the diagnosis of  
PT hypertension.  
PS Claim 1; Page 43; 53pp; English.  
XX The invention provides polymorphic fragments of genes associated with  
CC hypertension. The nucleic acids including the polymorphic sites can be  
CC used as probes or primers for expressing variant proteins. Detection of  
CC the polymorphisms is useful in designing prophylactic and therapeutic  
CC regimes customized to underlying abnormalities. The polymorphisms can be  
CC used for association studies for hypertension, and in hypertension  
CC diagnostic assays. Where the polymorphisms have strong correlation with  
CC hypertension, within a gene, they are likely to have a causative role in  
CC hypertension. This information can be used to find the precise role of a  
CC polymorphism in the disease, and this can be used to identify potential  
CC drugs which combat the disease. The polymorphisms can be tested for  
CC association with other diseases e.g. agammaglobulinemia, diabetes  
CC insipidus, Leisch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich  
CC syndrome, Fabry's disease, familial hypercholesterolemia, polycystic  
CC kidney disease, hereditary spherocytosis, von Willebrand's disease,  
CC tuberous sclerosis, hereditary hemorrhagica telangiectasia, familial  
CC colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and  
CC acute intermittent porphyria. The polymorphic forms can also be used in  
CC forensics to identify individuals  
XX Sequence 29 BP; 5 A; 8 C; 10 G; 5 T; 0 U; 1 Other;  
SQ  
Query Match 2.8%; Score 27.6; DB 1; Length 29;  
Best Local Similarity 96.4%; Pred. No. 6.3e+02;  
Matches 27; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Gy 643 CCCAGGCTGAGTGCAGTGGCCATCT 670  
Db 1 CCCAGGCTGAGTGCAGTGGCCATCT 28  
RESULT 252  
AAH37977/C  
ID AAH37977 standard; DNA; 29 BP.  
XX AAH37977;  
AC  
XX 14-AUG-2001 (first entry)  
DT  
XX SNP specific upper PCR primer SEQ ID 773.  
DE  
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
KW SNP; genotyping; agammaglobulinemia; diabetes insipidus; cancer;  
KW Leisch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolemia;  
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
KW inflammation; forensic investigation; paternity analysis; PCR primer; ss.  
XX Homo sapiens.  
OS  
XX MO200129262-A2.  
PN  
XX 26-APR-2001.  
PD  
XX 13-OCT-2000; 2000WO-US028436.  
PF  
XX 15-OCT-1999; 99US-0160096P.  
PR  
XX (ORCH-) ORCHID BIOSCIENCES INC.  
PA  
XX Picoult-Newburg L, Fohl M;  
PI  
XX MPI, 2001-290930/30.  
DR  
XX New genotyping oligonucleotide, useful for detecting the presence,  
PT absence or identity of single polynucleotide polymorphism in a nucleic  
PT acid sample.

XX Claim 1; Page 53; 83pp; English.  
PS Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
XX primer extension (SNPE) primers, and the sequences of regions flanking  
CC sites of single nucleotide polymorphisms SNPs. The present invention  
CC includes kits for determining the presence or absence of a SNP, using the  
CC oligonucleotides of the invention. The PCR primers are used to amplify a  
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.  
CC The oligonucleotides are useful for genotyping a nucleic acid sample by  
CC performing a single-nucleotide primer extension reaction. The  
CC oligonucleotides are useful for determining the presence, absence or  
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
CC assess by association analysis the genotype of an individual or group of  
CC individuals, having a pathological phenotypic trait suspected of being  
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
CC agammaglobulinemia, diabetes insipidus, Leisch-Nyhan syndrome, muscular  
CC dystrophy, familial hypercholesterolemia, polycystic kidney disease,  
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
CC traits also include symptoms of or susceptibility to multifactorial  
CC diseases of which a component is or may be genetic such as autoimmune  
CC diseases, including, rheumatoid arthritis, multiple sclerosis,  
CC inflammation, cancer, nervous system diseases and infection by pathogenic  
CC microorganism. The method is also useful in forensic investigations and  
CC paternity analysis. The present sequence represents a PCR primer specific  
CC for a human SNP containing DNA sequence  
XX Sequence 29 BP; 12 A; 7 C; 3 G; 7 T; 0 U; 0 Other;  
SQ  
Query Match 2.8%; Score 27.4; DB 1; Length 29;  
Best Local Similarity 96.6%; Pred. No. 6.4e+02;  
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Gy 774 GTATTTTAGTAGAGATGGGTTCCACCAT 802  
Db 29 GTATTTTAGTAGAGATGGGTTCCACCAT 1  
RESULT 253  
AAH06467  
ID AAH06467 standard; DNA; 31 BP.  
XX AAH06467;  
AC  
XX 31-MAR-1999 (first entry)  
DT  
XX Human biallelic polymorphic DNA fragment SGC34924.  
DE  
XX Polymorphism; biallelic; paternity testing; forensic; genetic mapping;  
KW phenotypic typing; medication; disease; marker; human; ss.  
KW Homo sapiens.  
OS  
XX MO9858529-A2.  
PN  
XX 30-DEC-1998.  
PD  
XX 22-JUN-1998; 98WO-US012930.  
PF  
XX 24-JUN-1997; 97US-0050594P.  
PR  
XX (AFFY-) AFFYMETRIX INC.  
PA  
XX Lipshutz RJ, Chee M, Fan J, Berno A;  
PI  
XX MPI; 1999-080963/07.  
DR  
XX New nucleic acid segments containing polymorphic sites - used for, e.g.  
PT detecting a disease phenotype, in forensics, paternity testing or genetic  
PT mapping of phenotypic traits.  
XX Claim 1; Page 29; 61pp; English.

CC Sequences AAX06101-X06558 represent human DNA fragments which contain  
CC diallelic polymorphic markers. The base occupying the polymorphic site is  
CC indicated by the appropriate IUPAC-IUB ambiguity code. These fragments  
CC can be used in a method for determining polymorphic forms in an  
CC individual. The invention further provides computer-readable storage  
CC medium for storing data for access by an application programme being  
CC executed on a data processing system. Such a method comprises a data  
CC structure stored in the computer-readable storage medium, the data  
CC structure including information resident in a database used by the  
CC application programme and including records, each record comprising  
CC information identifying a polymorphism shown in the above sequences. The  
CC products and methods can be used for analysing polymorphic sites in  
CC individuals for testing for the presence of a disease phenotype or in  
CC forensics, paternity testing or genetic mapping of phenotypic traits.  
CC They can also be used for the production of polypeptides expressed by  
CC variant genes and for the production of transgenic animals. The nucleic  
CC acid segments can also be used in the manufacture of medicaments for the  
CC treatment or prophylaxis of diseases

XX Sequence 31 BP; 8 A; 9 C; 8 G; 5 T; 0 U; 1 Other;

Query Match 2.8%; Score 27.4; DB 1; Length 31;  
Best Local Similarity 90.3%; Pred. No. 6.7e+02;  
Matches 28; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 863 TCGTGGATTACAGCGGTGAGCCACCCGCC 893  
DB 1 TCGTAGATTACAGGTGTGAGCCACCCACC 31

RESULT 254

AAQ27389  
ID AAQ27389 standard; DNA; 32 BP.

XX AAQ27389;

DT 25-MAR-2003 (revised)

PT 27-JAN-1993 (first entry)

XX Inter-Alu specific primer PDJ33A.

XX Polymerase chain reaction; PCR; repetitive element; ss.

XX Synthetic.

XX MO9213101-Al.

XX 06-AUG-1992.

XX 24-JAN-1992; 92WO-NL000018.

XX 25-JAN-1991; 91NL-00000132.

XX (INGE-) INGENY BV.

XX Ulfterlinden AG, Vißg J;

XX WPI; 1992-284683/34.

XX Detection of genetic variation by 2-D electrophoresis of fragments - and  
XX hybridisation with labelled probes, carried out on fragments consisting  
XX of inter-repeat sequences generated by PCR.

XX Claim 6; Page 6; 31pp; English.

XX Primer PDJ33A is one of several primers which are preferred for use in  
XX amplifying inter-Alu regions of DNA. The amplified fragments are then  
XX subjected to 2-D electrophoresis on the basis of length and differences  
XX in base sequence. The resulting separation pattern is transferred to a  
XX filter for screening with a probe. The method can be used to detect  
XX genetic variation. See also AAQ27390-Q27404 and AAQ33141-Q33144. (Updated  
XX on 25-MAR-2003 to correct PN field.)

XX Sequence 32 BP; 7 A; 9 C; 10 G; 6 T; 0 U; 0 Other;

Query Match 2.8%; Score 27.4; DB 1; Length 32;  
Best Local Similarity 96.6%; Pred. No. 6.9e+02;  
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 379 TCAGCTCCCAAGTGTGGATTACAG 407  
DB 4 TCGGCTCCCAAGTGTGGATTACAG 32

RESULT 255

AD814206/c  
ID AD814206 standard; DNA; 32 BP.

XX AD814206;

DT 29-JAN-2004 (first entry)

XX Optineurin promoter motif, repeat element or regulatory region #315.

XX Human; optineurin; de; ophthalmological; single nucleotide polymorphism;

XX SNP; glaucoma; progressive ocular hypertensive disorder;

XX glaucoma related disorder; motif; repeat element; regulatory region.

XX Homo sapiens.

XX US2003190617-Al.

XX 09-OCT-2003.

XX 06-MAR-2002; 2002US-00091281.

XX 06-MAR-2002; 2002US-00091281.

XX (SIEE/) SI E.

XX (RAYM/) RAYMOND V.

XX (MORI/) MORISSETTE J.

XX Raymond V, Morissette J, Si E;

XX WPI; 2003-864168/80.

XX Claim 11; SEQ ID NO 317; 159pp; English.

XX The invention relates to an isolated nucleic acid (NI) comprising at  
XX least 20 but not more than 1500 consecutive nucleotides of the optineurin  
XX promoter appearing as AD813890. Also included are the optineurin promoter  
XX operably linked to a heterologous nucleic acid, a nucleic acid capable of  
XX detecting a single nucleotide polymorphism (SNP) in the optineurin  
XX promoter, a host cell comprising the promoter operably linked to a  
XX heterologous sequence, diagnosing or prognosing glaucoma in a sample  
XX obtained from a cell or bodily fluid (comprising detecting a polymorphism  
XX in a promoter region of the optineurin gene, associated with a glaucoma  
XX phenotype), detecting a SNP sequence variation in a sample containing  
XX DNA, detecting the presence of an optineurin promoter sequence variation  
XX in a sample containing DNA, determining the presence or increased  
XX susceptibility to glaucoma or to a progressive ocular hypertensive  
XX disorder resulting in loss of visual field in a patient (or the severity  
XX or progression of glaucoma in a patient, comprising providing  
XX amplification reaction primers that direct amplification of a selected  
XX nucleic acid region containing the variation within the optineurin  
XX promoter and amplifying the DNA) and detecting a polymorphism (comprising  
XX obtaining a sample containing human genomic DNA, providing a nucleic acid  
XX capable of detecting a SNP located within an optineurin promoter, and  
XX detecting the polymorphism). The invention is used to diagnose and  
XX prognose glaucoma and also to treat glaucoma related disorders. The  
XX present sequence is an optineurin promoter motif, repeat element or

CC putative regulatory region.  
XX Sequence 32 BP; 7 A; 12 C; 6 G; 7 T; 0 U; 0 Other;  
SQ  
Query Match 2.8%; Score 27.4; DB 1; Length 32;  
Best Local Similarity 96.6%; Pred. No. 6.9e+02;  
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Oy 860 AAGTCTGAGATTACAGCGGTGAGCCACC 888  
Db 32 AAGTCTGAGATTACAGCGGTGAGCCACC 4  
RESULT 256  
AA162688/C  
ID AA162688 standard; DNA; 33 BP.  
AC AA162688;  
XX  
DT 19-OCT-2001 (first entry)  
XX  
DE Human breast or ovarian antigen genomic DNA SEQ ID NO: 338.  
XX  
KW Human; breast antigen; ovarian antigen; cancer; metastasis; gene therapy;  
KW ds.  
XX  
OS Homo sapiens.  
XX  
FN WO200155324-A2.  
XX  
PD 02-AUG-2001.  
XX  
PF 17-JAN-2001; 2001WO-US001344.  
XX  
PR 31-JAN-2000; 2000US-0179065P.  
PR 04-FEB-2000; 2000US-0180628P.  
PR 24-FEB-2000; 2000US-0184664P.  
PR 02-MAR-2000; 2000US-0186350P.  
PR 16-MAR-2000; 2000US-0189874P.  
PR 17-MAR-2000; 2000US-0190076P.  
PR 18-APR-2000; 2000US-0198123P.  
PR 19-MAY-2000; 2000US-0205515P.  
PR 07-JUN-2000; 2000US-0209467P.  
PR 28-JUN-2000; 2000US-0214886P.  
PR 30-JUN-2000; 2000US-0215135P.  
PR 07-JUL-2000; 2000US-0216647P.  
PR 07-JUL-2000; 2000US-0216880P.  
PR 11-JUL-2000; 2000US-0217487P.  
PR 14-JUL-2000; 2000US-0218290P.  
PR 26-JUL-2000; 2000US-0220963P.  
PR 26-JUL-2000; 2000US-0220964P.  
PR 14-AUG-2000; 2000US-0224518P.  
PR 14-AUG-2000; 2000US-0224519P.  
PR 14-AUG-2000; 2000US-0225213P.  
PR 14-AUG-2000; 2000US-0225214P.  
PR 14-AUG-2000; 2000US-0225266P.  
PR 14-AUG-2000; 2000US-0225267P.  
PR 14-AUG-2000; 2000US-0225268P.  
PR 14-AUG-2000; 2000US-0225270P.  
PR 14-AUG-2000; 2000US-0225447P.  
PR 14-AUG-2000; 2000US-0225758P.  
PR 14-AUG-2000; 2000US-0225759P.  
PR 14-AUG-2000; 2000US-0225799P.  
PR 18-AUG-2000; 2000US-0226681P.  
PR 22-AUG-2000; 2000US-0226682P.  
PR 22-AUG-2000; 2000US-0227182P.  
PR 23-AUG-2000; 2000US-0227009P.  
PR 30-AUG-2000; 2000US-0228924P.  
PR 01-SEP-2000; 2000US-0229287P.  
PR 01-SEP-2000; 2000US-0229343P.  
PR 01-SEP-2000; 2000US-0229344P.

PR 01-SEP-2000; 2000US-0229345P.  
PR 05-SEP-2000; 2000US-0229509P.  
PR 05-SEP-2000; 2000US-0229513P.  
PR 06-SEP-2000; 2000US-0230437P.  
PR 06-SEP-2000; 2000US-0230438P.  
PR 08-SEP-2000; 2000US-0231242P.  
PR 08-SEP-2000; 2000US-0231243P.  
PR 08-SEP-2000; 2000US-0231244P.  
PR 08-SEP-2000; 2000US-0231413P.  
PR 08-SEP-2000; 2000US-0231414P.  
PR 08-SEP-2000; 2000US-0232080P.  
PR 08-SEP-2000; 2000US-0232081P.  
PR 12-SEP-2000; 2000US-0231968P.  
PR 14-SEP-2000; 2000US-0232397P.  
PR 14-SEP-2000; 2000US-0232398P.  
PR 14-SEP-2000; 2000US-0232399P.  
PR 14-SEP-2000; 2000US-0232400P.  
PR 14-SEP-2000; 2000US-0232401P.  
PR 14-SEP-2000; 2000US-0233063P.  
PR 14-SEP-2000; 2000US-0233064P.  
PR 21-SEP-2000; 2000US-0234223P.  
PR 21-SEP-2000; 2000US-0234224P.  
PR 25-SEP-2000; 2000US-0234997P.  
PR 25-SEP-2000; 2000US-0234998P.  
PR 26-SEP-2000; 2000US-0235484P.  
PR 27-SEP-2000; 2000US-0235836P.  
PR 27-SEP-2000; 2000US-0235837P.  
PR 29-SEP-2000; 2000US-0236327P.  
PR 29-SEP-2000; 2000US-0236327P.  
PR 29-SEP-2000; 2000US-0236367P.  
PR 29-SEP-2000; 2000US-0236368P.  
PR 29-SEP-2000; 2000US-0236369P.  
PR 29-SEP-2000; 2000US-0236370P.  
PR 02-OCT-2000; 2000US-0236802P.  
PR 02-OCT-2000; 2000US-0237037P.  
PR 02-OCT-2000; 2000US-0237038P.  
PR 02-OCT-2000; 2000US-0237039P.  
PR 13-OCT-2000; 2000US-0237904P.  
PR 13-OCT-2000; 2000US-0239935P.  
PR 13-OCT-2000; 2000US-0239937P.  
PR 20-OCT-2000; 2000US-0240960P.  
PR 20-OCT-2000; 2000US-0241221P.  
PR 20-OCT-2000; 2000US-0241785P.  
PR 20-OCT-2000; 2000US-0241786P.  
PR 20-OCT-2000; 2000US-0241787P.  
PR 20-OCT-2000; 2000US-0241808P.  
PR 20-OCT-2000; 2000US-0241809P.  
PR 20-OCT-2000; 2000US-0241826P.  
PR 01-NOV-2000; 2000US-0244617P.  
PR 08-NOV-2000; 2000US-0246474P.  
PR 08-NOV-2000; 2000US-0246475P.  
PR 08-NOV-2000; 2000US-0246476P.  
PR 08-NOV-2000; 2000US-0246477P.  
PR 08-NOV-2000; 2000US-0246478P.  
PR 08-NOV-2000; 2000US-0246523P.  
PR 08-NOV-2000; 2000US-0246524P.  
PR 08-NOV-2000; 2000US-0246525P.  
PR 08-NOV-2000; 2000US-0246526P.  
PR 08-NOV-2000; 2000US-0246527P.  
PR 08-NOV-2000; 2000US-0246528P.  
PR 08-NOV-2000; 2000US-0246532P.  
PR 08-NOV-2000; 2000US-0246609P.  
PR 08-NOV-2000; 2000US-0246610P.  
PR 08-NOV-2000; 2000US-0246611P.  
PR 08-NOV-2000; 2000US-0246613P.  
PR 17-NOV-2000; 2000US-0249207P.  
PR 17-NOV-2000; 2000US-0249208P.  
PR 17-NOV-2000; 2000US-0249209P.  
PR 17-NOV-2000; 2000US-0249210P.  
PR 17-NOV-2000; 2000US-0249211P.  
PR 17-NOV-2000; 2000US-0249212P.  
PR 17-NOV-2000; 2000US-0249213P.  
PR 17-NOV-2000; 2000US-0249214P.



PR 17-NOV-2000; 2000US-0249215P.  
PR 17-NOV-2000; 2000US-0249216P.  
PR 17-NOV-2000; 2000US-0249217P.  
PR 17-NOV-2000; 2000US-0249218P.  
PR 17-NOV-2000; 2000US-0249244P.  
PR 17-NOV-2000; 2000US-0249245P.  
PR 17-NOV-2000; 2000US-0249264P.  
PR 17-NOV-2000; 2000US-0249265P.  
PR 17-NOV-2000; 2000US-0249297P.  
PR 17-NOV-2000; 2000US-0249299P.  
PR 17-NOV-2000; 2000US-0249300P.  
PR 01-DEC-2000; 2000US-0250160P.  
PR 01-DEC-2000; 2000US-0250391P.  
PR 05-DEC-2000; 2000US-0251030P.  
PR 05-DEC-2000; 2000US-0251988P.  
PR 05-DEC-2000; 2000US-0256719P.  
PR 06-DEC-2000; 2000US-0251779P.  
PR 08-DEC-2000; 2000US-0251856P.  
PR 08-DEC-2000; 2000US-0251868P.  
PR 08-DEC-2000; 2000US-0251869P.  
PR 08-DEC-2000; 2000US-0251989P.  
PR 08-DEC-2000; 2000US-0254990P.  
PR 11-DEC-2000; 2000US-0254997P.  
PR 05-JAN-2001; 2001US-0259678P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Barash SC, Ruben SM;  
XX WPI; 2001-488785/53.  
XX  
XX New isolated nucleic acids and polypeptides, useful for diagnosing,  
PT treating and/or preventing human diseases and disorders.  
XX  
XX Disclosure; SEQ ID NO 338; 520pp + Sequence Listing; English.  
XX  
XX The present invention provides the protein and coding sequences of a  
CC number of ovarian and breast antigens. These are shown in AAL62467-  
CC AAL62572 and AAM42240-AAM42345. The sequences can be used in the  
CC diagnosis, prevention and treatment of breast and ovarian cancers, and  
CC their metastases. The present sequence is a genomic sequence of the  
CC invention. Note: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 33 BP; 8 A; 12 C; 9 G; 4 T; 0 U; 0 Other:  
SQ  
Query Match 2.7%; Score 27.2; DB 1; Length 33;  
Best Local Similarity 90.6%; Pred. No. 7.2e+02;  
Matches 29; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 932 TCACTCTGTTACCCAGGCTGAGTGCATGCG 963  
DB 33 TCGCTCTGTTGCCAGGCTGAGTGCATGCGC 2  
RESULT 257  
AAL06807/c  
ID AAL06807 standard; DNA; 33 BP.  
XX  
XX AAL06807;  
XX  
XX 21-NOV-2001 (first entry)  
DT  
XX  
XX Human reproductive system related antigen DNA SEQ ID NO: 9495.  
DE  
XX  
XX Human; reproductive system related antigen; reproductive system disorder;  
KM cancer; gene therapy; ds.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200155320-A2.  
XX  
XX

PD 02-AUG-2001;  
XX 17-JAN-2001; 2001WO-US001339.  
XX  
XX 31-JAN-2000; 2000US-0179065P.  
PR 04-FEB-2000; 2000US-0180628P.  
PR 24-FEB-2000; 2000US-0184664P.  
PR 02-MAR-2000; 2000US-0186350P.  
PR 16-MAR-2000; 2000US-0189874P.  
PR 17-MAR-2000; 2000US-0190076P.  
PR 18-APR-2000; 2000US-0198123P.  
PR 19-MAY-2000; 2000US-0205155P.  
PR 07-JUN-2000; 2000US-0209467P.  
PR 28-JUN-2000; 2000US-0214886P.  
PR 30-JUN-2000; 2000US-0215135P.  
PR 07-JUL-2000; 2000US-0216647P.  
PR 07-JUL-2000; 2000US-0216880P.  
PR 11-JUL-2000; 2000US-0217487P.  
PR 11-JUL-2000; 2000US-0217496P.  
PR 14-JUL-2000; 2000US-0218290P.  
PR 26-JUL-2000; 2000US-0220963P.  
PR 26-JUL-2000; 2000US-0220964P.  
PR 14-AUG-2000; 2000US-0224518P.  
PR 14-AUG-2000; 2000US-0224519P.  
PR 14-AUG-2000; 2000US-0225213P.  
PR 14-AUG-2000; 2000US-0225214P.  
PR 14-AUG-2000; 2000US-0225266P.  
PR 14-AUG-2000; 2000US-0225267P.  
PR 14-AUG-2000; 2000US-0225268P.  
PR 14-AUG-2000; 2000US-0225270P.  
PR 14-AUG-2000; 2000US-0225447P.  
PR 14-AUG-2000; 2000US-0225757P.  
PR 14-AUG-2000; 2000US-0225758P.  
PR 14-AUG-2000; 2000US-0225759P.  
PR 18-AUG-2000; 2000US-0226279P.  
PR 22-AUG-2000; 2000US-0226681P.  
PR 22-AUG-2000; 2000US-0226686P.  
PR 22-AUG-2000; 2000US-0227182P.  
PR 23-AUG-2000; 2000US-0227009P.  
PR 30-AUG-2000; 2000US-0228924P.  
PR 01-SEP-2000; 2000US-0229287P.  
PR 01-SEP-2000; 2000US-0229343P.  
PR 01-SEP-2000; 2000US-0229344P.  
PR 01-SEP-2000; 2000US-0229345P.  
PR 05-SEP-2000; 2000US-0229509P.  
PR 05-SEP-2000; 2000US-0229513P.  
PR 06-SEP-2000; 2000US-0230437P.  
PR 06-SEP-2000; 2000US-0230438P.  
PR 08-SEP-2000; 2000US-0231242P.  
PR 08-SEP-2000; 2000US-0231243P.  
PR 08-SEP-2000; 2000US-0231244P.  
PR 08-SEP-2000; 2000US-0231413P.  
PR 08-SEP-2000; 2000US-0231414P.  
PR 08-SEP-2000; 2000US-0232080P.  
PR 08-SEP-2000; 2000US-0232081P.  
PR 12-SEP-2000; 2000US-0231968P.  
PR 14-SEP-2000; 2000US-0232397P.  
PR 14-SEP-2000; 2000US-0232398P.  
PR 14-SEP-2000; 2000US-0232399P.  
PR 14-SEP-2000; 2000US-0232400P.  
PR 14-SEP-2000; 2000US-0232401P.  
PR 14-SEP-2000; 2000US-0233063P.  
PR 14-SEP-2000; 2000US-0233064P.  
PR 14-SEP-2000; 2000US-0233065P.  
PR 21-SEP-2000; 2000US-0234223P.  
PR 21-SEP-2000; 2000US-0234274P.  
PR 25-SEP-2000; 2000US-0234997P.  
PR 25-SEP-2000; 2000US-0234998P.  
PR 26-SEP-2000; 2000US-0235844P.  
PR 27-SEP-2000; 2000US-0235843P.  
PR 27-SEP-2000; 2000US-0235836P.  
PR 29-SEP-2000; 2000US-0236327P.  
PR 29-SEP-2000; 2000US-0236367P.  
PR

[illegible]

Db 2 ATGATCCTCATCTGTATACCAAGCTGAGT 33

RESULT 259  
ACC84460  
ID ACC84460 standard; DNA; 27 BP.  
XX  
XX  
AC ACC84460;  
XX  
DT 28-AUG-2003 (first entry)  
XX  
XX NTP peptide encoding sequence #7.  
DE  
XX  
XX Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;  
KW  
KW neural thread protein; NTP; tumour; ds.  
XX  
OS Unidentified.  
XX  
PN WO2003008443-A2.  
XX  
XX 30-JAN-2003.  
PD  
XX  
PF 19-JUL-2002; 2002WO-CA001105.  
XX  
PR 19-JUL-2001; 2001US-0306150P.  
XX  
PR 19-JUL-2001; 2001US-0306161P.  
XX  
PR 16-NOV-2001; 2001US-0331477P.  
XX  
PA (NYMO-) NYMOX CORP.  
XX  
PI Averbach PA;  
XX  
XX WPI: 2003-247999/24.  
DR  
XX  
XX P-PSDB; ABR63255.  
PT  
XX  
XX Novel neural thread protein peptide, referred as cell death peptide,  
PT useful for treating prostatic hyperplasia, psoriasis, eczema, dermatosis,  
PT atherosclerosis, cosmetic modification to skin, throat, mouth, muscle.  
XX  
XX Disclosure; Page 17; 77pp; English.  
XX  
XX The present invention relates to a neural thread protein (NTP) peptide  
CC referred to as cell death peptide. Thought to be cytostatic,  
CC antibacterial, immunosuppressive and antiinflammatory. It is useful for  
CC treating a condition in a patient requiring removal or destruction of  
CC cell, for treating a condition such as benign or malignant tumor.  
CC inflammatory disease, autoimmune disease and infectious disease. The  
CC peptide useful for treatment is derived from the amino acid sequence for  
CC a pancreatic thread protein. The peptide is conjugated, linked or bound  
CC to a molecule chosen from antibody or its fragment, antibody-like binding  
CC molecule, where the molecule has a higher affinity for binding to a tumor  
CC or other target than binding to other cells. Treatment using NTP peptides  
CC can remove benign tumors with less risk and fewer of the undesirable side  
CC effects of surgery. The present sequence is an NTP encoding sequence  
XX  
XX  
SQ Sequence 27 BP; 6 A; 10 C; 6 G; 5 T; 0 U; 0 Other;  
Query Match 2.7%; Score 27; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 6.4e+02;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1017 CTCAGCTCCCAAGCAGCTGGATTAC 1043  
Db 1 CTCAGCTCCCAAGCAGCTGGATTAC 27

RESULT 260  
AAA04371  
ID AAA04371 standard; DNA; 29 BP.  
XX  
XX  
AC AAA04371;  
XX  
DT 22-MAY-2000 (first entry)  
XX

XX  
DE Polymorphic fragment of hypertension associated gene HSTSGENE.  
XX  
XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;  
KW  
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;  
KW Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;  
KW polycystic kidney disease; von Willebrand's disease; forensic; human;  
KW tuberculous scleritis; hereditary hemorrhagica telangiectasia;  
KW familial colonic polyposis; osteogenesis imperfecta; porphyria;  
KW Ehlers-Danlos syndrome; ss.  
XX  
XX  
OS Homo sapiens.  
XX  
XX EP955382-A2.  
PN  
XX  
XX 10-NOV-1999.  
PD  
XX  
XX 07-MAY-1999; 99EP-00250150.  
PF  
XX  
XX 07-MAY-1998; 98US-0084641P.  
PR  
XX  
PR 03-MAY-1999; 99US-00304232.  
XX  
XX  
PA (APFY-) AFFYMERIX INC.  
XX (UYCA-) UNIT CASE WESTERN RESERVE.  
XX  
XX Fan JB, Chakravarti A, Haluska MK;  
XX  
XX WPI: 2000-107928/10.  
DR  
XX  
XX Novel nucleic acids containing polymorphisms used in the diagnosis of  
PT hypertension.  
PT  
XX  
XX Claim 1; Page 34; 53pp; English.  
PS  
XX  
XX The invention provides polymorphic fragments of genes associated with  
CC hypertension. The nucleic acids including the polymorphic sites can be  
CC used as probes or primers for expressing variant proteins. Detection of  
CC the polymorphisms is useful in designing prophylactic and therapeutic  
CC regimens customized to underlying abnormalities. The polymorphisms can be  
CC used for association studies for hypertension, and in hypertension  
CC diagnostic assays. Where the polymorphisms have strong correlation with  
CC hypertension, within a gene, they are likely to have a causative role in  
CC hypertension. This information can be used to find the precise role of a  
CC polymorphism in the disease, and this can be used to identify potential  
CC drugs which combat the disease. The polymorphisms can be tested for  
CC association with other diseases e.g. agammaglobulinemia, diabetes  
CC insipidus, Lesch-Nyhan syndrome, muscular dystrophy, polycystic  
CC syndrome, Fabry's disease, familial hypercholesterolemia, polycystic  
CC kidney disease, hereditary spherocytosis, von Willebrand's disease,  
CC tuberculous scleritis, hereditary hemorrhagica telangiectasia, familial  
CC colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and  
CC acute intermittent porphyria. The polymorphic forms can also be used in  
CC forensics to identify individuals  
XX  
XX  
SQ Sequence 29 BP; 6 A; 8 C; 9 G; 5 T; 0 U; 1 Other;  
Query Match 2.7%; Score 27; DB 1; Length 29;  
Best Local Similarity 93.1%; Pred. No. 6.7e+02;  
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 856 CCCAAGTGTGGATTACAGCGGTAGC 884  
Db 1 CCCAAGTGTGGATTACAGCGGTAGC 29

RESULT 261  
AAA04506  
ID AAA04506 standard; DNA; 29 BP.  
XX  
XX  
AC AAA04506;  
XX  
DT 22-MAY-2000 (first entry)  
XX

DE Polymorphic fragment of hypertension associated gene PGIS.  
 XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;  
 XX Leisch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;  
 XX Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;  
 XX polycystic kidney disease; von Willebrand's disease; fornicis; human;  
 XX tuberculous sclerosis; hereditary hemorrhagica telangiectasia;  
 XX familial colonic polypoid; osteogenesis imperfecta; porphyria;  
 XX Ehlers-Danlos syndrome; ss.  
 XX Homo sapiens.  
 OS EP955382-A2.  
 XX 10-NOV-1999.  
 PD 07-MAY-1999; 99EP-00250150.  
 XX 07-MAY-1998; 98US-0084641P.  
 XX 03-MAY-1999; 99US-00304232.  
 XX (AFY-) AFFYMETRIX INC.  
 PA (UYCA-) UNIV CASE WESTERN RESERVE.  
 XX Fan JB, Chakravarti A, Haluska MK;  
 XX WPI; 2000-107928/10.  
 DR Novel nucleic acids containing polymorphisms used in the diagnosis of  
 XX hypertension.  
 PT Claim 1; Page 38; 53pp; English.  
 XX The invention provides polymorphic fragments of genes associated with  
 XX hypertension. The nucleic acids including the polymorphic sites can be  
 XX used as probes or primers for expressing variant proteins. Detection of  
 XX the polymorphisms is useful in designing prophylactic and therapeutic  
 XX regimens customized to underlying abnormalities. The polymorphisms can be  
 XX used for association studies for hypertension, and in hypertension  
 XX diagnostic assays. Where the polymorphisms have strong correlation with  
 XX hypertension, within a gene, they are likely to have a causative role in  
 XX hypertension. This information can be used to find the precise role of a  
 XX polymorphism in the disease, and this can be used to identify potential  
 XX drugs which combat the disease. The polymorphisms can be tested for  
 XX association with other diseases e.g. agammaglobulinemia, diabetes  
 XX insipidus, Leisch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich  
 XX syndrome, Fabry's disease, familial hypercholesterolemia, polycystic  
 XX kidney disease, hereditary spherocytosis, von Willebrand's disease,  
 XX tuberculous sclerosis, hereditary hemorrhagica telangiectasia, familial  
 XX colonic polypoid, Ehlers-Danlos syndrome, osteogenesis imperfecta, and  
 XX acute intermittent porphyria. The polymorphic forms can also be used in  
 XX forensics to identify individuals  
 XX Sequence 29 BP; 5 A; 8 C; 11 G; 4 T; 0 U; 1 Other;  
 SQ  
 XX Query Match 2.7%; Score 27; DB 1; Length 29;  
 XX Best Local Similarity 93.1%; Pred. No. 6.7e+02;  
 XX Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 OY 864 GCTGGATTACAGCGGTAGCCACCGC 892  
 DB 1 GCTGGATTACAGCGGTAGCCACCGC 29  
 RESULT 262  
 ID AAA04303 standard; DNA; 29 BP.  
 AC AAA04303;  
 XX 22-MAY-2000 (first entry)  
 DT Polymorphic fragment of hypertension associated gene GLUT4.  
 DE

XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;  
 XX Leisch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;  
 XX Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;  
 XX polycystic kidney disease; von Willebrand's disease; fornicis; human;  
 XX tuberculous sclerosis; hereditary hemorrhagica telangiectasia;  
 XX familial colonic polypoid; osteogenesis imperfecta; porphyria;  
 XX Ehlers-Danlos syndrome; ss.  
 XX Homo sapiens.  
 OS EP955382-A2.  
 XX 10-NOV-1999.  
 PD 07-MAY-1999; 99EP-00250150.  
 XX 07-MAY-1998; 98US-0084641P.  
 XX 03-MAY-1999; 99US-00304232.  
 XX (AFY-) AFFYMETRIX INC.  
 PA (UYCA-) UNIV CASE WESTERN RESERVE.  
 XX Fan JB, Chakravarti A, Haluska MK;  
 XX WPI; 2000-107928/10.  
 DR Novel nucleic acids containing polymorphisms used in the diagnosis of  
 XX hypertension.  
 PT Claim 1; Page 32; 53pp; English.  
 XX The invention provides polymorphic fragments of genes associated with  
 XX hypertension. The nucleic acids including the polymorphic sites can be  
 XX used as probes or primers for expressing variant proteins. Detection of  
 XX the polymorphisms is useful in designing prophylactic and therapeutic  
 XX regimens customized to underlying abnormalities. The polymorphisms can be  
 XX used for association studies for hypertension, and in hypertension  
 XX diagnostic assays. Where the polymorphisms have strong correlation with  
 XX hypertension, within a gene, they are likely to have a causative role in  
 XX hypertension. This information can be used to find the precise role of a  
 XX polymorphism in the disease, and this can be used to identify potential  
 XX drugs which combat the disease. The polymorphisms can be tested for  
 XX association with other diseases e.g. agammaglobulinemia, diabetes  
 XX insipidus, Leisch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich  
 XX syndrome, Fabry's disease, familial hypercholesterolemia, polycystic  
 XX kidney disease, hereditary spherocytosis, von Willebrand's disease,  
 XX tuberculous sclerosis, hereditary hemorrhagica telangiectasia, familial  
 XX colonic polypoid, Ehlers-Danlos syndrome, osteogenesis imperfecta, and  
 XX acute intermittent porphyria. The polymorphic forms can also be used in  
 XX forensics to identify individuals  
 XX Sequence 29 BP; 5 A; 8 C; 10 G; 5 T; 0 U; 1 Other;  
 SQ  
 XX Query Match 2.7%; Score 27; DB 1; Length 29;  
 XX Best Local Similarity 93.1%; Pred. No. 6.7e+02;  
 XX Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 OY 862 GTGCTGGATTACAGCGGTAGCCACAC 890  
 DB 1 GTGCTGGATTACAGCGGTAGCCACAC 29  
 RESULT 263  
 ID AAA04500 standard; DNA; 29 BP.  
 AC AAA04500;  
 XX 22-MAY-2000 (first entry)  
 DT Polymorphic fragment of hypertension associated gene PGIS.  
 DE

KM Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;  
 KM Leech-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;  
 KM Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;  
 KM polycystic kidney disease; von Willebrand's disease; forensic; human;  
 KM tuberculous sclerosis; hereditary hemorrhagica telangiectasia;  
 KM familial colonic polyposis; osteogenesis imperfecta; porphyria;  
 KM Ehlers-Danlos syndrome; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP955382-A2.  
 XX  
 PD 10-NOV-1999.  
 XX  
 PF 07-MAY-1999; 99EP-00250150.  
 XX  
 PR 07-MAY-1998; 98US-0084641P.  
 PR 03-MAY-1999; 99US-00304232.  
 XX  
 PA (APFV-) APFVETRIX INC.  
 PA (UYCA-) UNIV CASE WESTERN RESERVE.  
 XX  
 PI Fan JB, Chakravarti A, Haluska MK;  
 XX  
 DR WPI; 2000-107928/10.  
 XX  
 PT Novel nucleic acids containing polymorphisms used in the diagnosis of  
 PT hypertension.  
 XX  
 PS Claim 1; Page 38; 53pp; English.  
 XX  
 CC The invention provides polymorphic fragments of genes associated with  
 CC hypertension. The nucleic acids including the polymorphic sites can be  
 CC used as probes or primers for expressing variant proteins. Detection of  
 CC the polymorphisms is useful in designing prophylactic and therapeutic  
 CC regimes customized to underlying abnormalities. The polymorphisms can be  
 CC used for association studies for hypertension, and in hypertension  
 CC diagnostic assays. Where the polymorphisms have strong correlation with  
 CC hypertension, within a gene, they are likely to have a causative role in  
 CC hypertension. This information can be used to find the precise role of a  
 CC polymorphism in the disease, and this can be used to identify potential  
 CC drugs which combat the disease. The polymorphisms can be tested for  
 CC association with other diseases e.g. agammaglobulinemia, diabetes  
 CC insipidus, Leech-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich  
 CC syndrome, Fabry's disease, familial hypercholesterolemia, polycystic  
 CC kidney disease, hereditary spherocytosis, von Willebrand's disease,  
 CC tuberculous sclerosis, hereditary hemorrhagica telangiectasia, familial  
 CC colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and  
 CC acute intermittent porphyria. The polymorphic forms can also be used in  
 CC forensics to identify individuals  
 XX  
 SQ Sequence 29 BP; 4 A; 10 C; 8 G; 6 T; 0 U; 1 Other;  
 XX  
 QY Query Match 2.7%; Score 27; DB 1; Length 29;  
 Best Local Similarity 93.1%; Pred. No. 6.7e+02;  
 Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 Db 713 CTGGCCAGCCTCTGAGTAGTGGAGACT 741  
 1 CTGGCTCAGCCTCTGAGTAGTGGAGACT 29  
 XX  
 RESULT 264  
 ID AAA03996  
 XX AAA03996 standard; DNA; 29 BP.  
 AC AAA03996;  
 XX  
 DT 22-MAY-2000 (first entry)  
 XX  
 DB Polymorphic fragment of hypertension associated gene APOC4.  
 XX  
 KM Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;

KM Leech-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;  
 KM Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;  
 KM polycystic kidney disease; von Willebrand's disease; forensic; human;  
 KM tuberculous sclerosis; hereditary hemorrhagica telangiectasia;  
 KM familial colonic polyposis; osteogenesis imperfecta; porphyria;  
 KM Ehlers-Danlos syndrome; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP955382-A2.  
 XX  
 PD 10-NOV-1999.  
 XX  
 PF 07-MAY-1999; 99EP-00250150.  
 XX  
 PR 07-MAY-1998; 98US-0084641P.  
 PR 03-MAY-1999; 99US-00304232.  
 XX  
 PA (APFV-) APFVETRIX INC.  
 PA (UYCA-) UNIV CASE WESTERN RESERVE.  
 XX  
 PI Fan JB, Chakravarti A, Haluska MK;  
 XX  
 DR WPI; 2000-107928/10.  
 XX  
 PT Novel nucleic acids containing polymorphisms used in the diagnosis of  
 PT hypertension.  
 XX  
 PS Claim 1; Page 22; 53pp; English.  
 XX  
 CC The invention provides polymorphic fragments of genes associated with  
 CC hypertension. The nucleic acids including the polymorphic sites can be  
 CC used as probes or primers for expressing variant proteins. Detection of  
 CC the polymorphisms is useful in designing prophylactic and therapeutic  
 CC regimes customized to underlying abnormalities. The polymorphisms can be  
 CC used for association studies for hypertension, and in hypertension  
 CC diagnostic assays. Where the polymorphisms have strong correlation with  
 CC hypertension, within a gene, they are likely to have a causative role in  
 CC hypertension. This information can be used to find the precise role of a  
 CC polymorphism in the disease, and this can be used to identify potential  
 CC drugs which combat the disease. The polymorphisms can be tested for  
 CC association with other diseases e.g. agammaglobulinemia, diabetes  
 CC insipidus, Leech-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich  
 CC syndrome, Fabry's disease, familial hypercholesterolemia, polycystic  
 CC kidney disease, hereditary spherocytosis, von Willebrand's disease,  
 CC tuberculous sclerosis, hereditary hemorrhagica telangiectasia, familial  
 CC colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and  
 CC acute intermittent porphyria. The polymorphic forms can also be used in  
 CC forensics to identify individuals  
 XX  
 SQ Sequence 29 BP; 6 A; 7 C; 9 G; 6 T; 0 U; 1 Other;  
 XX  
 QY Query Match 2.7%; Score 27; DB 1; Length 29;  
 Best Local Similarity 93.1%; Pred. No. 6.7e+02;  
 Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 Db 849 TCGGCTCCCAAGTGTGGATTACAG 877  
 1 TTGGCTCCCAAGTGTGGATTACAG 29  
 XX  
 RESULT 265  
 ID AAA04505  
 XX AAA04505 standard; DNA; 29 BP.  
 AC AAA04505;  
 XX  
 DT 22-MAY-2000 (first entry)  
 XX  
 DB Polymorphic fragment of hypertension associated gene PCS.  
 XX  
 KM Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;  
 KM Leech-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;

KM Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;  
 KM polycystic kidney disease; von Willebrand's disease; forensic; human;  
 KM tuberculous sclerosis; hereditary hemorrhagica telangiectasia;  
 KM familial colonic polyposis; osteogenesis imperfecta; porphyria;  
 KM Ehlers-Danlos syndrome; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP955382-A2.  
 XX  
 PD 10-NOV-1999.  
 XX  
 PD 07-MAY-1999; 99EP-00250150.  
 XX  
 PF 07-MAY-1998; 98US-0084641P.  
 XX  
 PR 03-MAY-1999; 99US-00304232.  
 XX  
 PA (AFPY-) AFPMETRIX INC.  
 XX  
 PA (UYCA-) UNIV CASE WESTERN RESERVE.  
 XX  
 PI Fan JB, Chakravarti A, Haluska MK;  
 XX  
 DR WPI; 2000-107928/10.  
 XX  
 PT Novel nucleic acids containing polymorphisms used in the diagnosis of  
 PT hypertension.  
 XX  
 PS Claim 1; Page 38; 53pp; English.  
 XX  
 CC The invention provides polymorphic fragments of genes associated with  
 CC hypertension. The nucleic acids including the polymorphic sites can be  
 CC used as probes or primers for expressing variant proteins. Detection of  
 CC the polymorphisms is useful in designing prophylactic and therapeutic  
 CC regimes customized to underlying abnormalities. The polymorphisms can be  
 CC used for association studies for hypertension, and in hypertension  
 CC diagnostic assays. Where the polymorphisms have strong correlation with  
 CC hypertension, within a gene, they are likely to have a causative role in  
 CC hypertension. This information can be used to find the precise role of a  
 CC polymorphism in the disease, and this can be used to identify potential  
 CC drugs which combat the disease. The polymorphisms can be tested for  
 CC association with other diseases e.g. agammaglobulinemia, diabetes  
 CC insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich  
 CC syndrome, Fabry's disease, familial hypercholesterolemia, polycystic  
 CC kidney disease, hereditary spherocytosis, von Willebrand's disease,  
 CC tuberculous sclerosis, hereditary hemorrhagica telangiectasia, familial  
 CC colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and  
 CC acute intermittent porphyria. The polymorphic forms can also be used in  
 CC forensics to identify individuals  
 XX  
 SQ Sequence 29 BP; 4 A; 11 C; 7 G; 6 T; 0 U; 1 Other;  
 XX  
 Query Match 2.7%; Score 27; DB 1; Length 29;  
 Best Local Similarity 93.1%; Pred. No. 6.7e+02;  
 Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 QY 836 TGATCTGCTGCTGCTGCTGCCAAGTG 864  
 Db 1 TGATCTGCCGCTTGCTGCTGCCAAGTG 29  
 XX  
 RESULT 266  
 AAQ73570  
 ID AAQ73570 standard; DNA; 32 BP.  
 XX  
 AC AAQ73570;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 25-JUN-1995 (first entry)  
 XX  
 DE Enhancer element er-3 conserved basepair sequence.  
 XX  
 KW Enhancer element; carcinoma; tumor; cancer; SLPI gene;  
 KM secretory leukoprotease-inhibitor gene; cyokeratin gene-8; ss.

XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT misc\_difference 29 /\*tag= a  
 FT FT /label= pyrimidine  
 XX  
 PN MO9421118-A1.  
 XX  
 PD 29-SEP-1994.  
 XX  
 PD 24-MAR-1994; 94WO-US003197.  
 XX  
 PF 24-MAR-1993; 93US-00035435.  
 XX  
 PR 24-MAR-1993; 93US-00035435.  
 XX  
 PA (UABR-) UAB RES FOUND.  
 XX  
 PI Garver RI, Sorocher EJ;  
 XX  
 DR WPI; 1994-316537/39.  
 XX  
 PT DNA construct for treating human carcinoma - includes a cancer-  
 PT therapeutic gene under the control of a promoter and a gp. of enhancer  
 PT sequences.  
 XX  
 PS Claim 1; Fig 6; 54pp; English.  
 XX  
 CC This enhancer element is part of a DNA construct used for treating human  
 CC carcinoma which contains a cancer therapeutic protein under the control  
 CC of a promoter and 3 enhancer sequences in a specific 5'-3' order. This  
 CC enhancer element is derived from the flanking region of the human  
 CC epithelial cell cyokeratin-8 gene. (Updated on 25-MAR-2003 to correct PN  
 CC field.)  
 XX  
 SQ Sequence 32 BP; 7 A; 1 C; 8 G; 15 T; 0 U; 1 Other;  
 XX  
 Query Match 2.7%; Score 27; DB 1; Length 32;  
 Best Local Similarity 100.0%; Pred. No. 7.2e+02;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 769 TTTTGTATTTTGTATGTAGATGGGCT 795  
 Db 2 TTTTGTATTTTGTATGTAGATGGGCT 28  
 XX  
 RESULT 267  
 AAK91040  
 ID AAK91040 standard; DNA; 32 BP.  
 XX  
 AC AAK91040;  
 XX  
 DT 05-NOV-2001 (first entry)  
 XX  
 DE Human digestive system antigen genomic sequence SEQ ID NO: 4616.  
 XX  
 DE Human digestive system antigen; gene therapy; cancer; appendicitis;  
 KM ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;  
 KM digestive system disorder; Meckel's diverticulum; de.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO200155314-A2.  
 XX  
 PD 02-AUG-2001.  
 XX  
 DT 17-JAN-2001; 2001WO-US001324.  
 XX  
 PF 31-JAN-2000; 2000US-0179065P.  
 PR 04-FEB-2000; 2000US-0180628P.  
 PR 24-FEB-2000; 2000US-0184664P.  
 PR 02-MAR-2000; 2000US-0186350P.  
 PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.  
PR 18-APR-2000; 2000US-0198123P.  
PR 19-MAY-2000; 2000US-020515P.  
PR 07-JUN-2000; 2000US-0209467P.  
PR 28-JUN-2000; 2000US-0214886P.  
PR 30-JUN-2000; 2000US-0215135P.  
PR 07-JUL-2000; 2000US-0216647P.  
PR 07-JUL-2000; 2000US-0216880P.  
PR 11-JUL-2000; 2000US-0217487P.  
PR 11-JUL-2000; 2000US-021796P.  
PR 14-JUL-2000; 2000US-0218290P.  
PR 26-JUL-2000; 2000US-0220963P.  
PR 26-JUL-2000; 2000US-0220964P.  
PR 14-AUG-2000; 2000US-0224518P.  
PR 14-AUG-2000; 2000US-0224519P.  
PR 14-AUG-2000; 2000US-0225213P.  
PR 14-AUG-2000; 2000US-0225214P.  
PR 14-AUG-2000; 2000US-0225267P.  
PR 14-AUG-2000; 2000US-0225268P.  
PR 14-AUG-2000; 2000US-0225270P.  
PR 14-AUG-2000; 2000US-0225447P.  
PR 14-AUG-2000; 2000US-0225757P.  
PR 14-AUG-2000; 2000US-0225758P.  
PR 14-AUG-2000; 2000US-0225759P.  
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PR 05-DEC-2000; 2000US-0256719P.  
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PR 05-JAN-2001; 2001US-0259678P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Barash SC, Ruben SM;  
XX  
XX WPI; 2001-502630/55.  
XX  
XX Polynucleotides encoding digestive system antigens, useful for  
PT diagnosing, treating, preventing and/or prognostizing disorders of the  
PT digestive system, particularly cancer and cancer metastases.  
XX  
XX Disclosure; SEQ ID NO 4616; 986bp; English.  
XX  
XX The present invention provides the protein and coding sequences of a  
CC number of human digestive system antigens. These can be used in the

CC diagnosis, treatment and prevention of digestive system disorders,  
CC including cancer, Meckel's diverticulum, bacterial or parasitic  
CC infections, appendicitis, Hirschsprung's disease, chronic colitis or  
CC ulcerative colitis. The present sequence is a genomic DNA fragment  
CC encoding a digestive system antigen of the invention  
XX  
SQ Sequence 32 BP; 7 A; 3 C; 7 G; 15 T; 0 U; 0 Other;  
  
Query Match 2.7%; Score 26.8; DB 1; Length 32;  
Best Local Similarity 93.3%; Pred. No. 7.3e+02;  
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
CY 768 TTTTGTATTATTAGTACAGATGGGCTTC 797  
Db 1 TTTTGTATTATTAGTACAGAGGCTTC 30  
  
RESULT 268  
AAS32075 AAS32075 standard; DNA; 32 BP.  
XX  
AC AAS32075;  
XX  
DT 04-DEC-2001 (first entry)  
XX  
DE Human liver associated genomic DNA #249.  
XX  
KW Liver associated protein; human; mouse; rabbit; goat; horse; cat; dog;  
KW chicken; sheep; immunosuppressive; antiarthritic; vasotropic;  
KW antirheumatic; antiproliferative; cytostatic; cardiatic; neuroprotective;  
KW cerebroprotective; nootropic; antibacterial; virucide; fungicide; cancer;  
KW ophthalmological; vulnery; gene therapy; autoimmune disease; neoplasm;  
KW hyperproliferative disorder; breast; liver; cardiovascular disorder; ds;  
KW cerebrovascular disorder; nervous system disorder; bacterial infection;  
KW fungal infection; viral infection; ocular disorder; endocrine disorder;  
KW gastrointestinal disorder; renal disorder; respiratory disorder;  
KW wound healing; skin aging; organ transplantation; tissue regeneration;  
KW anti-infectility.  
XX  
XX Homo sapiens.  
XX OS  
XX PN WO20015355-A1.  
XX  
XX 02-AUG-2001.  
XX  
PF 17-JAN-2001; 2001WO-US001351.  
XX  
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PR 08-NOV-2000; 2000US-0246527P.  
PR 08-NOV-2000; 2000US-0246528P.



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 PR 05-JAN-2001; 2001US-0259678P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PI Rosen CA, Barash SC, Ruben SM;  
 XX  
 DR WPI; 2001-457728/49.  
 XX  
 PT Isolated nucleic acid molecule encoding a human liver related protein is  
 PT used in preventing, treating or ameliorating disorders of the liver  
 PT particularly cancer of the liver.  
 PS  
 PS Claim 1; SEQ ID NO 551; 526bp; English.  
 XX  
 CC Sequences AAS31827-AAS32182 represent genomic DNA molecules, which encode  
 CC the liver associated polypeptides of the invention. Liver associated  
 CC polypeptides and their associated polynucleotides are useful in the  
 CC diagnosis, treatment and prevention of various types of disorders in e.g.  
 CC humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A  
 CC pathological condition can be determined by detecting the presence or  
 CC absence of a mutation in a liver associated polynucleotide. The treatable  
 CC disorders include autoimmune diseases such as rheumatoid arthritis,  
 CC hyperproliferative disorders such as neoplasms of the breast or liver,  
 CC cardiovascular disorders such as cardiac arrest, cerebrovascular  
 CC disorders such as cerebral ischaemia, nervous system disorders such as  
 CC Alzheimer's disease, infections caused by bacteria, viruses and fungi,  
 CC ocular disorders such as corneal infection, endocrine disorders such as  
 CC premature labour and infertility, gastrointestinal disorders such as  
 CC Crohn's disease, renal disorders such as glomerulonephritis and  
 CC respiratory disorders such as asthma and pleurisy. The polypeptides can  
 CC also be used to aid wound healing, to prevent skin aging due to sunburn,  
 CC to maintain organs before transplantation, to regenerate tissues and in  
 CC chemotaxis. Note: The sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 32 BP; 7 A; 3 C; 7 G; 15 T; 0 U; 0 Other;

Query Match 2.7%; Score 26.8; DB 1; Length 32;  
 Best Local Similarity 93.3%; Pred. No. 7.3e+02;  
 Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Oy 768 TTTTGTATTTTGTAGATGGGCTTC 797  
 Db 1 TTTTGTATTTTGTAGATGGGCTTC 30  
 RESULT 269  
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 ID ABR90430 standard; DNA; 32 BP.  
 XX  
 AC ABR90430;  
 XX  
 DT 24-JUL-2002 (first entry)  
 XX  
 DE Human liver antigen HLDV38 genomic sequence, SEQ ID NO:551.  
 XX  
 KW Human; liver antigen; liver disorder; hepatic disorder; infection;  
 KW hepatitis; viral; parasitic; bacterial; fungal; inflammatory condition;  
 KW cirrhosis; granulomatous hepatitis; toxin damage; drug damage;  
 KW autoimmune disease; Wilson's disease; primary biliary cirrhosis;  
 KW neoplastic disorder; cancer; tumour; portal hypertension;  
 KW gastrointestinal disorder; hepatitis; drug screening; gene therapy;  
 KW chromosome mapping; forensic analysis; antibody preparation;  
 KW hepatotropic; cytostatic; antiinflammatory; virocidic; antibacterial;  
 KW fungicide; parasiticicide; antidote; immunosuppressive; gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2002042096-A1.  
 XX  
 PD 11-APR-2002.  
 XX  
 PF 17-JAN-2001; 2001US-00764887.  
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 PR 28-JUN-2000; 2000US-0214886P.  
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 PR 26-JUL-2000; 2000US-0220963P.  
 PR 26-JUL-2000; 2000US-0220964P.  
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 PR 05-SEP-2000; 2000US-0229513P.  
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 PR 21-SEP-2000; 2000US-0231423P.  
 PR 21-SEP-2000; 2000US-0234274P.  
 PR 25-SEP-2000; 2000US-0234997P.  
 PR 27-SEP-2000; 2000US-0235834P.  
 PR 29-SEP-2000; 2000US-0236327P.  
 PR 29-SEP-2000; 2000US-0236367P.  
 PR 29-SEP-2000; 2000US-0236368P.  
 PR 29-SEP-2000; 2000US-0236369P.

29-SEP-2000; 2000US-0236370P.  
PR 02-OCT-2000; 2000US-0236802P.  
PR 02-OCT-2000; 2000US-0237037P.  
PR 02-OCT-2000; 2000US-0237038P.  
PR 02-OCT-2000; 2000US-0237039P.  
PR 02-OCT-2000; 2000US-0237040P.  
PR 13-OCT-2000; 2000US-0239335P.  
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XX  
XX (ROSE/) ROSEN C A.  
PA (ROBE/) ROSEN S M.  
PA (BARA/) BARASH S C.  
XX  
XX Rosen CA, Ruben SM, Barash SC;  
PI WPI: 2002-381944/41.  
XX  
XX New nucleic acid encoding human liver antigens, useful for diagnosis,  
PT treatment and prevention of e.g. hepatitis and hepatic cancer, also  
PT related polypeptides and antibodies.  
XX  
XX Disclosure; SEQ ID NO 551; 181bp; English.  
XX  
XX The invention relates to 145 novel human liver antigens (ABP0831-  
CC ABP0975) and to cDNAs encoding them (ABN90036-ABN90180), and also  
CC encompasses polypeptides 90% identical and polynucleotides 95% identical  
CC to the sequences of the invention. The invention additionally relates to  
CC recombinant vectors and host cells comprising human liver antigen  
CC polynucleotides, antibodies against human liver antigens, and the use of  
CC liver antigen polynucleotides and polypeptides in diagnosing, treating,  
CC prognosing or preventing various disorders of the liver. Such conditions  
CC include viral infections (e.g., cytomegalovirus, Epstein-Barr virus,  
CC hepatitis A virus, hepatitis B virus and hepatitis C virus), parasitic  
CC infections (e.g., Clonorchis sinensis, Echinococcus granulosus and  
CC Entamoeba histolytica), and also bacterial and fungal infections. Other  
CC disorders that may be treated include inflammatory conditions (e.g.,  
CC cirrhosis and granulomatous hepatitis), damage caused by drugs or toxins,  
CC autoimmune diseases (e.g., Wilson's disease, primary biliary cirrhosis),  
CC neoplastic disorders (e.g., adenomas, haemangiomas and hepatocellular  
CC carcinoma), portal hypertension, or gastrointestinal disorders (e.g.,  
CC peptic ulcers, gastritis and peritoneal diseases). Liver antigen  
CC polypeptides and polynucleotides may also be used in screening for  
CC compounds which modulate liver antigen expression or activity. The  
CC polynucleotides may further be used for gene therapy, chromosome mapping,  
CC in the identification of individuals and in forensic analysis, and the  
CC polypeptides may be used as molecular weight markers or to prepare  
CC antibodies useful in disease diagnosis, drug targeting and phenotyping.  
CC Sequences ABN90182-ABN90537 represent human liver antigen genomic  
CC sequences. Note: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from the USPTO at seqdata.uspto.gov/sequence/  
XX  
XX Sequence 32 BP; 7 A; 3 C; 7 G; 15 T; 0 U; 0 Other;  
SQ

XX ADJ15343;  
AC 20-MAY-2004 (first entry)  
XX  
DT Human liver-related genomic DNA - SEQ ID 551.  
XX  
XX liver; vitruide; fungicide; antibacterial; antiparasitic; hepatotropic;  
XX antiinflammatory; cytostatic; litholytic; antirheumatic; antiarthritic;  
XX neuroprotective; antidiabetic; anticoagulant; thrombolytic;  
XX antidiarrhoeal; cardiac; haemostatic; antiarrhythmic;  
XX ophthalmological; antiseriosclerotic; vasotropic; osteopathic;  
XX noctropic; antiparkinsonian; anticonvulsant; neuroleptic; vasotropic;  
XX cytostatic; gynaecological; viral; fungal; bacterial;  
XX parasitic infection; cirrhosis; Wilson's disease;  
XX gastrointestinal disorder; pancreatic; gallbladder; immune; blood;  
XX hyperproliferative; cardiovascular; respiratory; musculoskeletal system;  
XX neurological; endocrine; reproductive system; developmental; inherited;  
XX human; ds.  
XX  
XX Homo sapiens.  
OS  
XX  
XX US2003077602-A1.  
XX  
XX 24-APR-2003.  
XX  
XX 14-FEB-2002; 2002US-00073961.  
XX  
XX 31-JAN-2000; 2000US-0179065P.  
PR 04-FEB-2000; 2000US-0180628P.  
PR 24-FEB-2000; 2000US-0184664P.  
PR 02-MAR-2000; 2000US-0186350P.  
PR 16-MAR-2000; 2000US-0189874P.  
PR 17-MAR-2000; 2000US-0190076P.  
PR 18-APR-2000; 2000US-0198123P.  
PR 19-MAY-2000; 2000US-0205515P.  
PR 07-JUN-2000; 2000US-0209467P.  
PR 28-JUN-2000; 2000US-0214886P.  
PR 30-JUN-2000; 2000US-0215135P.  
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PR 26-JUL-2000; 2000US-0220964P.  
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PR 14-AUG-2000; 2000US-0224519P.  
PR 14-AUG-2000; 2000US-0225213P.  
PR 14-AUG-2000; 2000US-0225214P.  
PR 14-AUG-2000; 2000US-0225267P.  
PR 14-AUG-2000; 2000US-0225267P.  
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PR 14-AUG-2000; 2000US-0225757P.  
PR 14-AUG-2000; 2000US-0225758P.  
PR 14-AUG-2000; 2000US-0225759P.  
PR 18-AUG-2000; 2000US-0226279P.  
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PR 22-AUG-2000; 2000US-0226681P.  
PR 22-AUG-2000; 2000US-0227182P.  
PR 23-AUG-2000; 2000US-0227182P.  
PR 30-AUG-2000; 2000US-0228924P.  
PR 01-SEP-2000; 2000US-0229287P.  
PR 01-SEP-2000; 2000US-0229343P.  
PR 01-SEP-2000; 2000US-0229344P.  
PR 01-SEP-2000; 2000US-0229345P.  
PR 05-SEP-2000; 2000US-0229509P.  
PR 05-SEP-2000; 2000US-0229513P.  
PR 06-SEP-2000; 2000US-0230437P.  
PR 06-SEP-2000; 2000US-0230438P.  
PR 08-SEP-2000; 2000US-0231242P.

PR 08-SEP-2000; 2000US-0231243P.  
PR 08-SEP-2000; 2000US-0231244P.  
PR 08-SEP-2000; 2000US-0231413P.  
PR 08-SEP-2000; 2000US-0231414P.  
PR 08-SEP-2000; 2000US-0232080P.  
PR 08-SEP-2000; 2000US-0232081P.  
PR 12-SEP-2000; 2000US-0231968P.  
PR 14-SEP-2000; 2000US-0232397P.  
PR 14-SEP-2000; 2000US-0232398P.  
PR 14-SEP-2000; 2000US-0232399P.  
PR 14-SEP-2000; 2000US-0232400P.  
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PR 14-SEP-2000; 2000US-0233063P.  
PR 14-SEP-2000; 2000US-0233064P.  
PR 14-SEP-2000; 2000US-0233065P.  
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PR 21-SEP-2000; 2000US-0234274P.  
PR 25-SEP-2000; 2000US-0234997P.  
PR 25-SEP-2000; 2000US-0234998P.  
PR 26-SEP-2000; 2000US-0235844P.  
PR 27-SEP-2000; 2000US-0235834P.  
PR 27-SEP-2000; 2000US-0235836P.  
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PR 29-SEP-2000; 2000US-0236367P.  
PR 29-SEP-2000; 2000US-0236368P.  
PR 29-SEP-2000; 2000US-0236369P.  
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PR 02-OCT-2000; 2000US-0237038P.  
PR 02-OCT-2000; 2000US-0237039P.  
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PR 08-NOV-2000; 2000US-0246477P.  
PR 08-NOV-2000; 2000US-0246478P.  
PR 08-NOV-2000; 2000US-0246523P.  
PR 08-NOV-2000; 2000US-0246524P.  
PR 08-NOV-2000; 2000US-0246525P.  
PR 08-NOV-2000; 2000US-0246526P.  
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PR 08-NOV-2000; 2000US-0246611P.  
PR 08-NOV-2000; 2000US-0246613P.  
PR 17-NOV-2000; 2000US-0249207P.  
PR 17-NOV-2000; 2000US-0249208P.  
PR 17-NOV-2000; 2000US-0249209P.  
PR 17-NOV-2000; 2000US-0249210P.  
PR 17-NOV-2000; 2000US-0249211P.  
PR 17-NOV-2000; 2000US-0249212P.  
PR 17-NOV-2000; 2000US-0249213P.  
PR 17-NOV-2000; 2000US-0249214P.  
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PR 17-NOV-2000; 2000US-0249218P.  
PR 17-NOV-2000; 2000US-0249244P.  
PR 17-NOV-2000; 2000US-0249245P.

PR 17-NOV-2000; 2000US-0249264P.  
PR 17-NOV-2000; 2000US-0249265P.  
PR 17-NOV-2000; 2000US-0249297P.  
PR 17-NOV-2000; 2000US-0249299P.  
PR 17-NOV-2000; 2000US-0249300P.  
PR 01-DEC-2000; 2000US-0250160P.  
PR 01-DEC-2000; 2000US-0250191P.  
PR 05-DEC-2000; 2000US-0251030P.  
PR 05-DEC-2000; 2000US-0251088P.  
PR 05-DEC-2000; 2000US-0256719P.  
PR 06-DEC-2000; 2000US-0251479P.  
PR 08-DEC-2000; 2000US-0251856P.  
PR 08-DEC-2000; 2000US-0251868P.  
PR 08-DEC-2000; 2000US-0251869P.  
PR 08-DEC-2000; 2000US-0251989P.  
PR 08-DEC-2000; 2000US-0251990P.  
PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2000US-0259678P.  
PR 17-JAN-2001; 2000US-00764887.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX PI Rosen CA, Ruben SM, Barash SC,  
XX WPI, 2003-765398/72.  
XX  
XX DR  
XX  
XX PT New liver related polypeptide, useful for diagnosis, treatment and/or  
XX prevention of liver, gastrointestinal, pancreatic, immune, blood related,  
XX endocrine, reproductive, hyperproliferative or reproductive disorders.  
XX  
XX PS disclosure, SEQ ID NO 551; 181pp; English.

XX  
XX The invention relates to a novel isolated, liver related polypeptide. The  
XX polypeptide of the invention demonstrates vitruicide, fungicide,  
XX antibacterial, antiparasitic, hepatotropic, antiinflammatory, cyostatic,  
XX litholytic, antirheumatic, antiarthritic, neuroprotective, antidiabetic,  
XX anticoagulant, thrombolytic, antiatherosclerotic, cardiac, haemostatic,  
XX antirhythmic, ophthalmological, antiatherosclerotic, vasotropic,  
XX osteopathic, cytostatic and gynaecological activities. The polypeptides  
XX vasotropic, cyostatic and gynaecological activities. The polypeptides  
XX and polynucleotides of the invention may be useful for diagnosis,  
XX detection, treatment and/or prevention of disorders of the liver such as  
XX viral, fungal, bacterial or parasitic infections, cirrhosis, Wilson's  
XX disease, gastrointestinal disorders, pancreatic disorders, gallbladder  
XX diseases, immune disorders, blood related disorders, hyperproliferative  
XX disorders, cardiovascular disorders, respiratory disorders,  
XX musculoskeletal system disorders, neurological diseases, endocrine  
XX disorders, reproductive system disorders or developmental and inherited  
XX disorders. The current sequence is that of the human liver-related  
XX genomic DNA of the invention. The current sequence is not shown within  
XX the specification per se but was obtained electronically from the USPTO  
XX web-site.

Query Match 2.7%; Score 26.8; DB 1; Length 32;  
Best Local Similarity 93.3%; Pred. No. 7.3e+02;  
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 768 TTTTGTATTTTGTAGAGATGGGCTT 797  
Db 1 TTTTGTATTTTGTAGAGACAGGGCTT 30

RESULT 271  
AAQ77890/c  
AAQ77890 standard; cDNA; 30 BP.

XX  
XX AC AAQ77890;  
XX  
XX 25-MAR-2003 (revised)  
DT 06-JUL-1995 (first entry)  
XX  
DE Neural thread protein AD10-7 cDNA 5' antisense oligonucleotide.

XX Neural thread protein AD10-7; Alzheimer's; neuroectodermal tumours;  
 KW malignant astrocytomas; glioblastomas; 5' antisense therapy; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9423756-A1.  
 XX  
 PD 27-OCT-1994.  
 XX  
 PF 20-APR-1994; 94WO-US004321.  
 XX  
 PR 20-APR-1993; 93US-00050559.  
 XX  
 PA (GENO ) GEN HOSPITAL CORP.  
 XX  
 PI De La Monte SM, Wanda JR;  
 XX  
 DR WPI; 1994-341497/42.  
 XX  
 PT Detection of neural thread proteins - to detect sporadic and familial  
 PT Alzheimer's disease, neuroectodermal tumours, malignant astrocytomas and  
 PT glioblastomas (Eng).  
 XX  
 PS Disclosure; Page 48; 158pp; English.  
 XX  
 CC AO77888-Q77890 are AD10-7 neural thread protein (NTP) antisense  
 CC oligonucleotides, that can be used to down regulate or inhibit the  
 CC expression of the NTP gene. These oligonucleotides could be used in the  
 CC treatment of the following conditions Alzheimer's disease, neuroectodermal  
 CC tumours, malignant astrocytomas and glioblastomas. (Updated on 25-MAR-  
 CC 2003 to correct PN field.)  
 XX  
 SQ Sequence 30 BP; 8 A; 4 C; 14 G; 4 T; 0 U; 0 Other;

Query Match 2.7%; Score 26.4; DB 1; Length 30;  
 Best Local Similarity 96.4%; Pred. No. 7.3e+02;  
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1000 TCAAGCGATTCTCCTGCTCAGCCTCCC 1027  
 ||||||||||||||||||  
 DB 29 TCAAGCGATTCTCCTGCTCAGCCTCCC 2

RESULT 272  
 AAT27744/C  
 ID AAT27744 standard; DNA; 30 BP.  
 XX  
 AC AAT27744;  
 XX  
 DT 14-NOV-1996 (first entry)  
 XX  
 DE Neural thread protein antisense sequence.  
 XX  
 KW Neural thread protein; NTP; diagnosis; detection; Alzheimer's disease;  
 KW neuroectodermal tumour; malignant astrocytoma; monoclonal antibody;  
 KW binding fragment; ds.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9615272-A1.  
 XX  
 PD 23-MAY-1996.  
 XX  
 PF 14-NOV-1995; 95WO-US017111.  
 XX  
 PR 14-NOV-1994; 94US-00340426.  
 XX  
 PA (GENO ) GEN HOSPITAL CORP.  
 XX  
 PI De La Monte S, Wanda JR;  
 XX  
 DR WPI; 1996-259865/26.

XX  
 PT Detection of neural thread protein in diagnosis of Alzheimer's disease -  
 PT also NTP DNA and protein sequences used in gene and anti:sense therapy.  
 XX  
 PS Disclosure; Page 48; 238pp; English.  
 XX  
 CC A method for detecting the presence of neural thread protein (NTP) having  
 CC a molecular weight of 8, 14, 17, 21, 26 or 42 kD in a human subject  
 CC comprises (a) contacting a sample from a human subject that is suspected  
 CC of containing the NTP with at least one molecule capable of binding to  
 CC the protein; and (b) detecting any of the molecule bound to the protein.  
 CC The binding molecule is selected from an antibody free of natural  
 CC impurities, a monoclonal antibody or a binding fragment of either of  
 CC these. The method may be used for diagnosing the presence of Alzheimer's  
 CC disease, neuroectodermal tumours and a malignant astrocytoma in a human.  
 CC Expression of NTP nucleic acid may be inhibited using antisense  
 CC oligonucleotides (See AAT27739-44)  
 XX  
 SQ Sequence 30 BP; 8 A; 4 C; 14 G; 4 T; 0 U; 0 Other;

Query Match 2.7%; Score 26.4; DB 1; Length 30;  
 Best Local Similarity 96.4%; Pred. No. 7.3e+02;  
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1000 TCAAGCGATTCTCCTGCTCAGCCTCCC 1027  
 ||||||||||||||||||  
 DB 29 TCAAGCGATTCTCCTGCTCAGCCTCCC 2

RESULT 273  
 AAH91474/C  
 ID AAH91474 standard; DNA; 32 BP.  
 XX  
 AC AAH91474;  
 XX  
 DT 09-OCT-2001 (first entry)  
 XX  
 DE Human inflammatory bowel disease associated polymorphic site #549.

Human inflammatory bowel disease associated polymorphic site #549.  
 KW Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;  
 KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;  
 KW chromosome 5q31-33; forensic test; gene therapy; ds.  
 XX  
 OS Homo sapiens.

Key Location/Qualifiers  
 FT misc\_feature 17  
 FT /\*tag= a  
 FT /note= "SNP, optionally C or G at this position"  
 XX

WC200142511-A2.

14-JUN-2001.

11-DEC-2000; 2000WO-US033632.

10-DEC-1999; 99US-0170257P.

10-APR-2000; 2000US-0196046P.

(WHEB ) WHITEHEAD INST BIOMEDICAL RES.

(ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.

Daly M, Hudson TV, Lander ES, Rioux J, Siminovitch K;

WPI; 2001-367874/38.

Testing for the presence of polymorphisms associated with inflammatory  
 bowel disease, using a hybridization assay.

Claim 1; Page 62; 463pp; English.

The present invention describes a method for detecting the presence of  
 polymorphisms associated with inflammatory bowel diseases such as

CC ulcerative colitis and Crohn's disease. The methods can be used to detect  
CC the presence of genetic polymorphisms associated with inflammatory bowel  
CC disease and correlating their occurrence with disease states. They may be  
CC used in this way for phenotypic correlations, forensics, paternity  
CC testing, medicine and genetic analysis. The present sequence is a  
CC polymorphic site described in the exemplification of the invention  
XX

SQ Sequence 32 BP; 8 A; 6 C; 10 G; 7 T; 0 U; 1 Other;

Query Match 2.6%; Score 26.2; DB 1; Length 32;  
Best Local Similarity 87.5%; Pred. No. 7.8e+02;  
Matches 28; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 679 TCGAACCTCTGCTCCCGGGTTCAGTTATTC 710  
|||  
DB 32 TCGAACCTCTGCTCCGAGTTTCAAGATTC 1

RESULT 274  
AAA04663  
ID AAA04663 standard; DNA; 29 BP.  
XX  
AC AAA04663;  
XX  
XX

DT 22-MAY-2000 (first entry)

DE Polymorphic fragment of hypertension associated gene TBXA2R.

XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;  
XX Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;  
XX Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;  
XX polycystic kidney disease; von Willebrand's disease; forensic; human;  
XX tubercous sclerosis; hereditary hemorrhagica telangiectasia;  
XX familial colonic polyposis; osteogenesis imperfecta; porphyria;  
XX Ehlers-Danlos syndrome; ss.

OS Homo sapiens.

XX  
XX  
PN BP955382-A2.

PD 10-NOV-1999.

PF 07-MAY-1999; 99BP-00250150.

PR 07-MAY-1998; 98US-0084641P.

PR 03-MAY-1999; 99US-00304232.

XX  
XX  
PA (AFY-) AFFYMETRIX INC.

PA (UYCA-) UNIV CASE WESTERN RESERVE.

PI Fan JB, Chakravarti A, Haluska MK;

DR WPI; 2000-107928/10.

XX  
XX  
PT Novel nucleic acids containing polymorphisms used in the diagnosis of  
XX hypertension.

PS Claim 1; Page 44; 53pp; English.

XX The invention provides polymorphic fragments of genes associated with  
CC hypertension. The nucleic acids including the polymorphic sites can be  
CC used as probes or primers for expressing variant proteins. Detection of  
CC the polymorphisms is useful in designing prophylactic and therapeutic  
CC regimens customized to underlying abnormalities. The polymorphisms can be  
CC used for association studies for hypertension, and in hypertension  
CC diagnostic assays. Where the polymorphisms have strong correlation with  
CC hypertension, within a gene, they are likely to have a causative role in  
CC hypertension. This information can be used to find the precise role of a  
CC polymorphism in the disease, and this can be used to identify potential  
CC drugs which combat the disease. The polymorphisms can be tested for  
CC association with other diseases e.g. agammaglobulinemia, diabetes  
CC insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich  
CC syndrome, Fabry's disease, familial hypercholesterolemia, polycystic

CC kidney disease, hereditary spherocytosis, von Willebrand's disease,  
CC tubercous sclerosis, hereditary hemorrhagica telangiectasia, familial  
CC colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and  
CC acute intermittent porphyria. The polymorphic forms can also be used in  
CC forensics to identify individuals

SQ Sequence 29 BP; 4 A; 12 C; 4 G; 8 T; 0 U; 1 Other;

Query Match 2.6%; Score 26; DB 1; Length 29;  
Best Local Similarity 92.9%; Pred. No. 7.5e+02;  
Matches 26; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1000 TCAAGGATTCCTGCTCCAGCCTCCC 1027  
|||  
DB 2 TCAAGGATTCCTGCTCCAGCCTCCC 29

RESULT 275  
AAA03961/C  
ID AAA03961 standard; DNA; 29 BP.  
XX  
AC AAA03961;  
XX  
XX

DT 22-MAY-2000 (first entry)

DE Polymorphic fragment of hypertension associated gene APOC1.

XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;  
XX Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;  
XX Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;  
XX polycystic kidney disease; von Willebrand's disease; forensic; human;  
XX tubercous sclerosis; hereditary hemorrhagica telangiectasia;  
XX familial colonic polyposis; osteogenesis imperfecta; porphyria;  
XX Ehlers-Danlos syndrome; ss.

OS Homo sapiens.

XX  
XX  
PN BP955382-A2.

PD 10-NOV-1999.

PF 07-MAY-1999; 99BP-00250150.

PR 07-MAY-1998; 98US-0084641P.

PR 03-MAY-1999; 99US-00304232.

XX  
XX  
PA (AFY-) AFFYMETRIX INC.

PA (UYCA-) UNIV CASE WESTERN RESERVE.

PI Fan JB, Chakravarti A, Haluska MK;

DR WPI; 2000-107928/10.

XX  
XX  
PT Novel nucleic acids containing polymorphisms used in the diagnosis of  
XX hypertension.

PS Claim 1; Page 21; 53pp; English.

XX The invention provides polymorphic fragments of genes associated with  
CC hypertension. The nucleic acids including the polymorphic sites can be  
CC used as probes or primers for expressing variant proteins. Detection of  
CC the polymorphisms is useful in designing prophylactic and therapeutic  
CC regimens customized to underlying abnormalities. The polymorphisms can be  
CC used for association studies for hypertension, and in hypertension  
CC diagnostic assays. Where the polymorphisms have strong correlation with  
CC hypertension, within a gene, they are likely to have a causative role in  
CC hypertension. This information can be used to find the precise role of a  
CC polymorphism in the disease, and this can be used to identify potential  
CC drugs which combat the disease. The polymorphisms can be tested for  
CC association with other diseases e.g. agammaglobulinemia, diabetes  
CC insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich  
CC syndrome, Fabry's disease, familial hypercholesterolemia, polycystic  
CC kidney disease, hereditary spherocytosis, von Willebrand's disease,

CC tuberosus sclerosis, hereditary hemorrhagica telangiectasia, familial  
CC colonic polypoidosis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and  
CC acute intermittent porphyria. The polymorphic forms can also be used in  
CC forensics to identify individuals

XX SQ Sequence 29 BP; 9 A; 5 C; 11 G; 3 T; 0 U; 1 Other;

Query Match 2.6%; Score 26; DB 1; Length 29;  
Best Local Similarity 92.9%; Pred. No. 7.5e+02;  
Matches 26; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 690 CCTCCCGGGTTCAGTATTCCTGCCC 717  
DB 29 CCTCCCGGGTTCAGTATTCCTGCCC 2

## RESULT 276

AAA03993  
ID AAA03993 standard; DNA; 29 BP.

XX AC AAA03993;

XX DT 22-MAY-2000 (first entry)

XX DE Polymorphic fragment of hypertension associated gene APOC4.

XX KM Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;  
XX KM Leesh-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;  
XX KM Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;  
XX KM polycystic kidney disease; von Willebrand's disease; forensic; human;  
XX KM tuberosus sclerosis; hereditary hemorrhagica telangiectasia;  
XX KM familial colonic polypoidosis; osteogenesis imperfecta; porphyria;  
XX KM Ehlers-Danlos syndrome; ss.

XX OS Homo sapiens.

XX PN EP955382-A2.

XX PD 10-NOV-1999.

XX PF 07-MAY-1999; 99BP-00250150.

XX PR 07-MAY-1999; 98US-0084641P.

XX PR 03-MAY-1999; 99US-00304232.

XX PA (AFRY-) AFFYMETRIX INC.

XX PA (UYCA-) UNIV CASE WESTERN RESERVE.

XX PI Fan JB, Chakravarti A, Haluska MK;

XX DR WPI; 2000-107928/10.

XX PT Novel nucleic acids containing polymorphisms used in the diagnosis of  
XX PT hypertension.

XX PS Claim 1; Page 22; 53pp; English.

XX CC The invention provides polymorphic fragments of genes associated with  
XX CC hypertension. The nucleic acids including the polymorphic sites can be  
XX CC used as probes or primers for expressing variant proteins. Detection of  
XX CC the polymorphisms is useful in designing prophylactic and therapeutic  
XX CC regimens customized to underlying abnormalities. The polymorphisms can be  
XX CC used for association studies for hypertension, and in hypertension can be  
XX CC diagnostic assays. Where the polymorphisms have strong correlation with  
XX CC hypertension, within a gene, they are likely to have a causative role in  
XX CC hypertension. This information can be used to find the precise role of a  
XX CC polymorphism in the disease, and this can be used to identify potential  
XX CC drugs which combat the disease. The polymorphisms can be tested for  
XX CC association with other diseases e.g. agammaglobulinemia, diabetes  
XX CC insipidus, Leesh-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich  
XX CC syndrome, Fabry's disease, familial hypercholesterolemia, polycystic  
XX CC kidney disease, hereditary spherocytosis, von Willebrand's disease,  
XX CC tuberosus sclerosis, hereditary hemorrhagica telangiectasia, familial

CC colonic polypoidosis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and  
CC acute intermittent porphyria. The polymorphic forms can also be used in  
CC forensics to identify individuals

XX SQ Sequence 29 BP; 8 A; 5 C; 9 G; 6 T; 0 U; 1 Other;

Query Match 2.6%; Score 26; DB 1; Length 29;  
Best Local Similarity 92.9%; Pred. No. 7.5e+02;  
Matches 26; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 860 AAGTCTGGGATTACAGCGCTGAGCCAC 887  
DB 1 AAGTCTGGGATTACAGCGCTGAGCCAC 28

## RESULT 277

AAQ77889/C  
ID AAQ77889 standard; CDNA; 30 BP.

XX AC AAQ77889;

XX DT 25-MAR-2003 (revised)  
XX DT 06-JUL-1995 (first entry)

XX DE Neural thread protein AD10-7 cDNA 5' antisense oligonucleotide.

XX KM Neural thread protein AD10-7; Alzheimer's; neuroectodermal tumours;  
XX KM malignant astrocytomas; glioblastomas; 5' antisense therapy; ss.

XX OS Synthetic.

XX PN WO9423756-A1.

XX PD 27-OCT-1994.

XX PF 20-APR-1994; 94WO-US004321.

XX PR 20-APR-1993; 93US-00050559.

XX PA (GEHO) GEN HOSPITAL CORP.

XX PI De La Monte SM, Wands JR;

XX DR WPI; 1994-341497/42.

XX PT Detection of neural thread proteins - to detect sporadic and familial  
XX PT Alzheimer's disease, neuroectodermal tumours, malignant astrocytomas and  
XX PT glioblastomas (Eng).

XX PS Disclosure; Page 48; 158pp; English.

XX CC AAQ77888-Q77890 are AD10-7 neural thread protein (NTP) antisense  
XX CC oligonucleotides, that can be used to down regulate or inhibit the  
XX CC expression of the NTP gene. These oligonucleotides could be used in the  
XX CC treatment of the following conditions Alzheimer's disease, neuroectodermal  
XX CC tumours, malignant astrocytomas and glioblastomas. (Updated on 25-MAR-  
XX CC 2003 to correct PN field.)

XX SQ Sequence 30 BP; 5 A; 7 C; 13 G; 5 T; 0 U; 0 Other;

Query Match 2.6%; Score 25.8; DB 1; Length 30;  
Best Local Similarity 93.1%; Pred. No. 7.8e+02;  
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 980 GCAACCTTGGCTCCCGGCTCAAGCGAT 1008  
DB 29 GCAACCTTGGCTCCCGGCTCAAGCGAT 1

## RESULT 278

AAT27743/C  
ID AAT27743 standard; DNA; 30 BP.

XX

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AC AAT27743;
XX
XX 14-NOV-1996 (first entry)
DT
XX
XX Neural thread protein antisense sequence.
DE
XX
XX Neural thread protein; NTP; diagnosis; detection; Alzheimer's disease;
KW neuroectodermal tumour; malignant astrocytoma; monoclonal antibody;
KW binding fragment; ds.
XX
XX Synthetic.
XX
XX WO9615272-A1.
XX
XX 23-MAY-1996.
XX
XX 14-NOV-1995; 95WO-US017111.
XX
XX 14-NOV-1994; 94US-00340426.
XX
XX (GEHO ) GEN HOSPITAL CORP.
XX
XX De la Monte S, Mands JR;
XX
XX WPI; 1996-259865/26.
XX
XX Detection of neural thread protein in diagnosis of Alzheimer's disease -
XX also NTP DNA and protein sequences used in gene and anti-sense therapy.
XX
XX Disclosure; Page 48; 238pp; English.
XX
XX A method for detecting the presence of neural thread protein (NTP) having
XX a molecular weight of 8, 14, 17, 21, 26 or 42 kD in a human subject
XX comprises (a) contacting a sample from a human subject that is suspected
XX of containing the NTP with at least one molecule capable of binding to
XX the protein; and (b) detecting any of the molecule bound to the protein.
XX The binding molecule is selected from an antibody free of natural
XX impurities, a monoclonal antibody or a binding fragment of either of
XX these. The method may be used for diagnosing the presence of Alzheimer's
XX disease, neuroectodermal tumours and a malignant astrocytoma in a human.
XX Expression of NTP nucleic acid may be inhibited using antisense
XX oligonucleotides (See AAT27739-44)
XX
XX
XX Sequence 30 BP; 5 A; 7 C; 13 G; 5 T; 0 U; 0 Other;
SQ
Query Match 2.6%; Score 25.8; DB 1; Length 30;
Best Local Similarity 93.1%; Pred. No. 7.8e+02;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 980 GCAACCTCTGCTCCCGGCTCAAGCGAT 1008
Db ||||| ||||| ||||| ||||| |||||
29 GCAACCTCGGCTCCCGGTTCAAGCGAT 1
AAQ73573
RESULT 279
ID AAQ73573 standard; DNA; 31 BP.
XX
XX AAQ73573;
XX
XX 25-MAR-2003 (revised)
DT 25-JUN-1995 (first entry)
XX
XX Enhancer element er-3 conserved basepair sequence.
DE
XX Enhancer element; carcinoma; tumor; cancer; SLP1 gene;
KW secretory leukoprotease-inhibitor gene; cyclokeratin gene-8; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT misc_difference 14
XX FT /*tag= a

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FT
FT misc_difference 24 /label= purine
FT /*tag= b
FT /label= pyrimidine
XX
XX WO9421118-A1.
XX
XX 29-SEP-1994.
XX
XX 24-MAR-1994; 94WO-US003197.
XX
XX 24-MAR-1993; 93US-00035435.
XX
XX (UABR-) UAB RES FOUND.
XX
XX Garver RI, Sorscher EJ;
XX
XX WPI; 1994-316537/39.
XX
XX DNA construct for treating human carcinoma - includes a cancer-
XX therapeutic gene under the control of a promoter and a gp. of enhancer
XX sequences.
XX
XX Claim 1; Fig 6; 54pp; English.
XX
XX This enhancer element is part of a DNA construct used for treating human
XX carcinoma which contains a cancer therapeutic protein under the control
XX of a promoter and 3 enhancer sequences in a specific 5'-3' order. This
XX enhancer element is derived from the flanking region of the human
XX epithelial cell secretory leukoprotease-inhibitor gene. (Updated on 25-
XX MAR-2003 to correct FN field.)
XX
XX
XX Sequence 31 BP; 7 A; 10 C; 7 G; 5 T; 0 U; 2 Other;
SQ
Query Match 2.6%; Score 25.8; DB 1; Length 31;
Best Local Similarity 87.1%; Pred. No. 8e+02;
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 378 CTCAGCCTCCCAAGTCTGGATTACAGGC 408
Db ||||| ||||| ||||| ||||| |||||
1 CTCAGCCTCCCAANTAGCTGGANTACAGGC 31
AA78748/c
RESULT 280
ID AA78748 standard; DNA; 31 BP.
XX
XX AA78748;
XX
XX 20-NOV-2000 (first entry)
DT
XX
XX Human genomic DNA polymorphic site sequence tag SEQ ID NO:118.
DE
XX Human; genomic DNA; polymorphism; genome; allele-specific; primer; probe;
KW hybridisation; polymorphic site; forensic; paternity testing; medicine;
KW phenotypic trait; genetic analysis; genetic mapping; ds.
XX
XX Homo sapiens.
XX
XX EP1024200-A2.
XX
XX 02-AUG-2000.
XX
XX 26-JAN-2000; 2000EP-00250023.
XX
XX 27-JUN-1999; 99US-00238402.
XX
XX (AFFY-) AFFYMETRIX INC.
XX
XX Patil N, Shah N, Warrington JA;
XX
XX WPI; 2000-500198/45.
XX

```

PT Human genomic polymorphic nucleic acid segments, allele specific primers  
PT and probes, and methods of analysis, useful for e.g. forensics, paternity  
PT testing, genetic mapping, .  
PS Claim 1; Page 8; 141pp; English.  
XX  
XX The present invention describes a nucleic acid segment of 10-100  
CC contiguous bases chosen from one of 632 fragments (AAAT8631 to AAAT9262),  
CC where the segment comprises a polymorphic site or an immediately adjacent  
CC base, or the complement of the segment. Also described are: (1) an allele  
CC -specific oligonucleotide that hybridizes to a segment of the novelty;  
CC (2) an isolated nucleic acid comprising a sequence of the novelty where  
CC the polymorphic site within the sequence is occupied by a base other than  
CC the reference base indicated in the specification; and (3) analysing a  
CC nucleic acid, comprising obtaining a nucleic acid from an individual, and  
CC determining a base occupying any one of the polymorphic sites of the  
CC novelty. The nucleic acid segments and method can be used to analyse an  
CC individual's nucleic acid sequences for the presence of polymorphisms. The  
CC method can also be used to test for a disease phenotype and correlate the  
CC presence of the phenotype with a particular polymorphism. The presence of  
CC polymorphic sites are useful for, e.g. forensics, paternity testing,  
CC correlation of polymorphisms with phenotypic traits and for genetic  
CC mapping of phenotypic traits. AAAT8631 to AAAT9262 represent sequence  
CC tags of human genomic DNA fragments containing polymorphic sites. The  
CC base occupying the polymorphic site is indicated using IUPAC-IUB  
CC nomenclature  
XX  
SQ Sequence 31 BP; 10 A; 11 C; 6 G; 3 T; 0 U; 1 Other;  
XX  
XX Query Match 2.6%; Score 25.8; DB 1; Length 31;  
XX Best Local Similarity 87.1%; Pred. No. 8e+02;  
XX Matches 27; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 191 GTTCTCATGTTGGTCAGCGCTGCTCGAA 221  
DB 31 GTTTCGCAATGTTGGTGTGGCTGCTCGAA 1  
XX  
XX RESULT 281  
XX AAD63091/C  
XX ID AAD63091 standard; DNA; 32 BP.  
XX AC AAD63091;  
XX XX  
XX 12-FEB-2004 (first entry)  
XX DT  
XX XX Human tandem tag DNA #25.  
XX DE  
XX XX Tandem tag; concatenated tag; human; ds.  
XX OS  
XX XX Homo sapiens.  
XX PN US2003190618-A1.  
XX PD 09-OCT-2003.  
XX PF 06-MAR-2002; 2002US-00092885.  
XX PR 06-MAR-2002; 2002US-00092885.  
XX  
XX (SAMA/) SAMAL B.  
XX PA (LIYY/) LI Y.  
XX PA (HERM/) HERMIDA L C.  
XX PA (HOPR/) HOPRA N L.  
XX PA (JOHE/) JOHE K K.  
XX PI Samal B, Li Y, Hermida LC, Hopra NL, Johe KK;  
XX DR WPI; 2003-831617/77.  
XX PT Generating five prime biased tandem tag libraries of cDNAs by isolating a  
XX sample of mRNAs, amplifying the released tags, concatenating the  
XX amplified tags to form concatenated tags, amplifying and isolating the

PT concatenated tags.  
XX  
XX Disclosure; Page 6; 0pp; English.  
PS  
XX The present invention discloses a method for generating five prime biased  
CC tandem tag libraries of cDNAs. The step involves isolating a sample of  
CC mRNAs, amplifying the released tags, concatenating the amplified tags to  
CC form concatenated tags, amplifying and isolating the concatenated tags.  
CC The present sequence is human tandem tag DNA  
XX  
SQ Sequence 32 BP; 11 A; 10 C; 6 G; 5 T; 0 U; 0 Other;  
XX  
XX Query Match 2.6%; Score 25.6; DB 1; Length 32;  
XX Best Local Similarity 87.5%; Pred. No. 8.3e+02;  
XX Matches 28; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 778 TTTTAGTAGAGATGGCGTTACCCATGTTGGCC 809  
DB 32 TTTTAGTAGAGACGGGTTTCGCAATGTTGGCC 1  
XX  
XX RESULT 282  
XX AAA04017  
XX ID AAA04017 standard; DNA; 29 BP.  
XX AC AAA04017;  
XX XX  
XX 22-MAY-2000 (first entry)  
XX DT  
XX XX Polymorphic fragment of hypertension associated gene APOC4.  
XX DE  
XX XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;  
XX KM Lesch-Nyhan syndrome; muscular dystrophy; Miskott-Aldrich syndrome;  
XX KM Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;  
XX KM polycystic kidney disease; von Willebrand's disease; forensic; human;  
XX KM tuberosus sclerosis; hereditary hemorrhagica telangiectasia;  
XX KM familial colonic polyposis; osteogenesis imperfecta; porphyria;  
XX KM Ehlers-Danlos syndrome; ss.  
XX KM  
XX OS  
XX XX Homo sapiens.  
XX PN EP955382-A2.  
XX PD 10-NOV-1999.  
XX PF 07-MAY-1999; 99EP-00250150.  
XX PR 07-MAY-1998; 98US-0084641P.  
XX PR 03-MAY-1999; 99US-00304232.  
XX PA (AFFY-) AFFYMETRIX INC.  
XX PA (UYCA-) UNIV CASE WESTERN RESERVE.  
XX PI Pan JB, Chakravarti A, Haineska MK;  
XX DR WPI; 2000-107928/10.  
XX PT Novel nucleic acids containing polymorphisms used in the diagnosis of  
XX hypertension.  
XX  
XX Claim 1; Page 23; 53pp; English.  
XX The invention provides polymorphic fragments of genes associated with  
XX hypertension. The nucleic acids including the polymorphic sites can be  
XX used as probes or primers for expressing variant proteins. Detection of  
XX the polymorphisms is useful in designing prophylactic and therapeutic  
XX regimes customized to underlying abnormalities. The polymorphisms can be  
XX used for association studies for hypertension, and in hypertension  
XX diagnostic assays. Where the polymorphisms have strong correlation with  
XX hypertension, within a gene, they are likely to have a causative role in  
XX hypertension. This information can be used to find the precise role of a  
XX polymorphism in the disease, and this can be used to identify potential  
XX drugs which combat the disease. The polymorphisms can be tested for



association with other diseases e.g. agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria. The polymorphic forms can also be used in forensics to identify individuals

Sequence 29 BP; 3 A; 6 C; 12 G; 7 T; 0 U; 1 Other;

Query Match 2.6%; Score 25.4; DB 1; Length 29;

Best Local Similarity 89.7%; Pred. No. 8e+02;

Matches 26; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

644 CCAAGCTGAGTGCAGTGGCGCAATCTTG 672

1 CCAAGCTGAGTGCAGTGGCGCAATCTTG 29

RESULT 283

AAA04065/c

ID AAA04065 standard; DNA; 29 BP.

AAA04065;

22-MAY-2000 (first entry)

Polymorphic fragment of hypertension associated gene BIR.

Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus; Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome; Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis; polycystic kidney disease; von Willebrand's disease; forensics; human; tuberous sclerosis; hereditary hemorrhagic telangiectasia; familial colonic polyposis; osteogenesis imperfecta; porphyria; Ehlers-Danlos syndrome; ss.

Homo sapiens.

EP955382-A2.

10-NOV-1999.

07-MAY-1999; 99EP-00250150.

07-MAY-1998; 98US-0084641P.

03-MAY-1999; 99US-00304232.

(AFPY-) AFFYMETRIX INC.

(UYCA-) UNIV CASE WESTERN RESERVE.

Fan JB, Chakravarti A, Haluska MK;

WPI; 2000-107928/10.

Novel nucleic acids containing polymorphisms used in the diagnosis of hypertension.

Claim 1; Page 24; 53pp; English.

The invention provides polymorphic fragments of genes associated with hypertension. The nucleic acids including the polymorphic sites can be used as probes or primers for expressing variant proteins. Detection of the polymorphisms is useful in designing prophylactic and therapeutic regimens customized to underlying abnormalities. The polymorphisms can be used for association studies for hypertension, and in hypertension diagnostic assays. Where the polymorphisms have strong correlation with hypertension, within a gene, they are likely to have a causative role in hypertension. This information can be used to find the precise role of a polymorphism in the disease, and this can be used to identify potential drugs which combat the disease. The polymorphisms can be tested for association with other diseases e.g. agammaglobulinemia, diabetes

insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria. The polymorphic forms can also be used in forensics to identify individuals

Sequence 29 BP; 7 A; 7 C; 11 G; 3 T; 0 U; 1 Other;

Query Match 2.6%; Score 25.4; DB 1; Length 29;

Best Local Similarity 89.7%; Pred. No. 8e+02;

Matches 26; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

670 TTGGCTCACTGCAACCTTGCTCCCGG 698

29 TTGGCTCACTGCAACCTTGCTCCCGG 1

RESULT 284

AAA03995

ID AAA03995 standard; DNA; 29 BP.

AAA03995;

22-MAY-2000 (first entry)

Polymorphic fragment of hypertension associated gene APOC4.

Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus; Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome; Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis; polycystic kidney disease; von Willebrand's disease; forensics; human; tuberous sclerosis; hereditary hemorrhagic telangiectasia; familial colonic polyposis; osteogenesis imperfecta; porphyria; Ehlers-Danlos syndrome; ss.

Homo sapiens.

EP955382-A2.

10-NOV-1999.

07-MAY-1999; 99EP-00250150.

07-MAY-1998; 98US-0084641P.

03-MAY-1999; 99US-00304232.

(AFPY-) AFFYMETRIX INC.

(UYCA-) UNIV CASE WESTERN RESERVE.

Fan JB, Chakravarti A, Haluska MK;

WPI; 2000-107928/10.

Novel nucleic acids containing polymorphisms used in the diagnosis of hypertension.

Claim 1; Page 22; 53pp; English.

The invention provides polymorphic fragments of genes associated with hypertension. The nucleic acids including the polymorphic sites can be used as probes or primers for expressing variant proteins. Detection of the polymorphisms is useful in designing prophylactic and therapeutic regimens customized to underlying abnormalities. The polymorphisms can be used for association studies for hypertension, and in hypertension diagnostic assays. Where the polymorphisms have strong correlation with hypertension, within a gene, they are likely to have a causative role in hypertension. This information can be used to find the precise role of a polymorphism in the disease, and this can be used to identify potential drugs which combat the disease. The polymorphisms can be tested for association with other diseases e.g. agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich

CC syndrome, Fabry's disease, familial hypercholesterolemia, polycystic  
CC kidney disease, hereditary spherocytosis, von Willebrand's disease,  
CC tuberos sclerosi, hereditary hemorrhagica telangiectasia, familial  
CC colonic polypoid, Ehlers-Danlos syndrome, osteogenesis imperfecta, and  
CC acute intermittent porphyria. The polymorphic forms can also be used in  
CC forensics to identify individuals

SQ Sequence 29 BP; 4 A; 10 C; 8 G; 6 T; 0 U; 1 Other;

Query Match 2.6%; Score 25.4; DB 1; Length 29;  
Best Local Similarity 89.7%; Pred. No. 8e+02; Indels 0; Gaps 0;  
Matches 26; Conservative 1; Mismatches 2;

OY 843 CCTGCCTGCGCTCCCAAGTCTGGAT 871  
DB 1 CCCGCTTGCTCTCAAGTCTGGAT 29

RESULT 285  
AAA04512  
ID AAA04512 standard; DNA; 29 BP.  
AC AAA04512;  
DT 22-MAY-2000 (first entry)  
DE Polymorphic fragment of hypertension associated gene PGIS.  
XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;  
XX Leech-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;  
XX Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;  
XX polycystic kidney disease; von Willebrand's disease; forensic; human;  
XX tuberos sclerosi; hereditary hemorrhagica telangiectasia;  
XX familial colonic polypoid; osteogenesis imperfecta; porphyria;  
XX Ehlers-Danlos syndrome; ss.  
XX Homo sapiens.  
XX EP955382-A2.  
XX 10-NOV-1999.  
XX 07-MAY-1999; 99EP-00250150.  
XX PF 07-MAY-1998; 98US-0084641P.  
XX PR 03-MAY-1999; 99US-00304232.  
XX PA (AFRY-) AFFYMETRIX INC.  
XX PA (UYCA-) UNIV CASE WESTERN RESERVE.  
XX PI Fan JB, Chakravarti A, Haluska MK;  
XX WPI; 2000-107928/10.  
XX Novel nucleic acids containing polymorphisms used in the diagnosis of  
XX hypertension.  
XX Claim 1; Page 39; 53bp; English.

CC The invention provides polymorphic fragments of genes associated with  
CC hypertension. The nucleic acids including the polymorphic sites can be  
CC used as probes or primers for expressing variant proteins. Detection of  
CC the polymorphisms is useful in designing prophylactic and therapeutic  
CC regimes customized to underlying abnormalities. The polymorphisms can be  
CC used for association studies for hypertension, and in hypertension  
CC diagnostic assays. Where the polymorphisms have strong correlation with  
CC hypertension, within a gene, they are likely to have a causative role in  
CC hypertension. This information can be used to find the precise role of a  
CC polymorphism in the disease, and this can be used to identify potential  
CC drugs which combat the disease. The polymorphisms can be tested for  
CC association with other diseases e.g. agammaglobulinemia, diabetes  
CC insipidus, Leech-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich  
CC syndrome, Fabry's disease, familial hypercholesterolemia, polycystic

CC kidney disease, hereditary spherocytosis, von Willebrand's disease,  
CC tuberos sclerosi, hereditary hemorrhagica telangiectasia, familial  
CC colonic polypoid, Ehlers-Danlos syndrome, osteogenesis imperfecta, and  
CC acute intermittent porphyria. The polymorphic forms can also be used in  
CC forensics to identify individuals

SQ Sequence 29 BP; 7 A; 10 C; 7 G; 4 T; 0 U; 1 Other;

Query Match 2.6%; Score 25.4; DB 1; Length 29;  
Best Local Similarity 89.7%; Pred. No. 8e+02; Indels 0; Gaps 0;  
Matches 26; Conservative 1; Mismatches 2;

OY 869 GATTACAGCGCTGAGCCACCGCCGCGC 897  
DB 1 GATTACAGCGATGACCGACCGCCGCGC 29

RESULT 286  
AAA04499  
ID AAA04499 standard; DNA; 29 BP.  
AC AAA04499;  
DT 22-MAY-2000 (first entry)  
DE Polymorphic fragment of hypertension associated gene PGIS.  
XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;  
XX Leech-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;  
XX Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;  
XX polycystic kidney disease; von Willebrand's disease; forensic; human;  
XX tuberos sclerosi; hereditary hemorrhagica telangiectasia;  
XX familial colonic polypoid; osteogenesis imperfecta; porphyria;  
XX Ehlers-Danlos syndrome; ss.  
XX Homo sapiens.  
XX EP955382-A2.  
XX 10-NOV-1999.  
XX 07-MAY-1999; 99EP-00250150.  
XX PF 07-MAY-1998; 98US-0084641P.  
XX PR 03-MAY-1999; 99US-00304232.  
XX PA (AFRY-) AFFYMETRIX INC.  
XX PA (UYCA-) UNIV CASE WESTERN RESERVE.  
XX PI Fan JB, Chakravarti A, Haluska MK;  
XX WPI; 2000-107928/10.  
XX Novel nucleic acids containing polymorphisms used in the diagnosis of  
XX hypertension.  
XX Claim 1; Page 38; 53bp; English.

CC The invention provides polymorphic fragments of genes associated with  
CC hypertension. The nucleic acids including the polymorphic sites can be  
CC used as probes or primers for expressing variant proteins. Detection of  
CC the polymorphisms is useful in designing prophylactic and therapeutic  
CC regimes customized to underlying abnormalities. The polymorphisms can be  
CC used for association studies for hypertension, and in hypertension  
CC diagnostic assays. Where the polymorphisms have strong correlation with  
CC hypertension, within a gene, they are likely to have a causative role in  
CC hypertension. This information can be used to find the precise role of a  
CC polymorphism in the disease, and this can be used to identify potential  
CC drugs which combat the disease. The polymorphisms can be tested for  
CC association with other diseases e.g. agammaglobulinemia, diabetes  
CC insipidus, Leech-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich  
CC syndrome, Fabry's disease, familial hypercholesterolemia, polycystic  
CC kidney disease, hereditary spherocytosis, von Willebrand's disease,

CC tuberous sclerosis, hereditary hemorrhagica telangiectasia, familial  
CC colonic polyps, Ehlers-danlos syndrome, osteogenesis imperfecta, and  
CC acute intermittent porphyria. The polymorphic forms can also be used in  
CC forensics to identify individuals

Sequence 29 BP; 4 A; 12 C; 5 G; 7 T; 0 U; 1 Other;

Query Match	2.6%	Score 25.4	DB 1	length 29
Best Local Similarity	89.7%	Pred. No. 8e+02		
Matches 26	Conservative 1	Mismatches 2	Indels 0	Gaps 0

674 CTCACTGCAACCTCTGCCCTCCCGGTTCA 702

Db 1 CTCACCTGCAAGCTCYGCCCTCCCGTTC 29

RESULT 287  
AAA03984/C  
ID AAA03984 standard; DNA; 29 BP.

AC AAA03984;

DT 22-MAY-2000 (first entry)

DE Polymorphic fragment of hypertension associated gene APOC3.

KM Polymorbism; hypertension; agammaglobulinemia; diabetes insipidus;  
KM Leech-Nyhan syndrome; muscular dystrophy; Miskot-Aldrich syndrome;  
KM Fabry disease, familial hypercholesterolemia; hereditary spherocytosis  
KM polycystic kidney disease; von Willebrand disease; forensic; human,  
KM tuberos sclerosis; hereditary hemorrhagica telangiectasia;  
KM familial colonic polyposis; osteogenesis imperfecta; porphyria;  
KM Ehlers-Danlos syndrome; ss.

OS Homo sapiens.

PN EP955382-A2.

PD 10-NOV-1999.

PF 07-MAY-1999; 99EP-00250150.

PR 07-MAY-1998; 98US-0084641P.

XX	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
XX	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

PA (UYCA-) UNIV CASE WESTERN RESERVE.

PI Fan JB, Chakravarti A, Haluska MK;

WPI; 2000-107928/10.

PT Novel nucleic acids

XX

2000

the amino acid sequence of a protein. The polymorphic sites can be used as probes or primers for expressing variant proteins. Detection of the polymorphisms is useful in designing prophylactic and therapeutic regimes customized to underlying abnormalities. The polymorphisms can be used for association studies for hypertension, and in hypertension diagnostic assays. Where the polymorphisms have strong correlation with hypertension, within a gene, they are likely to have a causative role in hypertension. This information can be used to find the precise role of a polymorphism in the disease, and this can be used to identify potential drugs which combat the disease. The polymorphisms can be tested for association with other diseases e.g. agammaglobulinemia, diabetes insipidus, Leach-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, fibrous scleroses, hereditary hemorrhagica telangiectasia, familial

colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria. The polymorphic forms can also be used in forensics to identify individuals

SQ Sequence 29 BP; 7 A; 4 C; 12 G; 5 T; 0 U; 1 Other;

Query Match	2.6%	Score	25.4	DB	1	Length	29
Best Local Similarity	89.7%	Pred. No.	8e+02				
Matches	26	Conservative	1	Mismatches	2	Indels	0
						Gaps	0

675 TCACTGCAACCTCTGCCTCCCGGTTCAA 703

Db 29 TCACTGCAACCTCCRTCTCCCGGTTCAA 1

RESULT 288  
AAA04645  
ID AAA04645 standard; DNA; 29 BP

AC AAA046457

DT 22-MAY-2000 (first entry)

DE Polymorphic fragment of hypertension associated gene TBXA2R

KM Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;  
 KM Leach-Nathan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;  
 KM Fabry disease; familial hypercholesterolemia; hereditary spherocytosis  
 KM polycystic kidney disease; von Willebrand disease; forensic; human;  
 KM tuberous sclerosis; hereditary hemorrhagic telangiectasia;  
 KM familial colonic polyposis; osteogenesis imperfecta; porphyria;  
 KM Ehlers-Danlos syndrome; ss.

**Homo sapiens.**

PN EP955382-A2.

PD 10-NOV-1999

PF 07-MAY-1999; 99EP-00250150.

PR 07-MAY-1998; 98US-0084641P.

XX

PA (UYCA-) UNIV CASE WESTERN RESERVE.

PI Fan JB, Chakravarti A, Haluska MK

DR WPI; 2000-107928/10

PT Novel nucleic acids

XX

100

the transcription process. The nucleic acids including the polymorphic sites can be used as probes or primers for expressing variant proteins. Detection of the polymorphisms is useful in designing prophylactic and therapeutic regimens customized to underlying abnormalities. The polymorphisms can be used for association studies for hypertension, and in hypertension diagnostic assays. Where the polymorphisms have strong correlation with hypertension, within a gene, they are likely to have a causative role in hypertension. This information can be used to find the precise role of a polymorphism in the disease, and this can be used to identify potential drugs which combat the disease. The polymorphisms can be tested for association with other diseases e.g. agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand disease, familial tuberous sclerosis, hereditary hemorrhagica telangiectasia, familial colonic polyps, Ehlers-Danlos syndrome, osteogenesis imperfecta, and

CC acute intermittent porphyria. The polymorphic forms can also be used in  
CC forensics to identify individuals  
XX  
SQ Sequence 29 BP; 6 A; 9 C; 8 G; 5 T; 0 U; 1 Other;

Query Match 2.6%; Score 25.4; DB 1; Length 29;  
Best Local Similarity 89.7%; Pred. No. 8e+02;  
Matches 26; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1017 CTCAGCTCCGACGAGCTGGATTACGG 1045  
DB 1 CTCAGCTCCGAGAGCTGGATTACAG 29

## RESULT 289

AAH38989  
ID AAH38989 standard; DNA; 30 BP.

AC AAH38989;

DT 14-AUG-2001 (first entry)

DE SNP specific upper PCR primer SEQ ID 1785.

XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
XX SNP; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;  
XX Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;  
XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
XX inflammation; forensic investigation; paternity analysis; PCR primer; ss.  
OS Homo sapiens.

PN WO200129262-A2.

PD 26-APR-2001.

PF 13-OCT-2000; 2000WO-US028436.

PR 15-OCT-1999; 99US-0160096P.

PA (ORCH-) ORCHID BIOSCIENCES INC.

PI Picoult-Newburg L, Pohl M;

DR WPI; 2001-290930/30.

PT New genotyping oligonucleotide, useful for detecting the presence,  
PT absence or identity of single polynucleotide polymorphism in a nucleic  
PT acid sample.

PS Claim 1; Page 59; 83pp; English.

XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
XX primer extension (SNPE) primers, and the sequences of regions flanking  
XX sites of single nucleotide polymorphisms SNPs. The present invention  
XX includes kits for determining the presence or absence of a SNP, using the  
XX oligonucleotides of the invention. The PCR primers are used to amplify a  
XX SNP flanking sequence, the SNPs primer is used as a genotyping primer.  
XX The oligonucleotides are useful for genotyping a nucleic acid sample by  
XX performing a single-nucleotide primer extension reaction. The  
XX oligonucleotides are useful for determining the presence, absence or  
XX identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
XX assess by association analysis the genotype of an individual or group of  
XX individuals, having a pathological phenotypic trait suspected of being  
XX caused by one or more SNPs. Phenotypic traits include diseases e.g.  
XX agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular  
XX dystrophy, familial hypercholesterolaemia, polycystic kidney disease,  
XX osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
XX traits also include symptoms of or susceptibility to multifactorial  
XX disease of which a component is or may be genetic such as autoimmune  
XX diseases, including, rheumatoid arthritis, multiple sclerosis,  
XX inflammation, cancer, nervous system diseases and infection by pathogenic

CC microorganism. The method is also useful in forensic investigations and  
CC paternity analysis. The present sequence represents a PCR primer specific  
CC for a human SNP containing DNA sequence  
XX

SQ Sequence 30 BP; 6 A; 1 C; 7 G; 16 T; 0 U; 0 Other;

Query Match 2.6%; Score 25.4; DB 1; Length 30;  
Best Local Similarity 96.3%; Pred. No. 8.2e+02;  
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 767 TTTTGTGATTTTGTAGAGATGGG 793  
DB 4 TTTTGTGATTTTGTAGAGACGG 30

## RESULT 290

AAH40734  
ID AAH40734 standard; DNA; 30 BP.

AC AAH40734;

DT 14-AUG-2001 (first entry)

DE SNP specific lower PCR primer SEQ ID 3530.

XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
XX SNP; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;  
XX Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;  
XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
XX inflammation; forensic investigation; paternity analysis; PCR primer; ss.  
OS Homo sapiens.

PN WO200129262-A2.

PD 26-APR-2001.

PF 13-OCT-2000; 2000WO-US028436.

PR 15-OCT-1999; 99US-0160096P.

PA (ORCH-) ORCHID BIOSCIENCES INC.

PI Picoult-Newburg L, Pohl M;

DR WPI; 2001-290930/30.

PT New genotyping oligonucleotide, useful for detecting the presence,  
PT absence or identity of single polynucleotide polymorphism in a nucleic  
PT acid sample.

PS Claim 1; Page 68; 83pp; English.

XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
XX primer extension (SNPE) primers, and the sequences of regions flanking  
XX sites of single nucleotide polymorphisms SNPs. The present invention  
XX includes kits for determining the presence or absence of a SNP, using the  
XX oligonucleotides of the invention. The PCR primers are used to amplify a  
XX SNP flanking sequence, the SNPE primer is used as a genotyping primer.  
XX The oligonucleotides are useful for genotyping a nucleic acid sample by  
XX performing a single-nucleotide primer extension reaction. The  
XX oligonucleotides are useful for determining the presence, absence or  
XX identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
XX assess by association analysis the genotype of an individual or group of  
XX individuals, having a pathological phenotypic trait suspected of being  
XX caused by one or more SNPs. Phenotypic traits include diseases e.g.  
XX agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular  
XX dystrophy, familial hypercholesterolaemia, polycystic kidney disease,  
XX osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
XX traits also include symptoms of or susceptibility to multifactorial  
XX disease of which a component is or may be genetic such as autoimmune  
XX diseases, including, rheumatoid arthritis, multiple sclerosis,

CC inflammation, cancer, nervous system diseases and infection by pathogenic  
CC microorganism. The method is also useful in forensic investigations and  
CC paternity analysis. The present sequence represents a PCR primer specific  
CC for a human SNP containing DNA sequence

XX SQ Sequence 30 BP; 7 A; 2 C; 8 G; 13 T; 0 U; 0 Other;

Query Match 2.5%; Score 25.2; DB 1; Length 30;  
Best Local Similarity 90.0%; Pred. No. 8.3e+02;  
Matches 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1066 CTAATTTTGTATTTTCATTAGAGCGCGG 1095  
DB 1 CTAATTTTGTATTTTGTAGAGCGCGG 30

RESULT 291  
AAQ25353/C  
ID AAQ25353 standard; DNA; 25 BP.

XX AC AAQ25353;

XX DT 21-NOV-1992 (first entry)

XX DE Sequence of probe Alu 1.

XX KM Hybridisation rate; chondroitin sulphate; probe; probe cocktail; Alu 1;  
XX 88.

XX OS Synthetic.

XX PN US5116727-A.

XX PD 26-MAY-1992.

XX PF 31-AUG-1989; 89US-00404990.

XX PR 31-AUG-1989; 89US-00404990.

XX PA (INIT-) INITIATIVE MARITIME 1991 SRL.

XX PI Brigati DJ;

XX DR WPI; 1992-199514/24.

XX PT Increasing hybridisation rate between complementary polynucleotide cpds.

XX PT - using water-soluble hetero:polysaccharide with sulphated N-  
XX acetyl:galactosamine units.

XX PS Example; Col 7; 6pp; English.

XX CC Alu 1 and Alu 2 probes were used in hybridisations carried out in an aq.

XX CC medium comprising a cocktail of: 10% chondroitin sulphate A; 45%  
XX CC furmamide; 5% saline citrate; 25mm phosphate; & 250 micro-g/ml sheared

XX CC herring sperm DNA. The probes were chemically labelled with 3-4 biotin

XX CC molecules per probe at the 3' termin. Excellent staining of the DNA of

XX CC human cell nuclei resulted when either of the Alu 1 or Alu 2 probes were

XX CC present at 60 ng/ml (or each was present at 30 ng/ml) of the probe

XX CC cocktail

XX SQ Sequence 25 BP; 5 A; 6 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 2.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 381 AGCCTCCCAAGTCTGGATTACA 405  
DB 25 AGCCTCCCAAGTCTGGATTACA 1

RESULT 292  
AAH40799

ID AAH40799 standard; DNA; 25 BP.

XX AAH40799;

XX AC 14-AUG-2001 (first entry)

XX DT SNP specific SNPE primer SEQ ID 3595.

XX DE Single nucleotide polymorphism; SNP; single nucleotide primer extension;

XX SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

XX Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;

XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;

XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;

XX inflammation; forensic investigation; paternity analysis; primer; 89.

XX OS Homo sapiens.

XX PN WO200129262-A2.

XX PD 26-APR-2001.

XX PF 13-OCT-2000; 2000WO-US028436.

XX PR 15-OCT-1999; 99US-0160096P.

XX PA (ORCH-) ORCHID BIOSCIENCES INC.

XX PI Picoult-Newburg L; Pohl M;

XX DR WPI; 2001-290930/30.

XX PT New genotyping oligonucleotide, useful for detecting the presence,

XX PT absence or identity of single polynucleotide polymorphism in a nucleic

XX PT acid sample.

XX PS Claim 1; Page 68; 83pp; English.

XX CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide

XX CC primer extension (SNPE) primers, and the sequences of regions flanking

XX CC sites of single nucleotide polymorphisms SNPs. The present invention

XX CC includes kits for determining the presence or absence of a SNP, using the

XX CC oligonucleotides of the invention. The PCR primers are used to amplify a

XX CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.

XX CC The oligonucleotides are useful for genotyping a nucleic acid sample by

XX CC performing a single-nucleotide primer extension reaction. The

XX CC oligonucleotides are useful for determining the presence, absence or

XX CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to

XX CC assess by association analysis the genotype of an individual or group of

XX CC individuals, having a pathological phenotypic trait suspected of being

XX CC caused by one or more SNPs. Phenotypic traits include diseases e.g.

XX CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular

XX CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,

XX CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic

XX CC traits also include symptoms of or susceptibility to multifactorial

XX CC disease of which a component is or may be genetic such as autoimmune

XX CC diseases, including, rheumatoid arthritis, multiple sclerosis,

XX CC inflammation, cancer, nervous system diseases and infection by pathogenic

XX CC microorganism. The method is also useful in forensic investigations and

XX CC paternity analysis. The present sequence represents a single nucleotide

XX CC primer extension (SNPE) primer specific for a human SNP containing DNA

XX CC sequence

XX SQ Sequence 25 BP; 6 A; 4 C; 10 G; 5 T; 0 U; 0 Other;

Query Match 2.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 860 AAGTCTGGATTACAGCGCTGAGC 884  
DB 1 AAGTCTGGATTACAGCGCTGAGC 25

RESULT 293  
 AAS15700  
 ID AAS15700 standard; DNA; 25 BP.  
 XX  
 AC AAS15700;  
 XX  
 DT 29-JAN-2002 (first entry)  
 XX  
 DE Human Alu sequence PCR primer #2.  
 XX  
 KW Human; Alu sequence; ss; PCR primer; human immunodeficiency virus;  
 KW latent HIV detection; LTR; long terminal repeat;  
 KW anti-retroviral drug therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200181541-A2.  
 XX  
 PD 01-NOV-2001.  
 XX  
 PF 19-APR-2001; 2001WO-US012711.  
 XX  
 PR 19-APR-2000; 2000US-0198884P.  
 XX  
 PA (RERE-) RES DEV FOUND.  
 XX  
 PI Cloyd MW, Yeh CM, Chen J;  
 XX  
 DR WPI; 2002-026164/03.  
 XX  
 PT Detecting integrated retroviruses in human sample, comprises amplifying  
 PT DNA in sample using primers specific for Alu and retroviral sequences and  
 PT detecting hybridization of probe recognizing amplified retroviral  
 PT sequence.  
 XX  
 PS Claim 10; Page 9; 28pp; English.  
 XX  
 CC The invention relates to detecting integrated retroviruses in a human  
 CC tissue sample comprising amplifying DNA in the sample with polymerase  
 CC chain reaction (PCR) using one primer for an Alu sequence and the other  
 CC primer for a retroviral sequence (e.g. human immunodeficiency virus 1  
 CC long terminal repeat, LTR), hybridising the PCR-amplified DNA with a  
 CC probe that specifically recognises the amplified retroviral sequence and  
 CC detecting hybridisation of the probe, where the hybridisation indicates  
 CC presence of integrated retrovirus in the sample. The method is useful for  
 CC detecting integrated retroviruses in human tissue sample such as paraffin  
 CC embedded tissue sections or frozen tissue sections of lymphocytes, blood,  
 CC or lymph nodes. The method quantitatively determines the number of cells  
 CC with integrated HIV in the human tissue sample. The method is useful for  
 CC determining and monitoring latent infection, preferably human  
 CC immunodeficiency virus (HIV) latent infection in patients. The method  
 CC only detects integrated retroviruses, and thus allows accurate assessment  
 CC of the frequency of productively and latently infected cells together in  
 CC patients. The method may be adapted in many forms of quantitative assays  
 CC of latent human immunodeficiency virus (HIV) infection in infected  
 CC subjects undergoing anti-retroviral drug therapy and allows physicians to  
 CC monitor the presence of latently infected cells so that they can  
 CC determine whether treatment should be discontinued or not. The present  
 CC sequence is a human Alu sequence PCR primer used in the method of the  
 CC invention  
 CC  
 SQ Sequence 25 BP; 6 A; 7 C; 7 G; 5 T; 0 U; 0 Other;  
 Query Match 2.5%; Score 25; DB 1; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 382 GCCTCCCAAGTGGGATTACAG 406  
 Db 1 GCCTCCCAAGTGGGATTACAG 25

ABT03658  
 ID ABT03658 standard; DNA; 25 BP.  
 XX  
 AC ABT03658;  
 XX  
 DT 13-SEP-2002 (first entry)  
 XX  
 DE Human Med-6 gene PCR primer SEQ ID NO: 179.  
 XX  
 KW Human; cancer; neoplastic disease; tumour specific marker; cytostatic;  
 KW transcription factor; PCR; primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200240716-A2.  
 XX  
 PD 23-MAY-2002.  
 XX  
 PF 13-NOV-2001; 2001WO-US043461.  
 XX  
 PR 16-NOV-2000; 2000US-0249508P.  
 XX  
 PA (CEMT-) CEMINES LLC.  
 XX  
 PI Palm K;  
 XX  
 DR WPI; 2002-537346/57.  
 XX  
 PT Determining the presence of neoplastic molecular markers, by identifying  
 PT the presence of markers in host test sample using array of neoplastic  
 PT molecular marker specific reagents and analyzing the array of the  
 PT reagents.  
 XX  
 PS Example 1; Page 16; 41pp; English.  
 XX  
 CC The present invention relates to a method for determining the presence of  
 CC neoplastic molecular markers in a host, involving the use of neoplastic  
 CC molecular marker specific reagents to detect such markers and analysing  
 CC the array of reagents, allowing the identification of the neoplastic  
 CC disease present. This can be used to determine the best treatment for  
 CC cancer, in particular neural cell, lung and prostate tumours. The  
 CC present sequence is a PCR primer useful for detecting the coding  
 CC sequences of markers of the invention  
 CC  
 SQ Sequence 25 BP; 7 A; 4 C; 9 G; 5 T; 0 U; 0 Other;  
 Query Match 2.5%; Score 25; DB 1; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 858 CAAAGTGTGGGATTACAGGCGTGA 882  
 Db 1 CAAAGTGTGGGATTACAGGCGTGA 25

RESULT 295  
 AAH91598  
 ID AAH91598 standard; DNA; 29 BP.  
 XX  
 AC AAH91598;  
 XX  
 DT 09-OCT-2001 (first entry)  
 XX  
 DE Human inflammatory bowel disease associated polymorphic site #673.  
 XX  
 KW Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;  
 KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;  
 KW chromosome 5q31-33; forensic test; gene therapy; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 Key Location/Qualifiers  
 FH misc\_feature 15  
 FT

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FT      /tag= a
FT      /note= "SNP, optionally A or C at this position"
XX      WO200142511-A2.
XX      14-JUN-2001.
XX      11-DEC-2000; 2000WO-US033632.
XX      10-DEC-1999; 99US-0170257P.
XX      10-APR-2000; 2000US-0196046P.
XX      (WHEED ) WHITEHEAD INST BIOMEDICAL RES.
XX      (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.
XX      Daly M, Hudson TJ, Lander ES, Rixou J, Simionovitch K;
XX      WPI, 2001-367874/38.
XX      Testing for the presence of polymorphisms associated with inflammatory
XX      bowel disease, using a hybridization assay.
XX      Claim 1, Page 67; 463pp; English.
XX      The present invention describes a method for detecting the presence of
XX      polymorphisms associated with inflammatory bowel diseases such as
XX      ulcerative colitis and Crohn's disease. The methods can be used to detect
XX      the presence of genetic polymorphisms associated with inflammatory bowel
XX      disease and correlating their occurrence with disease states. They may be
XX      used in this way for phenotypic correlations, forensic, paternity
XX      testing, medicine and genetic analysis. The present sequence is a
XX      polymorphic site described in the exemplification of the invention
XX      SO      Sequence 29 BP; 4 A; 12 C; 6 G; 6 T; 0 U; 1 Other;
XX      Query Match      2.5%; Score 24.8; DB 1; Length 29;
XX      Best Local Similarity 89.7%; Pred. No. 8.5e+02;
XX      Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY      670 TTGGCTCAGTCGCACTGCTGCTCCGGG 698
DB      1 TTGGCTCAGTCGCACTGCTCCGGG 29
XX      RESULT 296
XX      ID      AAA03985/C
XX      ID      AAA03985 standard; DNA; 29 BP.
XX      AC      AAA03985;
XX      XX      22-MAY-2000 (first entry)
XX      DE      Polymorphic fragment of hypertension associated gene APOC3.
XX      XX      Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus; *
XX      KM      Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
XX      KM      Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;
XX      KM      polycystic kidney disease; von Willebrand's disease; forensic; human;
XX      KM      tuberous sclerosis; hereditary hemorrhagic telangiectasia;
XX      KM      familial colonic polyposis; osteogenesis imperfecta; porphyria;
XX      KM      Ehlers-Danlos syndrome; ss.
XX      XX      Homo sapiens.
XX      OS      Homo sapiens.
XX      PN      EP95382-A2.
XX      XX      10-NOV-1999.
XX      PD      07-MAY-1999; 99EP-00250150.
XX      PF      07-MAY-1999; 99US-0084641P.
XX      PR      03-MAY-1999; 99US-00304232.
XX      PT
XX

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PA      (AFRY-) AFRYMETRIX INC.
PA      (UYCA-) UNIV CASE WESTERN RESERVE.
XX      PI      Fan JB, Chakravarti A, Haluska MK;
XX      DR      WPI; 2000-107928/10.
XX      PT      Novel nucleic acids containing polymorphisms used in the diagnosis of
XX      PT      hypertension.
XX      PS      Claim 1, Page 22; 53pp; English.
XX      The invention provides polymorphic fragments of genes associated with
XX      hypertension. The nucleic acids including the polymorphic sites can be
XX      used as probes or primers for expressing variant proteins. Detection of
XX      the polymorphisms is useful in designing prophylactic and therapeutic
XX      regimes customized to underlying abnormalities. The polymorphisms can be
XX      used for association studies for hypertension, and in hypertension
XX      diagnostic assays. Where the polymorphisms have strong correlation with
XX      hypertension, within a gene, they are likely to have a causative role in
XX      hypertension. This information can be used to find the precise role of a
XX      polymorphism in the disease, and this can be used to identify potential
XX      drugs which combat the disease. The polymorphisms can be tested for
XX      association with other diseases e.g. agammaglobulinemia, diabetes
XX      insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich
XX      syndrome, Fabry's disease, familial hypercholesterolemia, polycystic
XX      kidney disease, hereditary spherocytosis, von Willebrand's disease,
XX      tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial
XX      colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and
XX      acute intermittent porphyria. The polymorphic forms can also be used in
XX      forensics to identify individuals
XX      SO      Sequence 29 BP; 6 A; 8 C; 10 G; 4 T; 0 U; 1 Other;
XX      Query Match      2.5%; Score 24.6; DB 1; Length 29;
XX      Best Local Similarity 96.0%; Pred. No. 8.7e+02;
XX      Matches 24; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY      635 CTCTGTACCCAGGCTGAGTGAG 659
DB      25 CTCTGTACCCAGGCTGAGTGAG 1
XX      RESULT 297
XX      ID      ABK65978
XX      ID      ABK65978 standard; DNA; 26 BP.
XX      AC      ABK65978;
XX      XX      02-JUL-2002 (first entry)
XX      DE      Human gene specific PCR primer #66.
XX      KM      Primer; ss; DNA microarray; differential expression analysis; human.
XX      OS      Homo sapiens.
XX      PN      US6352829-B1.
XX      PD      05-MAR-2002.
XX      PF      05-JAN-1999; 99US-00225928.
XX      PR      21-MAY-1997; 97US-00859998.
XX      XX      (CLON-) CLONTECH LAB INC.
XX      PA      Chenchik A, Jekhadze G, Bibilashvili R;
XX      DR      WPI; 2002-314699/35.
XX      PT      Producing sub-population of labeled nucleic acids, useful for analyzing
XX      PT      differences in RNA profiles between several different physiological
XX

```

PT sources, using set of distinct gene specific primers.  
XX  
XX Example 3; SEQ ID NO 66; 11pp; English.  
XX  
XX The invention relates to producing a sub-population of labeled nucleic acids (NAs) comprising contacting a NA sample from a physiological source, with a pool of 50 distinct gene specific primers under suitable conditions to enzymatically generate sub-population of NAs, where each CC gene specific primer has a sequence complementary to a distinct mRNA, and CC each labeled NA is generated using a single gene specific primer. The CC method is useful for producing a sub-population of labeled NAs which is CC useful for analysing the differences in the RNA profiles between several CC different physiological sources, where the method comprises producing CC subpopulation of labeled NAs for the different physiological sources, CC comprising the populations for each physiological source to identify CC differences in the population, where the comparison is preferably CC performed by hybridising the labeled NAs for each of the distinct CC physiological sources to an array of probe NAs stably associated with the CC surface of a substrate to produce a hybridisation pattern for each of the CC sources, and comparing the patterns for each of the sources, where CC differential gene expression assays are utilised in differential CC tissue, or different tissue or sub-tissue types. The present sequence is a CC human gene specific PCR primer used in the method of the invention. Note: CC The sequence data for this patent did not form part of the printed CC specification, but was obtained in electronic format directly from USPTO CC at <http://wipo.segdata.uspto.gov/sequence.html?docID=6352829B1>  
XX  
SQ Sequence 26 BP; 8 A; 4 C; 9 G; 5 T; 0 U; 0 Other;  
XX  
Query Match 2.5%; Score 24.4; DB 1; Length 26;  
Best Local Similarity 96.2%; Pred. No. 8.3e+02;  
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 859 AAAGTCGCGGATTACAGCGCTGAGC 884  
DB 1 AAAGTCGCGGATTACAGCGCTGAGC 26  
RESULT 298  
ABK66984  
ID ABK66984 standard; DNA; 26 BP.  
XX  
XX ABK66984;  
XX  
XX 02-JUL-2002 (first entry)  
XX  
XX Human gene specific PCR primer #1072.  
XX  
XX Primer; ss; DNA microarray; differential expression analysis; human.  
XX  
XX Homo sapiens.  
XX  
XX US6352829-B1.  
XX  
XX 05-MAR-2002.  
XX  
XX 05-JAN-1999; 99US-00225928.  
XX  
XX 21-MAY-1997; 97US-00859998.  
XX  
XX (CLON-) CLONTECH LAB INC.  
XX  
XX Chenchik A, Johadze G, Bibilashvili R;  
XX  
XX WPI; 2002-314699/35.  
XX  
XX Producing sub-population of labeled nucleic acids, useful for analyzing PT differences in RNA profiles between several physiological  
PT sources, using set of distinct gene specific primers.  
XX  
XX Example 3; SEQ ID NO 1072; 11pp; English.  
XX  
XX

CC The invention relates to producing a sub-population of labeled nucleic acids (NAs) comprising contacting a NA sample from a physiological source, with a pool of 50 distinct gene specific primers under suitable conditions to enzymatically generate sub-population of NAs, where each CC gene specific primer has a sequence complementary to a distinct mRNA, and CC each labeled NA is generated using a single gene specific primer. The CC method is useful for producing a sub-population of labeled NAs which is CC useful for analysing the differences in the RNA profiles between several CC different physiological sources, where the method comprises producing CC subpopulation of labeled NAs for the different physiological sources, CC comprising the populations for each physiological source to identify CC differences in the population, where the comparison is preferably CC performed by hybridising the labeled NAs for each of the distinct CC physiological sources to an array of probe NAs stably associated with the CC surface of a substrate to produce a hybridisation pattern for each of the CC sources, and comparing the patterns for each of the sources, where CC differential gene expression assays are utilised in differential CC tissue, or different tissue or sub-tissue types. The present sequence is a CC human gene specific PCR primer used in the method of the invention. Note: CC The sequence data for this patent did not form part of the printed CC specification, but was obtained in electronic format directly from USPTO CC at <http://wipo.segdata.uspto.gov/sequence.html?docID=6352829B1>  
XX  
SQ Sequence 26 BP; 5 A; 5 C; 9 G; 7 T; 0 U; 0 Other;  
XX  
Query Match 2.5%; Score 24.4; DB 1; Length 26;  
Best Local Similarity 96.2%; Pred. No. 8.3e+02;  
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 650 TGAAGTGCAGTGGCGCAATCTTGCT 675  
DB 1 TGAAGTGCAGTGGCGCAATCTTGCT 26  
RESULT 299  
AAH91530  
ID AAH91530 standard; DNA; 28 BP.  
XX  
XX AAH91530;  
XX  
XX 09-OCT-2001 (first entry)  
XX  
XX Human inflammatory bowel disease associated polymorphic site #605.  
XX  
XX Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis; KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test; KW chromosome 5q31-33; forensic test; gene therapy; ds.  
XX  
XX Homo sapiens.  
XX  
XX OS  
XX  
XX Key location/Qualifiers  
FT misc\_feature 14  
FT /\*tag= a  
FT /note= "SNP, optionally C or G at this position"  
XX  
XX WO200142511-A2.  
XX  
XX 14-JUN-2001.  
XX  
XX 11-DEC-2000; 2000WO-US033632.  
XX  
XX 10-DEC-1999; 99US-0170257P.  
XX  
XX 10-APR-2000; 2000US-0196046P.  
XX  
XX (WHEED ) WHITEHEAD INST BIOMEDICAL RES.  
XX  
XX (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.  
XX  
XX Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;  
XX  
XX WPI; 2001-367874/38.  
XX  
XX Testing for the presence of polymorphisms associated with inflammatory PT



PT bowel disease, using a hybridization assay.  
XX  
XX  
PS Claim 1; Page 64; 463pp; English.  
XX  
CC The present invention describes a method for detecting the presence of  
CC polymorphisms associated with inflammatory bowel diseases such as  
CC ulcerative colitis and Crohn's disease. The methods can be used to detect  
CC the presence of genetic polymorphisms associated with inflammatory bowel  
CC disease and correlating their occurrence with disease states. They may be  
CC used in this way for phenotypic correlations, forensics, paternity  
CC testing, medicine and genetic analysis. The present sequence is a  
CC polymorphic site described in the exemplification of the invention  
XX  
SQ Sequence 28 BP; 4 A; 9 C; 4 G; 10 T; 0 U; 1 Other;  
XX  
Query Match 2.5%; Score 24.4; DB 1; Length 28;  
Best Local Similarity 92.6%; Pred. No. 8.7e+02;  
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1000 TCAAGGATTCTCTGCTCAGCCTCC 1026  
DB 2 TCAAGGATTCTCTGCTCAGCCTCC 28  
XX  
RESULT 300  
AAA04000/c  
ID AAA04000 standard; DNA; 29 BP.  
XX  
AC AAA04000;  
XX  
DT 22-MAY-2000 (first entry)  
XX  
DE Polymorphic fragment of hypertension associated gene APOC4.  
XX  
XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;  
XX Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;  
XX Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;  
XX polycystic kidney disease; von Willebrand's disease; forensic; human;  
XX tubercous sclerosis; hereditary hemorrhagica telangiectasia;  
XX familial colonic polyposis; osteogenesis imperfecta; porphyria;  
XX Ehlers-Danlos syndrome; ss.  
XX  
XX Homo sapiens.  
XX  
OS  
XX  
PN EP955382-A2.  
XX  
PD 10-NOV-1999.  
XX  
PF 07-MAY-1999; 99EP-00250150.  
XX  
PR 07-MAY-1998; 98US-0084641P.  
XX  
PR 03-MAY-1999; 99US-00304232.  
XX  
XX (AFFY-) AFFMETRIX INC.  
XX (UYCA-) UNIV CASE WESTERN RESERVE.  
XX  
PI Fan JB, Chakravarti A, Haluska MK;  
XX  
XX WPI; 2000-107928/10.  
XX  
PT Novel nucleic acids containing polymorphisms used in the diagnosis of  
PT hypertension.  
XX  
PS Claim 1; Page 22; 53pp; English.  
XX  
CC The invention provides polymorphic fragments of genes associated with  
CC hypertension. The nucleic acids including the polymorphic sites can be  
CC used as probes or primers for expressing variant proteins. Detection of  
CC the polymorphisms is useful in designing prophylactic and therapeutic  
CC regimes customized to underlying abnormalities. The polymorphisms can be  
CC used for association studies for hypertension, and in hypertension  
CC diagnostic assays. Where the polymorphisms have strong correlation with  
CC hypertension, within a gene, they are likely to have a causative role in

CC hypertension. This information can be used to find the precise role of a  
CC polymorphism in the disease, and this can be used to identify potential  
CC drugs which combat the disease. The polymorphisms can be tested for  
CC association with other diseases e.g. agammaglobulinemia, diabetes  
CC insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich  
CC syndrome, Fabry's disease, familial hypercholesterolemia, polycystic  
CC kidney disease, hereditary spherocytosis, von Willebrand's disease,  
CC tubercous sclerosis, hereditary hemorrhagica telangiectasia, familial  
CC colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and  
CC acute intermittent porphyria. The polymorphic forms can also be used in  
CC forensics to identify individuals  
XX  
SQ Sequence 29 BP; 7 A; 5 C; 12 G; 4 T; 0 U; 1 Other;  
XX  
Query Match 2.5%; Score 24.4; DB 1; Length 29;  
Best Local Similarity 89.3%; Pred. No. 8.9e+02;  
Matches 25; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1000 TCAAGGATTCTCTGCTCAGCCTCCC 1027  
DB 29 TCAAGGATTCTCTGCTCAGCCTCCC 2  
XX  
RESULT 301  
AAA04507  
ID AAA04507 standard; DNA; 29 BP.  
XX  
AC AAA04507;  
XX  
DT 22-MAY-2000 (first entry)  
XX  
DE Polymorphic fragment of hypertension associated gene PGLS.  
XX  
XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;  
XX Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;  
XX Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;  
XX polycystic kidney disease; von Willebrand's disease; forensic; human;  
XX tubercous sclerosis; hereditary hemorrhagica telangiectasia;  
XX familial colonic polyposis; osteogenesis imperfecta; porphyria;  
XX Ehlers-Danlos syndrome; ss.  
XX  
XX Homo sapiens.  
XX  
OS  
XX  
PN EP955382-A2.  
XX  
PD 10-NOV-1999.  
XX  
PF 07-MAY-1999; 99EP-00250150.  
XX  
PR 07-MAY-1998; 98US-0084641P.  
XX  
PR 03-MAY-1999; 99US-00304232.  
XX  
XX (AFFY-) AFFMETRIX INC.  
XX (UYCA-) UNIV CASE WESTERN RESERVE.  
XX  
PI Fan JB, Chakravarti A, Haluska MK;  
XX  
XX WPI; 2000-107928/10.  
XX  
PT Novel nucleic acids containing polymorphisms used in the diagnosis of  
PT hypertension.  
XX  
PS Claim 1; Page 38; 53pp; English.  
XX  
CC The invention provides polymorphic fragments of genes associated with  
CC hypertension. The nucleic acids including the polymorphic sites can be  
CC used as probes or primers for expressing variant proteins. Detection of  
CC the polymorphisms is useful in designing prophylactic and therapeutic  
CC regimes customized to underlying abnormalities. The polymorphisms can be  
CC used for association studies for hypertension, and in hypertension  
CC diagnostic assays. Where the polymorphisms have strong correlation with  
CC hypertension, within a gene, they are likely to have a causative role in  
CC hypertension. This information can be used to find the precise role of a

CC polymorphism in the disease, and this can be used to identify potential  
CC drugs which combat the disease. The polymorphisms can be tested for  
CC association with other diseases e.g. agammaglobulinemia, diabetes  
CC insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich  
CC syndrome, Fabry's disease, familial hypercholesterolemia, polycystic  
CC kidney disease, hereditary spherocytosis, von Willebrand's disease,  
CC tuberos sclerosis, hereditary hemorrhagica telangiectasia, familial  
CC colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and  
CC acute intermittent porphyria. The polymorphic forms can also be used in  
CC forensics to identify individuals

XX Sequence 29 BP; 6 A; 9 C; 9 G; 4 T; 0 U; 1 Other;

Query Match 2.5%; Score 24.4; DB 1; Length 29;

Best Local Similarity 89.3%; Pred. No. 8.9e+02;

Matches 25; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 867 GGGATTACAGCGCTGAGCCACCGCC 894

DB 1 GGGATTACAGCTGTGACCGCCGCC 28

## RESULT 302

AAA04369 standard; DNA; 29 BP.

AC AAA04369;

DT 22-MAY-2000 (first entry)

DE Polymorphic fragment of hypertension associated gene HSTSCGENE.

XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;  
XX Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;  
XX Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;  
XX polycystic kidney disease; von Willebrand's disease; forensics; human;  
XX tuberos sclerosis; hereditary hemorrhagica telangiectasia;  
XX familial colonic polyposis; osteogenesis imperfecta; porphyria;  
XX Ehlers-Danlos syndrome; ss.

OS Homo sapiens.

PN EP955382-A2.

PD 10-NOV-1999.

PF 07-MAY-1999; 99EP-00250150.

PR 07-MAY-1998; 98US-0084641P.

PR 03-MAY-1999; 99US-00304232.

PA (AFY-) AFFYMETRIX INC.

PA (UYCA-) UNIV CASE WESTERN RESERVE.

PI Pan JB, Chakravarti A, Haluska MK;

DR WPI; 2000-107928/10.

PT Novel nucleic acids containing polymorphisms used in the diagnosis of  
PT hypertension.

PS Claim 1; Page 34; 53pp; English.

XX The invention provides polymorphic fragments of genes associated with  
XX hypertension. The nucleic acids including the polymorphic sites can be  
XX used as probes or primers for expressing variant proteins. Detection of  
XX the polymorphisms is useful in designing prophylactic and therapeutic  
XX regimens customized to underlying abnormalities. The polymorphisms can be  
XX used for association studies for hypertension, and in hypertension  
XX diagnostic assays. Where the polymorphisms have strong correlation with  
XX hypertension, within a gene, they are likely to have a causative role in  
XX hypertension. This information can be used to find the precise role of a  
XX polymorphism in the disease, and this can be used to identify potential

CC drugs which combat the disease. The polymorphisms can be tested for  
CC association with other diseases e.g. agammaglobulinemia, diabetes  
CC insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich  
CC syndrome, Fabry's disease, familial hypercholesterolemia, polycystic  
CC kidney disease, hereditary spherocytosis, von Willebrand's disease,  
CC tuberos sclerosis, hereditary hemorrhagica telangiectasia, familial  
CC colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and  
CC acute intermittent porphyria. The polymorphic forms can also be used in  
CC forensics to identify individuals

XX Sequence 29 BP; 7 A; 9 C; 6 G; 6 T; 0 U; 1 Other;

Query Match 2.5%; Score 24.4; DB 1; Length 29;

Best Local Similarity 89.3%; Pred. No. 8.9e+02;

Matches 25; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1032 AGCTGGATTACAGCGCCTGCCACCC 1059

DB 2 AGCTGGATTACAGCGCCTGCCACCC 29

## RESULT 303

AAA03994 standard; DNA; 29 BP.

AC AAA03994;

DT 22-MAY-2000 (first entry)

DE Polymorphic fragment of hypertension associated gene APOC4.

XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;  
XX Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;  
XX Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;  
XX polycystic kidney disease; von Willebrand's disease; forensics; human;  
XX tuberos sclerosis; hereditary hemorrhagica telangiectasia;  
XX familial colonic polyposis; osteogenesis imperfecta; porphyria;  
XX Ehlers-Danlos syndrome; ss.

OS Homo sapiens.

PN EP955382-A2.

PD 10-NOV-1999.

PF 07-MAY-1999; 99EP-00250150.

PR 07-MAY-1998; 98US-0084641P.

PR 03-MAY-1999; 99US-00304232.

PA (AFY-) AFFYMETRIX INC.

PA (UYCA-) UNIV CASE WESTERN RESERVE.

PI Pan JB, Chakravarti A, Haluska MK;

DR WPI; 2000-107928/10.

PT Novel nucleic acids containing polymorphisms used in the diagnosis of  
PT hypertension.

PS Claim 1; Page 22; 53pp; English.

XX The invention provides polymorphic fragments of genes associated with  
XX hypertension. The nucleic acids including the polymorphic sites can be  
XX used as probes or primers for expressing variant proteins. Detection of  
XX the polymorphisms is useful in designing prophylactic and therapeutic  
XX regimens customized to underlying abnormalities. The polymorphisms can be  
XX used for association studies for hypertension, and in hypertension  
XX diagnostic assays. Where the polymorphisms have strong correlation with  
XX hypertension, within a gene, they are likely to have a causative role in  
XX hypertension. This information can be used to find the precise role of a  
XX polymorphism in the disease, and this can be used to identify potential  
XX drugs which combat the disease. The polymorphisms can be tested for

CC association with other diseases e.g. agammaglobulinemia, diabetes  
CC insipidus, Leesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich  
CC syndrome, Fabry's disease, familial hypercholesterolemia, polycystic  
CC kidney disease, hereditary spherocytosis, von Willebrand's disease,  
CC tuberculous sclerosis, hereditary hemorrhagica telangiectasia, familial  
CC colonic polypoidosis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and  
CC acute intermittent porphyria. The polymorphic forms can also be used in  
CC forensics to identify individuals

XX  
SQ Sequence 29 BP, 5 A; 7 C; 8 G; 8 T; 0 U; 1 Other;

Query Match 2.5%; Score 24.4; DB 1; Length 29;

Best Local Similarity 89.3%; Pred. No. 8.9e+02; Mismatches 2; Indels 0; Gaps 0;

Matches 25; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1112 AGGCTGCTCTCAACCTCGACCTCAGG 1139  
DB 1 AGGCTGCTCTTGAAATCTGACCTCAGG 28

RESULT 304

AAA04389/C  
ID AAA04389 standard; DNA; 29 BP.

XX  
AC AAA04389;

XX  
DT 22-MAY-2000 (first entry)

DE Polymorphic fragment of hypertension associated gene IAPP.

XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;  
XX Leesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;  
XX Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;  
XX polycystic kidney disease; von Willebrand's disease; forensic; human;  
XX tuberculous sclerosis; hereditary hemorrhagica telangiectasia;  
XX familial colonic polypoidosis; osteogenesis imperfecta; porphyria;  
XX Ehlers-Danlos syndrome; ss.

OS Homo sapiens.

XX  
PN EP955382-A2.

XX  
PD 10-NOV-1999.

XX  
PF 07-MAY-1999; 99EP-00250150.

XX  
PR 07-MAY-1998; 98US-0084641P.

XX  
PR 03-MAY-1999; 99US-00304232.

XX  
PA (AFPY-) AFFYMETRIX INC.

XX  
PI (UYCA-) UNIV CASE WESTERN RESERVE.

XX  
PI Fan JB, Chakravarti A, Haluska MK;

XX  
DR WPI; 2000-107928/10.

XX  
PT Novel nucleic acids containing polymorphisms used in the diagnosis of

XX  
PT hypertension.

XX  
PS Claim 1; Page 35; 53pp; English.

XX The invention provides polymorphic fragments of genes associated with  
XX hypertension. The nucleic acids including the polymorphic sites can be  
XX used as probes or primers for expressing variant proteins. Detection of  
XX the polymorphisms is useful in designing prophylactic and therapeutic  
XX regimens customized to underlying abnormalities. The polymorphisms can be  
XX used for association studies for hypertension, and in hypertension  
XX diagnostic assays. Where the polymorphisms have strong correlation with  
XX hypertension, within a gene, they are likely to have a causative role in  
XX hypertension. This information can be used to find the precise role of a  
XX polymorphism in the disease, and this can be used to identify potential  
XX drugs which combat the disease. The polymorphisms can be tested for  
XX association with other diseases e.g. agammaglobulinemia, diabetes

CC insipidus, Leesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich  
CC syndrome, Fabry's disease, familial hypercholesterolemia, polycystic  
CC kidney disease, hereditary spherocytosis, von Willebrand's disease,  
CC tuberculous sclerosis, hereditary hemorrhagica telangiectasia, familial  
CC colonic polypoidosis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and  
CC acute intermittent porphyria. The polymorphic forms can also be used in  
CC forensics to identify individuals

XX  
SQ Sequence 29 BP, 5 A; 8 C; 10 G; 5 T; 0 U; 1 Other;

Query Match 2.5%; Score 24.4; DB 1; Length 29;

Best Local Similarity 89.3%; Pred. No. 8.9e+02; Mismatches 2; Indels 0; Gaps 0;

Matches 25; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 927 GAATCTACTCTGTATCCAGGCTGAG 954  
DB 28 GAGTCTCACTCTGYCACCCAGGCTGAG 1

RESULT 305

AAA04314  
ID AAA04314 standard; DNA; 29 BP.

XX  
AC AAA04314;

XX  
DT 22-MAY-2000 (first entry)

DE Polymorphic fragment of hypertension associated gene GLUT4.

XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;  
XX Leesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;  
XX Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;  
XX polycystic kidney disease; von Willebrand's disease; forensic; human;  
XX tuberculous sclerosis; hereditary hemorrhagica telangiectasia;  
XX familial colonic polypoidosis; osteogenesis imperfecta; porphyria;  
XX Ehlers-Danlos syndrome; ss.

OS Homo sapiens.

XX  
PN EP955382-A2.

XX  
PD 10-NOV-1999.

XX  
PF 07-MAY-1999; 99EP-00250150.

XX  
PR 07-MAY-1998; 98US-0084641P.

XX  
PR 03-MAY-1999; 99US-00304232.

XX  
PA (AFPY-) AFFYMETRIX INC.

XX  
PI (UYCA-) UNIV CASE WESTERN RESERVE.

XX  
PI Fan JB, Chakravarti A, Haluska MK;

XX  
DR WPI; 2000-107928/10.

XX  
PT Novel nucleic acids containing polymorphisms used in the diagnosis of

XX  
PT hypertension.

XX  
PS Claim 1; Page 32; 53pp; English.

XX The invention provides polymorphic fragments of genes associated with  
XX hypertension. The nucleic acids including the polymorphic sites can be  
XX used as probes or primers for expressing variant proteins. Detection of  
XX the polymorphisms is useful in designing prophylactic and therapeutic  
XX regimens customized to underlying abnormalities. The polymorphisms can be  
XX used for association studies for hypertension, and in hypertension  
XX diagnostic assays. Where the polymorphisms have strong correlation with  
XX hypertension, within a gene, they are likely to have a causative role in  
XX hypertension. This information can be used to find the precise role of a  
XX polymorphism in the disease, and this can be used to identify potential  
XX drugs which combat the disease. The polymorphisms can be tested for  
XX association with other diseases e.g. agammaglobulinemia, diabetes  
XX insipidus, Leesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich

CC syndrome, Fabry's disease, familial hypercholesterolemia, polycystic  
 CC kidney disease, hereditary spherocytosis, von Willebrand's disease,  
 CC tuberos sclerosis, hereditary hemorhagica telangiectasia, familial  
 CC colonic polypsis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and  
 CC acute intermittent porphyria. The polymorphic forms can also be used in  
 CC forensics to identify individuals

SQ Sequence 29 BP; 3 A; 11 C; 6 G; 8 T; 0 U; 1 Other;

Query Match 2.5%; Score 24.4; DB 1; Length 29;  
 Best Local Similarity 89.3%; Pred. No. 8.9e+02;  
 Matches 25; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 821 GATCTCTGACCTGTGATCTGCTGCC 848  
 |||||  
 DB 2 GATCTCTGACCTGTGATCTGCTGCC 29

RESULT 306  
 AD182609/C  
 ID AD182609 standard; DNA; 30 BP.

AC AD182609;

DT 22-APR-2004 (first entry)

XX Prostate-specific membrane antigen enhancer PCR primer #2.

XX chimeric; prostate-specific-enhancing sequence promoter; PSES promoter;  
 XX androgen receptor core region promoter; AREC3 promoter;  
 XX prostate-specific-antigen; PSA;  
 XX prostate-specific membrane antigen enhancer; PSMA enhancer; PSMEdel2;  
 XX angiosgenesis reduction; prostate carcinoma cell; ss; PCR; primer.

OS Unidentified.

XX US2003235874-A1.

XX 25-DEC-2003.

XX 08-MAY-2003; 2003US-00431791.

XX 08-MAY-2002; 2002US-0378920P.

XX (KAO/C) KAO C.

XX (LEES/) LEE S.

XX (KIMH/) KIM H.

XX (LEEK/) LEE K.

XX (YURR/) YU R.

XX Kao C, Lee S, Kim H, Lee K, Yu R;

XX WPI; 2004-061500/06.

XX Novel chimeric PSES promoter construct comprising androgen receptor  
 PT enhancer core region promoter of prostate-specific-antigen gene and  
 PT PSME(del2) promoter of PSMA gene, useful for treating prostate cancer.

XX Example 1; SEQ ID NO 5; 29bp; English.

XX The invention comprises a chimeric prostate-specific-enhancing sequence  
 CC (PSES) promoter construct, which contains the androgen receptor core  
 CC region (AREC3) promoter of the prostate-specific-antigen (PSA) gene and  
 CC the prostate-specific membrane antigen (PSMA) enhancer (PSMEdel2)  
 CC promoter of the PSMA gene. The PSES promoter construct of the invention  
 CC is useful for reducing angiosgenesis in prostate carcinoma cells and in  
 CC targeting prostate carcinoma cells for destruction. The PSES promoter  
 CC construct is also useful for identifying an agent that modulates PSES  
 CC promoter activity. The present DNA sequence represents a PCR primer that  
 CC was used in an example of the invention.

XX Sequence 30 BP; 5 A; 8 C; 13 G; 4 T; 0 U; 0 Other;

Query Match 2.5%; Score 24.4; DB 1; Length 30;  
 Best Local Similarity 96.2%; Pred. No. 9.1e+02;  
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 673 GCTCAGTCAACCTCTGCTCCCGG 698  
 |||||  
 DB 30 GCTCAGTCAACCTCTGCTCCCGG 5

RESULT 307  
 AAQ29012/C  
 ID AAQ29012 standard; DNA; 25 BP.

AC AAQ29012;

DT 25-MAR-2003 (revised)

DT 23-FEB-1993 (first entry)

XX Alu family consensus sequence-derived probe #1.

XX Low frequency repeat; Alu restriction digest; genetic mapping; ss.

XX Synthetic.

XX EP505605-A2.

XX 30-SEP-1992.

XX 11-APR-1991; 91EP-00105802.

XX 28-MAR-1991; 91US-00676292.

XX (UYWA-) UNIV WAYNE STATE.

XX Duncan CH, Solus JF, Kaplan DJ;

XX WPI; 1992-324992/40.

XX New nucleic acid probes - have a labelled low frequency repetitive  
 PT sequence for detecting overlaps among cloned DNA.

XX Disclosure; Page 8; 41pp; English.

XX 500-1000bp fragments from an AluI-digest of human genomic DNA were  
 CC ligated to M13mp19 RF DNA. E.coli JM109 were transformed by the ligation  
 CC mixture. Filter replicates of the transformant colonies were screened  
 CC with probe #1 and a second probe. The probes were derived from the Alu  
 CC family consensus sequence. Phage which hybridised to both probes were  
 CC plated at lower density and rescreened with the same probes. Single-  
 CC stranded template DNA was extd. from cultures of these phage to isolate  
 CC low-frequency repeat sequence probes Lf1, Lf2, Lf3, Lf19, Lf20 and Lf21.  
 CC See also AAQ29013-Q29017 and AAQ29021-Q29038. (Updated on 25-MAR-2003 to  
 CC correct PN field.)

XX Sequence 25 BP; 5 A; 8 C; 5 G; 5 T; 0 U; 2 Other;

Query Match 2.4%; Score 24.2; DB 1; Length 25;  
 Best Local Similarity 92.0%; Pred. No. 8.2e+02;  
 Matches 23; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 863 TGCTGGATTACAGCGTGAGCCAC 887  
 |||||  
 DB 25 TGCTGGATTACAGGYRTGAGCCAC 1

RESULT 308

AAH91549  
 ID AAH91549 standard; DNA; 30 BP.

XX AAH91549;

XX 09-OCT-2001 (first entry)

```

DE Human inflammatory bowel disease associated polymorphic site #624.
XX Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
XX single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
XX chromosome 5q31-33; forensic test; gene therapy; ds.
XX Homo sapiens.
XX Location/Qualifiers
XX misc_feature 14
XX /tag= a
XX /note="SNP, optionally T or C at this position"
XX WO200142511-A2.
XX 14-JUN-2001.
XX 11-DEC-2000; 2000WO-US033632.
XX 10-DEC-1999; 99US-0170257P.
XX 10-APR-2000; 2000US-0196046P.
XX (WHEB) WHITEHEAD INST BIOMEDICAL RES.
XX (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.
XX Daily M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;
XX WPI; 2001-367874/38.
XX Testing for the presence of polymorphisms associated with inflammatory
XX bowel disease, using a hybridization assay.
XX Claim 1; Page 65; 463pp; English.
XX The present invention describes a method for detecting the presence of
XX polymorphisms associated with inflammatory bowel diseases such as
XX ulcerative colitis and Crohn's disease. The methods can be used to detect
XX the presence of genetic polymorphisms associated with inflammatory bowel
XX disease and correlating their occurrence with disease states. They may be
XX used in this way for phenotypic correlations, forensics, paternity
XX testing, medicine and genetic analysis. The present sequence is a
XX polymorphic site described in the exemplification of the invention
XX
XX Sequence 30 BP; 6 A; 11 C; 5 G; 7 T; 0 U; 1 Other;
XX
XX Query Match 2.4%; Score 24.2; DB 1; Length 30;
XX Best Local Similarity 86.7%; Pred. No. 9.3e+02;
XX Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 832 CTTGTGATCTGCTGCTCGGCTCCCAAA 861
XX 1 CATGTGATCTGCGGCTCGGCTCCCAAA 30
XX
XX RESULT 309
XX AAF29776
XX ID AAF29776 standard; DNA; 30 BP.
XX AC AAF29776;
XX 09-APR-2001 (first entry)
XX Presentline-1 gene promoter PCR primer Prom6F.
XX Human; PSEN1; Alzheimer's disease; polymorphism; diagnosis;
XX presentline-1; chromosome 14; PCR primer; ss.
XX Homo sapiens.
XX WO200079000-A1.
XX 28-DEC-2000.
XX

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PF 22-JUN-2000; 2000WO-EP005942.
XX 22-JUN-1999; 99EP-00201991.
XX (VLA-A-) VLAMMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX Theuns J, Cruts M, Van Broeckhoven C;
XX WPI; 2001-071402/08.
XX Determining whether a human subject has or is at risk of developing (early
XX onset) Alzheimer's disease comprises detecting the presence/absence of a
XX genetic lesion in the presentline-1 gene.
XX Example 1; Page 45; 56pp; English.
XX The present invention describes a method for determining the presence of
XX or susceptibility to Alzheimer's disease in humans, involving detecting a
XX genetic lesion in the presentline-1 (PSEN1) gene, found on chromosome 14.
XX The genetic lesion is a polymorphism in the promoter or upstream
XX regulatory region of the gene. The invention also describes transgenic
XX animals which can be used to identify compounds useful in treating
XX Alzheimer's disease
XX
XX Sequence 30 BP; 7 A; 9 C; 6 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 2.4%; Score 24.2; DB 1; Length 30;
XX Best Local Similarity 89.7%; Pred. No. 9.3e+02;
XX Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 205 GTTCAGGCTGTCTCGAATCCGACCTCA 233
XX 1 GTTAGGCTGTCTAGAACTCCCAACTCA 29
XX
XX RESULT 310
XX AAH45830/C
XX ID AAH45830 standard; DNA; 24 BP.
XX AAH45830;
XX 11-SEP-2001 (first entry)
XX Telomere size determination method related oligonucleotide #3.
XX Telomere size determination; chromosomal DNA; probe; primer;
XX repetitive sequence; tissue aging; cancer progression; ds.
XX Synthetic.
XX JP2001095586-A.
XX 10-APR-2001.
XX 30-SEP-1999; 99JP-00279948.
XX 30-SEP-1999; 99JP-00279948.
XX (IDET/) IDE T.
XX WPI; 2001-360495/38.
XX Determining telomere size useful for investigating aging in tissue and
XX progression of cancer.
XX Example 2; Page 6; 8pp; Japanese.
XX The present invention describes a method for determining the length of
XX telomeres, involving hybridizing a chromosomal DNA extracted from a
XX sample and a labeled DNA probe with a sequence complementary to a
XX repetitive telomeric sequence, and measuring the labeled signal of the
XX hybridised probe to give the size of telomere. This can be used to
XX investigate tissue aging and the progression of cancer and in monitoring
XX

```

CC the prognosis of patients. The present sequence is an oligonucleotide  
CC described in the exemplification of the invention  
XX  
SQ Sequence 24 BP; 5 A; 6 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 2.4%; Score 24; DB 1; Length 24;  
Best Local Similarity 100.0%; Pred. No. 8.2e+02;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 382 GCTCCCAAGTCTGGATTACA 405  
DB 24 GCTCCCAAGTCTGGATTACA 1

RESULT 311  
AAH45828  
ID AAH45828 standard; DNA; 24 BP.

AAH45828;  
AC  
XX  
DT 11-SEP-2001 (first entry)

XX Telomere size determination method related oligonucleotide #1.

KW Telomere size determination; chromosomal DNA; probe; primer;  
KW repetitive sequence; tissue aging; cancer progression; ds.

OS Synthetic.

FN JP2001095586-A.

XX 10-APR-2001.

XX 30-SEP-1999; 99JP-00279948.

XX 30-SEP-1999; 99JP-00279948.

XX (IDET/) IDE T.

DR WPI, 2001-360495/38.

FT Determining telomere size useful for investigating aging in tissue and  
PT progression of cancer.

PS Disclosure; Page 5; 8pp; Japanese.

CC The present invention describes a method for determining the length of  
CC telomeres, involving hybridizing a chromosomal DNA extracted from a  
CC sample and a labeled DNA probe with a sequence complementary to a  
CC repetitive telomeric sequence, and measuring the labeled signal of the  
CC hybridised probe to give the size of telomere. This can be used to  
CC investigate tissue aging and the progression of cancer and in monitoring  
CC the prognosis of patients. The present sequence is an oligonucleotide  
CC described in the exemplification of the invention  
XX

SQ Sequence 24 BP; 6 A; 7 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 2.4%; Score 24; DB 1; Length 24;  
Best Local Similarity 100.0%; Pred. No. 8.2e+02;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 382 GCTCCCAAGTCTGGATTACA 405  
DB 1 GCTCCCAAGTCTGGATTACA 24

RESULT 312  
ADL07545/C  
ID ADL07545 standard; DNA; 24 BP.

XX ADL07545;  
AC

DT 06-MAY-2004 (first entry)

XX DE Sec24 protein-31.35 RT-PCR primer #1.

XX ss; primer; Sec24 protein-31.35; cancer; HIV infection; PCR; RT-PCR;  
KW reverse transcriptase PCR.

XX Unidentified.

XX CN1393472-A.

XX 29-JAN-2003.

XX 29-JUN-2001; 2001CN-00113189.

XX 29-JUN-2001; 2001CN-00113189.

XX (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.

XX Mao Y, Xie Y;

XX WPI, 2003-422176/40.

XX Polypeptide-Sec24 protein-31.35.

PS Example 3; SEQ ID NO 3; 31pp; Chinese.

CC The invention relates to a polypeptide-Sec24 protein-31.35 and the  
CC polynucleotide encoding it. Also included are the process for preparing  
CC the polypeptide by recombinant DNA technology, the application of the  
CC polypeptide in treating diseases such as cancer and HIV infection, the  
CC antagonist against the polypeptide (and its therapeutic action) and the  
CC application of the polynucleotide encoding this polypeptide. The present  
CC sequence is an RT-(reverse transcriptase) PCR primer used to isolate cDNA  
CC encoding the Sec24 protein-31.35.  
XX

SQ Sequence 24 BP; 4 A; 9 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 2.4%; Score 24; DB 1; Length 24;  
Best Local Similarity 100.0%; Pred. No. 8.2e+02;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 864 GCTGGATTACAGCGTGAGCCAC 887  
DB 24 GCTGGATTACAGCGTGAGCCAC 1

RESULT 313  
AAH91303/C  
ID AAH91303 standard; DNA; 28 BP.

XX AAH91303;

XX 09-OCT-2001 (first entry)

XX Human inflammatory bowel disease associated polymorphic site #378.

KW Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;  
KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;

KW chromosome 5q31-33; forensic test; gene therapy; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

XX misc\_feature 15

XX WO200142511-A2.

XX 14-JUN-2001.

XX 11-DEC-2000; 2000WO-US033632.

xx Claim 1; Page 21; 53pp; English.

xx The invention provides polymorphic fragments of genes associated with  
cc hypertension. The nucleic acids including the polymorphic sites can be  
cc used as probes or primers for expressing variant proteins. Detection of  
cc the polymorphisms is useful in designing prophylactic and therapeutic  
cc regimens customized to underlying abnormalities. The polymorphisms can be  
cc used for association studies for hypertension, and in hypertension  
cc diagnostic assays. Where the polymorphisms have strong correlation with  
cc hypertension, within a gene, they are likely to have a causative role in  
cc hypertension. This information can be used to find the precise role of a  
cc polymorphism in the disease, and this can be used to identify potential  
cc drugs which combat the disease. The polymorphisms can be tested for  
cc association with other diseases e.g. agammaglobulinemia, diabetes  
cc insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich  
cc syndrome, Fabry's disease, familial hypercholesterolemia, polycystic  
cc kidney disease, hereditary spherocytosis, von Willebrand's disease,  
cc tuberculous sclerosis, Ehlers-Danlos syndrome, osteogenesis imperfecta, familial  
cc colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and  
cc acute intermittent porphyria. The polymorphic forms can also be used in  
cc forensics to identify individuals

SQ Sequence 29 BP; 7 A; 4 C; 6 G; 11 T; 0 U; 1 Other;

Query Match 2.4%; Score 23.8; DB 1; Length 29;  
Best Local Similarity 86.2%; Pred. No. 9.5e+02;  
Matches 25; Conservative 1; Mismatches 3; Indels 0; Gaps 0

Gy 1073 TTGTATTTTCATTAGAGCGGCGGTTTCCAC 1101  
||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 1 TTGTATTTTCATTAGAGCGGCGGTTTCCAC 29

RESULT 315  
AAAA04662  
ID AAAA04662 standard; DNA; 29 BP.  
AC AAAA04662;  
AD  
DT 22-MAY-2000 (first entry)  
XX  
DE Polymorphic fragment of hypertension associated gene TBXA2R.  
XX  
XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;  
XX Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;  
XX Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;  
XX polycystic kidney disease; von Willebrand's disease; forensic human;  
XX tuberculous sclerosis; hereditary hemorrhagica telangiectasia;  
XX familial colonic polyposis; osteogenesis imperfecta; porphyria;  
XX Ehlers-Danlos syndrome; ss.  
XX  
OS Homo sapiens.  
XX  
PN EP955382-A2.  
PD 10-NOV-1999.  
PF 07-MAY-1999; 99EP-00250150.  
PR 07-MAY-1998; 98US-0084641P.  
PR 03-MAY-1999; 99US-00304232.  
PA (AFPV-) APFYMETRIX INC.  
PA (UYCA-) UNIV CASE WESTERN RESERVE.  
XX Fan JB, Chakravarti A, Haluska MK;  
DR WPI, 2000-107928/10.  
PT Novel nucleic acids containing polymorphisms used in the diagnosis of  
XX hypertension.

PS Claim 1; Page 43; 53pp; English.

XX  
CC The invention provides polymorphic fragments of genes associated with  
CC hypertension. The nucleic acids including the polymorphic sites can be  
CC used as probes or primers for expressing variant proteins. Detection of  
CC the polymorphisms is useful in designing prophylactic and therapeutic  
CC regimens customized to underlying abnormalities. The polymorphisms can be  
CC used for association studies for hypertension, and in hypertension  
CC diagnostic assays. Where the polymorphisms have strong correlation with  
CC hypertension, within a gene, they are likely to have a causative role in  
CC hypertension. This information can be used to find the precise role of a  
CC polymorphism in the disease, and this can be used to identify potential  
CC drugs which combat the disease, and this can be used to identify potential  
CC association with other diseases e.g. agammaglobulinemia, diabetes  
CC insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich  
CC syndrome, Fabry disease, familial hypercholesterolemia, polycystic  
CC kidney disease, hereditary spherocytosis, von Willebrand disease,  
CC tuberculous sclerosis, hereditary hemorrhagica telangiectasia, familial  
CC colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and  
CC acute intermittent porphyria. The polymorphic forms can also be used in  
CC forensics to identify individuals

XX  
SQ Sequence 29 BP; 6 A; 8 C; 8 G; 6 T; 0 U; 1 Other;

Query Match 2.4%; Score 23.8; DB 1; Length 29;  
Best Local Similarity 86.2%; Pred. No. 9.5e+02;  
Matches 25; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 652 GAGTCAGATGGCGCATCTTGGCTCAGTG 680  
DB 1 GAGTCAGATGGCGCATCTTGGCTCAGTG 29

RESULT 316  
AAA04486/c  
ID AAA04486 standard; DNA; 29 BP.  
XX  
AC AAA04486;  
XX  
DT 22-MAY-2000 (first entry)

DE Polymorphic fragment of hypertension associated gene PGIS.

XX  
KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;  
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;  
KW Fabry disease; familial hypercholesterolemia; hereditary spherocytosis;  
KW polycystic kidney disease; von Willebrand disease; forensic; human;  
KW tuberculous sclerosis; hereditary hemorrhagica telangiectasia;  
KW familial colonic polyposis; osteogenesis imperfecta; porphyria;  
KW Ehlers-Danlos syndrome; ss.  
XX  
OS Homo sapiens.  
XX  
PN EP955382-A2.  
XX  
PD 10-NOV-1999.  
XX  
PF 07-MAY-1999; 99EP-00250150.  
XX  
PR 07-MAY-1998; 98US-0084641P.  
XX  
PR 03-MAY-1999; 99US-00304232.  
XX  
PA (AFY-) AFFYMETRIX INC.  
XX (UYCA-) UNIV CASE WESTERN RESERVE.  
XX  
PI Fan JB, Chakravarti A, Haluska MK;  
XX  
DR WPI; 2000-107928/10.  
XX  
PT Novel nucleic acids containing polymorphisms used in the diagnosis of  
XX hypertension.  
XX  
PS Claim 1; Page 38; 53pp; English.

XX  
CC The invention provides polymorphic fragments of genes associated with  
CC hypertension. The nucleic acids including the polymorphic sites can be  
CC used as probes or primers for expressing variant proteins. Detection of  
CC the polymorphisms is useful in designing prophylactic and therapeutic  
CC regimens customized to underlying abnormalities. The polymorphisms can be  
CC used for association studies for hypertension, and in hypertension  
CC diagnostic assays. Where the polymorphisms have strong correlation with  
CC hypertension, within a gene, they are likely to have a causative role in  
CC hypertension. This information can be used to find the precise role of a  
CC polymorphism in the disease, and this can be used to identify potential  
CC drugs which combat the disease. The polymorphisms can be tested for  
CC association with other diseases e.g. agammaglobulinemia, diabetes  
CC insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich  
CC syndrome, Fabry disease, familial hypercholesterolemia, polycystic  
CC kidney disease, hereditary spherocytosis, von Willebrand disease,  
CC tuberculous sclerosis, hereditary hemorrhagica telangiectasia, familial  
CC colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and  
CC acute intermittent porphyria. The polymorphic forms can also be used in  
CC forensics to identify individuals

XX  
SQ Sequence 29 BP; 9 A; 10 C; 4 G; 5 T; 0 U; 1 Other;

Query Match 2.4%; Score 23.8; DB 1; Length 29;  
Best Local Similarity 86.2%; Pred. No. 9.5e+02;  
Matches 25; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 177 TTAGTAGAGATGAGATTCTCCATGTTGG 205  
DB 29 TTAGTAGAGATGAGATTCTCCATGTTGG 1

RESULT 317  
AAA03878/c  
ID AAA03878 standard; DNA; 29 BP.  
XX  
AC AAA03878;  
XX  
DT 22-MAY-2000 (first entry)

DE Polymorphic fragment of hypertension associated gene AEL.

XX  
KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;  
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;  
KW Fabry disease; familial hypercholesterolemia; hereditary spherocytosis;  
KW polycystic kidney disease; von Willebrand disease; forensic; human;  
KW tuberculous sclerosis; hereditary hemorrhagica telangiectasia;  
KW familial colonic polyposis; osteogenesis imperfecta; porphyria;  
KW Ehlers-Danlos syndrome; ss.  
XX  
OS Homo sapiens.  
XX  
PN EP955382-A2.  
XX  
PD 10-NOV-1999.  
XX  
PF 07-MAY-1999; 99EP-00250150.  
XX  
PR 07-MAY-1998; 98US-0084641P.  
XX  
PR 03-MAY-1999; 99US-00304232.  
XX  
PA (AFY-) AFFYMETRIX INC.  
XX (UYCA-) UNIV CASE WESTERN RESERVE.  
XX  
PI Fan JB, Chakravarti A, Haluska MK;  
XX  
DR WPI; 2000-107928/10.  
XX  
PT Novel nucleic acids containing polymorphisms used in the diagnosis of  
XX hypertension.  
XX  
PS Claim 1; Page 18; 53pp; English.



CC The invention provides polymorphic fragments of genes associated with  
CC hypertension. The nucleic acids including the polymorphic sites can be  
CC used as probes or primers for expressing variant proteins. Detection of  
CC the polymorphisms is useful in designing prophylactic and therapeutic  
CC regimes customized to underlying abnormalities. The polymorphisms can be  
CC used for association studies for hypertension, and in hypertension with  
CC diagnostic assays. Where the polymorphisms have strong correlation with  
CC hypertension, within a gene, they are likely to have a causative role in  
CC hypertension. This information can be used to find the precise role of a  
CC polymorphism in the disease, and this can be used to identify potential  
CC drugs which combat the disease. The polymorphisms can be tested for  
CC association with other diseases e.g. agammaglobulinemia, diabetes  
CC insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich  
CC syndrome, Fabry's disease, familial hypercholesterolemia, polycystic  
CC kidney disease, hereditary spherocytosis, von Willebrand's disease,  
CC tuberous sclerosis, hereditary hemorrhagica telangiectasia, familial  
CC colonic polypsis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and  
CC acute intermittent porphyria. The polymorphic forms can also be used in  
CC forensics to identify individuals

SO Sequence 29 BP; 7 A; 6 C; 11 G; 4 T; 0 U; 1 Other;

Query Match 2.4%; Score 23.8; DB 1; Length 29;  
Best Local Similarity 86.2%; Pred. No. 9.5e+02;  
Matches 25; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 670 TTGGCTCAGTCAACCTGCTCCCGG 698

DB 29 TTGGCTCAGTCAACCTCCTCTCTGGG 1

RESULT 318

AAA04660 standard; DNA; 29 BP.

AAA04660;

22-MAY-2000 (first entry)

Polymorphic fragment of hypertension associated gene TBXA2R.

XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;  
XX Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;  
XX Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;  
XX polycystic kidney disease; von Willebrand's disease; forensic; human;  
XX tuberous sclerosis; hereditary hemorrhagica telangiectasia;  
XX familial colonic polypsis; osteogenesis imperfecta; porphyria;  
XX Ehlers-Danlos syndrome; ss.

XX Homo sapiens.

XX EP955382-A2.

XX 10-NOV-1999.

XX 07-MAY-1999; 99EP-00250150.

XX 07-MAY-1998; 98US-0084641P.

XX 03-MAY-1999; 99US-00304232.

XX (AFPM-) AFFMETRIX INC.

XX (UYCA-) UNIV CASE WESTERN RESERVE.

XX Fan JB, Chakravarti A, Haluska MK;

XX WPI; 2000-107928/10.

XX Novel nucleic acids containing polymorphisms used in the diagnosis of

XX hypertension.

XX Claim 1; Page 43; 53pp; English.

XX The invention provides polymorphic fragments of genes associated with

CC hypertension. The nucleic acids including the polymorphic sites can be  
CC used as probes or primers for expressing variant proteins. Detection of  
CC the polymorphisms is useful in designing prophylactic and therapeutic  
CC regimes customized to underlying abnormalities. The polymorphisms can be  
CC used for association studies for hypertension, and in hypertension with  
CC diagnostic assays. Where the polymorphisms have strong correlation with  
CC hypertension, within a gene, they are likely to have a causative role in  
CC hypertension. This information can be used to find the precise role of a  
CC polymorphism in the disease, and this can be used to identify potential  
CC drugs which combat the disease. The polymorphisms can be tested for  
CC association with other diseases e.g. agammaglobulinemia, diabetes  
CC insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich  
CC syndrome, Fabry's disease, familial hypercholesterolemia, polycystic  
CC kidney disease, hereditary spherocytosis, von Willebrand's disease,  
CC tuberous sclerosis, hereditary hemorrhagica telangiectasia, familial  
CC colonic polypsis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and  
CC acute intermittent porphyria. The polymorphic forms can also be used in  
CC forensics to identify individuals

SO Sequence 29 BP; 4 A; 11 C; 8 G; 5 T; 0 U; 1 Other;

Query Match 2.4%; Score 23.8; DB 1; Length 29;  
Best Local Similarity 86.2%; Pred. No. 9.5e+02;  
Matches 25; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 876 GGGGTGAGCCACCGCCGCTTATTTT 904

DB 1 GGGGCGCGCCACCAVCGCCGCTAATTTT 29

RESULT 319

AAA04502 standard; DNA; 29 BP.

AAA04502;

22-MAY-2000 (first entry)

Polymorphic fragment of hypertension associated gene PCIS.

XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;  
XX Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;  
XX Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;  
XX polycystic kidney disease; von Willebrand's disease; forensic; human;  
XX tuberous sclerosis; hereditary hemorrhagica telangiectasia;  
XX familial colonic polypsis; osteogenesis imperfecta; porphyria;  
XX Ehlers-Danlos syndrome; ss.

XX Homo sapiens.

XX EP955382-A2.

XX 10-NOV-1999.

XX 07-MAY-1999; 99EP-00250150.

XX 07-MAY-1998; 98US-0084641P.

XX 03-MAY-1999; 99US-00304232.

XX (AFPM-) AFFMETRIX INC.

XX (UYCA-) UNIV CASE WESTERN RESERVE.

XX Fan JB, Chakravarti A, Haluska MK;

XX WPI; 2000-107928/10.

XX Novel nucleic acids containing polymorphisms used in the diagnosis of

XX hypertension.

XX Claim 1; Page 38; 53pp; English.

XX The invention provides polymorphic fragments of genes associated with

used as probes or primers for expressing variant proteins. Detection of the polymorphisms is useful in designing prophylactic and therapeutic regimens customized to underlying abnormalities. The polymorphisms can be used for association studies for hypertension, and in hypertension diagnostic assays. Where the polymorphisms have strong correlation with hypertension, within a gene, they are likely to have a causative role in hypertension. This information can be used to find the precise role of a polymorphism in the disease, and this can be used to identify potential drugs which combat the disease. The polymorphisms can be tested for association with other diseases e.g. agammaglobulinemia, diabetes insipidus, Leech-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria. The polymorphic forms can also be used in forensics to identify individuals

Sequence 29 BP; 6 A; 14 C; 6 G; 2 T; 0 U; 1 Other;

Query Match 2.4%; Score 23.8; DB 1; Length 29;  
Best Local Similarity 86.2%; Pred. No. 9.5e+02;  
Matches 25; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1034 CTGGGATTACGGGACCTGCCACACACC 1062  
|||||  
DB 1 CTGGGACTACAGGCGCCGCCACACACC 29

RESULT 320  
AAA04661  
ID AAA04661 standard; DNA; 29 BP.

AC AAA04661;

DT 22-MAY-2000 (first entry)

DE Polymorphic fragment of hypertension associated gene TBXA2R.

XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;  
XX Leech-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;  
XX Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;  
XX polycystic kidney disease; von Willebrand's disease; forensic; human;  
XX tuberous sclerosis; hereditary hemorrhagic telangiectasia;  
XX familial colonic polyposis; osteogenesis imperfecta; porphyria;  
XX Ehlers-Danlos syndrome; ss.

OS Homo sapiens.

PN EP955382-A2.

PD 10-NOV-1999.

PF 07-MAY-1999; 99EP-00250150.

PR 07-MAY-1998; 98US-0084641P.

PR 03-MAY-1999; 99US-00304232.

PA (AFRY-) AFFYMETRIX INC.

PA (UYCA-) UNIV CASE WESTERN RESERVE.

PI Fan JB, Chakravarti A, Haluska MK;

DR WPI; 2000-107928/10.

PT Novel nucleic acids containing polymorphisms used in the diagnosis of hypertension.

PS Claim 1; Page 43; 53pp; English.

CC The invention provides polymorphic fragments of genes associated with hypertension. The nucleic acids including the polymorphic sites can be used as probes or primers for expressing variant proteins. Detection of

CC the polymorphisms is useful in designing prophylactic and therapeutic regimens customized to underlying abnormalities. The polymorphisms can be used for association studies for hypertension, and in hypertension diagnostic assays. Where the polymorphisms have strong correlation with hypertension, within a gene, they are likely to have a causative role in hypertension. This information can be used to find the precise role of a polymorphism in the disease, and this can be used to identify potential drugs which combat the disease. The polymorphisms can be tested for association with other diseases e.g. agammaglobulinemia, diabetes insipidus, Leech-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria. The polymorphic forms can also be used in forensics to identify individuals

Sequence 29 BP; 5 A; 8 C; 9 G; 6 T; 0 U; 1 Other;

Query Match 2.4%; Score 23.8; DB 1; Length 29;  
Best Local Similarity 86.2%; Pred. No. 9.5e+02;  
Matches 25; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 650 TGGAGTGCAGTGGCGCATCTTGCTCAC 678  
|||||  
DB 1 TGGAGTACAGTGGCGCATCTTGCTCAC 29

RESULT 321

AAA04307  
ID AAA04307 standard; DNA; 29 BP.

AC AAA04307;

DT 22-MAY-2000 (first entry)

DE Polymorphic fragment of hypertension associated gene GLUT4.

XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;  
XX Leech-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;  
XX Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;  
XX polycystic kidney disease; von Willebrand's disease; forensic; human;  
XX tuberous sclerosis; hereditary hemorrhagic telangiectasia;  
XX familial colonic polyposis; osteogenesis imperfecta; porphyria;  
XX Ehlers-Danlos syndrome; ss.

OS Homo sapiens.

PN EP955382-A2.

PD 10-NOV-1999.

PF 07-MAY-1999; 99EP-00250150.

PR 07-MAY-1998; 98US-0084641P.

PR 03-MAY-1999; 99US-00304232.

PA (AFRY-) AFFYMETRIX INC.

PA (UYCA-) UNIV CASE WESTERN RESERVE.

PI Fan JB, Chakravarti A, Haluska MK;

DR WPI; 2000-107928/10.

PT Novel nucleic acids containing polymorphisms used in the diagnosis of hypertension.

PS Claim 1; Page 32; 53pp; English.

CC The invention provides polymorphic fragments of genes associated with hypertension. The nucleic acids including the polymorphic sites can be used as probes or primers for expressing variant proteins. Detection of the polymorphisms is useful in designing prophylactic and therapeutic

regimes customized to underlying abnormalities. The polymorphisms can be used for association studies for hypertension, and in hypertension diagnostic assays. Where the polymorphisms have strong correlation with hypertension, within a gene, they are likely to have a causative role in hypertension. This information can be used to find the precise role of a polymorphism in the disease, and this can be used to identify potential drugs which combat the disease. The polymorphisms can be tested for association with other diseases e.g. agammaglobulinemia, diabetes insipidus, Leisch-Nyhan syndrome, muscular dystrophy, Miskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberculous scleritis, hereditary hemorrhagica telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria. The polymorphic forms can also be used in forensics to identify individuals

Sequence 29 BP; 7 A; 12 C; 6 G; 3 T; 0 U; 1 Other;

Query Match 2.4%; Score 23.8; DB 1; Length 29;  
Best Local Similarity 86.2%; Pred. No. 9.5e+02;  
Matches 25; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

1034 CTGGGATTACGGGACCTGCCACACACC 1062  
1 CTGGGACTACAGGCGCATGCGCACACACC 29

RESULT 322  
AA209548/C  
ID AA209548 standard; DNA; 25 BP.  
XX  
AC AA209548;  
XX  
DT 08-NOV-1999 (first entry)  
XX  
DE Human Apo E oligonucleotide primer 4.  
XX  
XX Apo E; Apo B; hyperlipidemia; human; treatment; hepatocyte; apoprotein;  
XX Apo A1; low density lipoprotein; LDL; blood; therapy; atherosclerosis;  
XX high density lipoprotein; HDL; cholesterol; coronary heart disease;  
XX Alzheimer's disease; hypobetalipoproteinemia; dysbetalipoproteinemia;  
XX primer; ss.  
XX  
OS Synthetic.  
XX Homo sapiens.  
XX  
PN MO940789-A1.  
XX  
PD 19-AUG-1999.  
XX  
PF 28-AUG-1998; 98WO-US017908.  
XX  
PR 12-FEB-1998; 98US-0074497P.  
XX  
PR 30-JUN-1998; 98US-00108006.  
XX  
XX (MINTU) UNIV MINNESOTA.  
XX (YESH) UNIV YESHIVA EINSTEIN COLLEGE.  
XX  
XX Steer CJ, Kren BT, Bandyopadhyay PT, Roy-Chowdhury J;  
XX WPI; 1999-527333/44.  
XX  
XX Mutating apolipoprotein genes in hepatocytes to control cholesterol  
XX levels, e.g. for treating or preventing hyperlipidemia, particularly  
XX atherosclerosis.  
XX  
XX Claim 31; Page 51; 106pp; English.  
XX  
XX This invention describes a novel method for the genetic treatment of  
XX hyperlipidemia by altering genes, in hepatocytes, for apoprotein (apo) B,  
XX E or A1. Low density lipoprotein (LDL) levels in the blood are reduced by  
XX altering an apo B gene (I) in a hepatocyte. The invention describes a  
XX method for the therapeutic and/or prophylactic method involving altering

an apo E gene in hepatocytes by introducing the mutations Arg112Cys, Arg158Cys or Cys158Arg and a method for ameliorating atherosclerosis by altering the apo A1 gene in a hepatocyte so that the altered protein can diesterise. Altering expression of apo genes regulates levels of high and low density lipoprotein cholesterol. Altering expression of apo B, E and A1 genes is used to treat or prevent atherosclerosis, coronary heart disease, Alzheimer's disease, hypobetalipoproteinemia, and dysbetalipoproteinemia. AA209545-209548 represent primers used in the manipulation of the human Apo E protein described in the method of the invention

Sequence 25 BP; 7 A; 5 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 2.4%; Score 23.4; DB 1; Length 25;  
Best Local Similarity 96.0%; Pred. No. 9e+02;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1113 GGCTGATCTCAACCTCGTCACTCA 1137  
25 GGCTGATCTCAACCTCGTCACTCACTTA 1

RESULT 323  
AA216609  
ID AA216609 standard; DNA; 25 BP.  
XX  
AC AA216609;  
XX  
DT 29-APR-1999 (first entry)  
XX  
DE Interleukin 1 (44112332) haplotype PCR primer #3.  
XX  
XX Interleukin 1; IL-1; haplotype; inflammatory disorder; alopecia areata;  
XX coronary artery disease; osteoporosis; nephropathy; diabetes mellitus;  
XX Graves disease; systemic lupus erythematosus; lichen sclerosis;  
XX ulcerative colitis; PCR primer; ss.  
XX  
OS Synthetic.  
XX Homo sapiens.  
XX  
PN MO9854359-A1.  
XX  
PD 03-DEC-1998.  
XX  
PF 21-MAY-1998; 98WO-GB001481.  
XX  
PR 29-MAY-1997; 97GB-00011040.  
XX  
XX (DUFF/) DUFF G.  
XX (COXA/) COX A.  
XX (CAMP/) CAMP N J.  
XX (DGIO/) DE GIOVINE F S.  
XX  
XX Duff G, Cox A, Camp NJ, De Giovine FS;  
XX WPI; 1999-080814/07.  
XX  
XX New method of determining a patient's susceptibility to inflammatory  
XX disorders - by detecting the presence of an IL-1 (44112332) haplotype,  
XX useful in designing treatment strategies that modulate the activity of  
XX proteins produced by the IL-1 gene cluster.  
XX  
XX Claim 3; Page 33; 49pp; English.  
XX  
XX A method has been developed for determining a patient's susceptibility to  
XX an inflammatory disorder. The method comprises the detection of an  
XX interleukin 1 (IL-1) (44112332) haplotype in a sample obtained from the  
XX patient, where its presence indicates susceptibility to an inflammatory  
XX disorder. AA216607 to AA216631 represent PCR primer used in the method  
XX for detecting the IL-1 (44112332) haplotype. The method provides kits for  
XX the early prediction of a patient's susceptibility to inflammatory  
XX disorders, including coronary artery disease, osteoporosis, nephropathy  
XX in diabetes mellitus, alopecia areata, Graves disease, systemic lupus

CC erythematous, lichen sclerosis and ulcerative colitis. The detection of  
CC alleles of the haplotype can be applied to particular inflammatory  
CC disorders, comprising diabetic retinopathy, juvenile chronic arthritis,  
CC psoriasis, and insulin dependent diabetes. The identification of a  
CC disease-associated haplotype enables determination of which alleles are  
CC causative, and this information is useful in designing treatment  
CC strategies, including gene therapy and treatment using various agents  
CC that modulate the activity of proteins produced by the IL-1 gene cluster.  
CC Some alleles from the IL-1 gene cluster are associated with particular  
CC inflammatory diseases, and insufficient IL-1 production appears to act  
CC centrally in the pathology of these diseases. Therefore, the use of IL-1  
CC gene clusters is useful in determining genetic susceptibility to  
CC inflammatory diseases, including those with a multifactorial etiology  
CC with a polygenic component  
XX  
SQ Sequence 25 BP; 5 A; 7 C; 10 G; 3 T; 0 U; 0 Other;  
Query Match 2.4%; Score 23.4; DB 1; Length 25;  
Best Local Similarity 96.0%; Pred. No. 9e+02;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 867 GGGATTACAGCGCTGAGCCACG 891  
DB 1 GGGATTACAGCGCTGAGCCACG 25  
RESULT 324  
AAS14584  
ID AAS14584 standard; DNA; 25 BP.  
XX  
AC AAS14584;  
XX  
DT 18-DEC-2001 (first entry)  
XX  
DE Human SNP23 SNP region #2 PCR primer #1.  
XX  
XX Human; single-nucleotide polymorphism; SNP; SNP23; ss; PCR primer;  
KW synaptosome associated protein of 23 kilodaltons; diabetes; obesity;  
KW cardiovascular disorder; hypertension; cancer; drug screening;  
KW forensic medicine; paternity testing.  
XX  
OS Homo sapiens.  
XX  
PN WO200164957-A1.  
XX  
PD 07-SEP-2001.  
XX  
PF 02-MAR-2001; 2001WO-US006830.  
XX  
PR 02-MAR-2000; 2000US-0187176P.  
XX  
PA (DNAS-) DNA SCI INC.  
XX  
PI Ma Y, Smith K, Bentley LG;  
XX  
DR WPI; 2001-602571/68.  
XX  
PT Polymorphic sites useful for the diagnosis of metabolic diseases  
PT involving glucose homeostasis e.g. diabetes, obesity and cardiovascular  
PT disorders.  
XX  
PS Disclosure; Page 8; 41pp; English.  
XX  
CC The invention relates to a nucleic acid between 10 and 100 bases  
CC comprising at least 10 contiguous nucleotides including a polymorphic  
CC site or an adjacent base, from 6 polymorphisms from 5 human genes, RG55  
CC (regulator of G-protein signalling 5), SNP23 (synaptosome associated  
CC protein of 23 kilodaltons), ALDOB (aldolase B), GOS8/RGS2 (helix-loop-  
CC helix basic phosphoprotein) and PPP1CB (not defined). The invention also  
CC relates to using such polymorphisms in a method comprising analysing a  
CC nucleic acid comprising by obtaining nucleic acid samples from  
CC individuals, determining a base occupying any one of the polymorphic or  
CC other sites in linkage disequilibrium with them and testing each

CC individual for the presence of a phenotype and correlating the presence  
CC of the disease phenotype with the base. The linkage disequilibrium thus  
CC determined is used as a diagnostic tool for diseases such as diabetes,  
CC obesity, cardiovascular disorders, hypertension and some forms of  
CC cancers. The polymorphisms may also be used for drug screening,  
CC forensics, paternity tests and could be tested for association with other  
CC diseases. The present sequence is a PCR primer used to amplify a region  
CC containing an SNP (single-nucleotide polymorphism) from human SNP23  
XX  
SQ Sequence 25 BP; 7 A; 7 C; 6 G; 5 T; 0 U; 0 Other;  
Query Match 2.4%; Score 23.4; DB 1; Length 25;  
Best Local Similarity 96.0%; Pred. No. 9e+02;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 383 CCTCCCAAGTGTGAGTTACAG 407  
DB 1 CCTCCCAAGTGTGAGTTACAG 25  
RESULT 325  
AAS14581  
ID AAS14581 standard; DNA; 25 BP.  
XX  
AC AAS14581;  
XX  
DT 18-DEC-2001 (first entry)  
XX  
DE Human SNP23 SNP region #1 PCR primer #1.  
XX  
XX Human; single-nucleotide polymorphism; SNP; SNP23; ss; PCR primer;  
KW synaptosome associated protein of 23 kilodaltons; diabetes; obesity;  
KW cardiovascular disorder; hypertension; cancer; drug screening;  
KW forensic medicine; paternity testing.  
XX  
OS Homo sapiens.  
XX  
PN WO200164957-A1.  
XX  
PD 07-SEP-2001.  
XX  
PF 02-MAR-2001; 2001WO-US006830.  
XX  
PR 02-MAR-2000; 2000US-0187176P.  
XX  
PA (DNAS-) DNA SCI INC.  
XX  
PI Ma Y, Smith K, Bentley LG;  
XX  
DR WPI; 2001-602571/68.  
XX  
PT Polymorphic sites useful for the diagnosis of metabolic diseases  
PT involving glucose homeostasis e.g. diabetes, obesity and cardiovascular  
PT disorders.  
XX  
PS Disclosure; Page 8; 41pp; English.  
XX  
CC The invention relates to a nucleic acid between 10 and 100 bases  
CC comprising at least 10 contiguous nucleotides including a polymorphic  
CC site or an adjacent base, from 6 polymorphisms from 5 human genes, RG55  
CC (regulator of G-protein signalling 5), SNP23 (synaptosome associated  
CC protein of 23 kilodaltons), ALDOB (aldolase B), GOS8/RGS2 (helix-loop-  
CC helix basic phosphoprotein) and PPP1CB (not defined). The invention also  
CC relates to using such polymorphisms in a method comprising analysing a  
CC nucleic acid comprising by obtaining nucleic acid samples from  
CC individuals, determining a base occupying any one of the polymorphic or  
CC other sites in linkage disequilibrium with them and testing each  
CC individual for the presence of a phenotype and correlating the presence  
CC of the disease phenotype with the base. The linkage disequilibrium thus  
CC determined is used as a diagnostic tool for diseases such as diabetes,  
CC obesity, cardiovascular disorders, hypertension and some forms of  
CC cancers. The polymorphisms may also be used for drug screening,  
CC forensics, paternity tests and could be tested for association with other

Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

CC the exemplification of the invention for genotyping IL-1A (g25/g26)



XX 28-OCT-1999.  
PD 14-APR-1999; 99WO-JP001997.  
XX 14-APR-1998; 98UP-00121805.  
XX 14-APR-1998; 98UP-00121805.  
XX (CHUS ) CHUGAI RES INST MOLECULAR MEDICINE INC.  
XX Hirata Y;  
XX WPI; 2000-013230/01.  
XX Novel cytokine-like protein, with activity of supporting proliferation of  
PT myeloid cells, useful in treating abnormality of cell proliferation in  
PT immune and hematopoiesis systems.  
XX Example 5; Page 23; 69pp; Japanese.  
XX This sequence represents a PCR primer used to isolate DNA encoding the  
CC Interleukin-6-G-CSF related factor (SGRF) protein of the invention. The  
CC protein is a member of the IL-6/G-CSF/MSF family. The protein can be used  
CC in drugs for treating diseases due to abnormality of cell proliferation  
CC in the immune system and haematopoietic system  
XX  
SQ Sequence 27 BP; 4 A; 5 C; 12 G; 6 T; 0 U; 0 Other;  
Query Match 2.4%; Score 23.4; DB 1; Length 27;  
Best Local Similarity 96.0%; Pred. No. 9.4e+02;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 537 CCTGCTCAAGCCCTCCCAAGTAGCTG 561  
DB 27 CCTGCTCAAGCCCTCCCAAGTAGCTG 3  
RESULT 331  
ID AAH38611/c  
AAH38611 standard; DNA; 27 BP.  
AC AAH38611;  
XX  
DT 14-AUG-2001 (first entry)  
XX  
DE SNP specific SNPE primer SEQ ID 1407.  
XX  
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
KW SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;  
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolemia;  
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
KW inflammation; forensic investigation; paternity analysis; primer; ss.  
XX  
XX Homo sapiens.  
OS  
XX WO200129262-A2.  
PN  
XX 26-APR-2001.  
PD  
XX 13-OCT-2000; 2000WO-US028436.  
PF  
XX 15-OCT-1999; 99US-0160096P.  
PR  
XX (ORCH-) ORCHID BIOSCIENCES INC.  
PA  
XX Picoult-Newburg L, Pohl M;  
PI  
XX WPI; 2001-290930/30.  
DR  
XX New genotyping oligonucleotide, useful for detecting the presence,  
PT absence or identity of single polymorphic polymorphism in a nucleic  
PT acid sample.  
XX

PS Claim 1; Page 57; 83pp; English.  
XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
CC primer extension (SNPE) primers, and the sequences of regions flanking  
CC sites of single nucleotide polymorphisms SNPs. The present invention  
CC includes kits for determining the presence or absence of a SNP, using the  
CC oligonucleotides of the invention. The PCR primers are used to amplify a  
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.  
CC The oligonucleotides are useful for genotyping a nucleic acid sample by  
CC performing a single-nucleotide primer extension reaction. The  
CC oligonucleotides are useful for determining the presence, absence or  
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
CC assess by association analysis the genotype of an individual or group of  
CC individuals, having a pathological phenotype trait suspected of being  
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular  
CC dystrophy, familial hypercholesterolemia, polycystic kidney disease,  
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
CC traits also include symptoms of or susceptibility to multifactorial  
CC disease of which a component is or may be genetic such as autoimmune  
CC diseases, including, rheumatoid arthritis, multiple sclerosis,  
CC inflammation, cancer, nervous system diseases and infection by pathogenic  
CC microorganism. The method is also useful in forensic investigations and  
CC paternity analysis. The present sequence represents a single nucleotide  
CC primer extension (SNPE) primer specific for a human SNP containing DNA  
CC sequence  
XX  
SQ Sequence 27 BP; 6 A; 6 C; 10 G; 3 T; 0 U; 2 Other;  
Query Match 2.4%; Score 23.4; DB 1; Length 27;  
Best Local Similarity 88.9%; Pred. No. 9.4e+02;  
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 673 GCTCACTGCAACCTCTGCTCCCGGCT 699  
DB 27 GCTCACTGCAACCTCTGCTCCCGGCT 1  
RESULT 332  
ID AAA27185  
AAA27185 standard; DNA; 28 BP.  
AC AAA27185;  
XX  
DT 11-SEP-2000 (first entry)  
XX  
DE Reverse primer IL10 for target sequence human interleukin 10.  
XX  
XX P2; CX5C chemokine; Chromosome 5q31; gene therapy; asthma; PCR primer;  
KW allergic rhinitis; urticaria; anaphylactic shock; hives; hay fever; human;  
KW ss.  
XX  
XX Homo sapiens.  
OS  
XX WO200029621-A2.  
PN  
XX 25-MAY-2000.  
PD  
XX 12-NOV-1999; 99WO-US026931.  
PF  
XX 16-NOV-1998; 98US-00193320.  
PR  
XX (GENE-) GENELABS TECHNOLOGIES INC.  
PA  
XX Dolganov G, Novikov A;  
PI  
XX WPI; 2000-387825/33.  
DR  
XX Measuring target polymorphic sequences in biological samples by  
PT contacting sequence-selective primer pairs, forming conjugates with  
PT adaptor molecules, polymerizing target-identifier dimers and quantifying  
PT them.  
XX

PS Disclosure; Page 100; 103pp; English.

CC A novel method for simultaneously determining the level of a number of  
CC target polynucleotides in a sample has been disclosed. The method  
CC involves forming double stranded copies of the target sequence in direct  
CC proportion to the target levels in the original sample. The target  
CC sequence is copied using primer pairs designed to flank a defined region  
CC in the target sequence. The double stranded copies are then cleaved and  
CC reacted with either first or second adaptor sequences. The first and  
CC second conjugate mixtures are then allowed to form dimers with each other  
CC through the target sequences. The adaptor sequences are then removed to  
CC leave target sequence dimers. These dimers are then polymerised to form  
CC multimer targets. The relative abundances of target identifiers in the  
CC multimer allow expression levels to be determined. This method is useful  
CC for developing polynucleotide abundance level profiles for cells and  
CC tissues under various conditions, stages of development and disease  
CC states, particularly where the target polynucleotide is present at low  
CC levels. The method may also be used in the discovery and evaluation of  
CC candidate therapeutic agents and their effective dosage levels. In  
CC addition to the method described above, the invention also includes the  
CC polynucleotide and polypeptide of P2. P2 is thought to be a member of a  
CC novel chemokine family, denoted CX5C and may be associated with immune  
CC function. Compositions of the P2 polypeptide may be useful in the  
CC treatment of asthma, allergic rhinitis (hay fever), urticaria (hives),  
CC anaphylactic shock and conditions involving immune system  
CC hypersensitivity. The P2 polynucleotide to treat conditions using gene  
CC therapy. The human P2 gene has been localised to chromosome 5, within the  
CC cytokine gene cluster at 5q31. The present sequence is the reverse primer  
CC IL10 for target sequence human interleukin 10

SQ Sequence 28 BP; 5 A; 8 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 2.4%; Score 23.4; DB 1; Length 28;  
Best Local Similarity 96.0%; Pred. No. 9.7e+02;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 635 CTCTGTCAACCCAGCTGAGTGACG 659  
|||  
4 CTCTGTCAACCCAGCTGAGTGACG 28

Db

RESULT 333  
ACC84463  
ID ACC84463 standard; DNA; 28 BP.  
XX AC AC84463;  
XX  
XX 28-AUG-2003 (first entry)  
XX  
XX NTP peptide encoding sequence #10.  
DE  
XX  
XX Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;  
KW neutral thread protein; NTP; tumour; ds.  
XX  
XX Unidentified.  
OS  
XX WO2003008443-A2.  
XX  
XX 30-JAN-2003.  
PD  
XX  
XX 19-JUL-2002; 2002WO-CA001105.  
XX  
XX 19-JUL-2001; 2001US-0306150P.  
XX  
XX 19-JUL-2001; 2001US-0306161P.  
PR  
XX 16-NOV-2001; 2001US-0331477P.  
XX  
XX (NYMO-) NYMOX CORP.  
PA  
XX Averbach PA;  
XX  
XX WPI; 2003-247999/24.  
DR  
XX P-PSDB; ABR63258.  
XX

PT Novel neural thread protein peptide, referred as cell death peptide,  
PT useful for treating prostatic hyperplasia, psoriasis, eczema, dermatosis,  
PT atherosclerosis, cosmetic modification to skin, throat, mouth, muscle.

XX  
XX  
XX Disclosure; Page 17; 77pp; English.

PS  
XX  
XX The present invention relates to a neural thread protein (NTP) peptide  
CC referred to as cell death peptide. Thought to be cytostatic,  
CC antibacterial, immunosuppressive and antiinflammatory. It is useful for  
CC treating a condition in a patient requiring removal or destruction of  
CC cells, for treating a condition such as benign or malignant tumor,  
CC inflammatory disease, autoimmune disease and infectious disease. The  
CC peptide useful for treatment is derived from the amino acid sequence for  
CC a pancreatic cholest protein. The peptide is conjugated, linked or bound  
CC to a molecule chosen from antibody or its fragment, antibody-like binding  
CC molecule, where the molecule has a higher affinity for binding to a tumor  
CC or other target than binding to other cells. Treatment using NTP peptides  
CC can remove benign tumors with less risk and fewer of the undesirable side  
CC effects of surgery. The present sequence is an NTP encoding sequence

SQ Sequence 28 BP; 6 A; 9 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 2.4%; Score 23.4; DB 1; Length 28;  
Best Local Similarity 96.0%; Pred. No. 9.7e+02;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 725 CCTGAGTAGCTGGACTACAGGCGC 749  
|||  
4 CCGAGTAGCTGGACTACAGGCGC 28

Db

RESULT 334  
ADP70455  
ID ADP70455 standard; DNA; 28 BP.  
XX AC ADP70455;  
XX  
XX 12-AUG-2004 (first entry)  
XX  
XX RT-PCR primer 2 related to human blood disease-related LRR8 mutant.  
DE  
XX  
XX LRR8; B-cell surface membrane; immunosuppressive;  
KW non-gamma globulin blood disease; maturation; human; ss; probe;  
KW chromosome 9; chromosome 20; translocation.  
XX  
XX Homo sapiens.  
OS  
XX  
XX JP2004141048-A.  
XX  
XX 20-MAY-2004.  
PD  
XX  
XX 23-OCT-2002; 2002JP-00308855.  
XX  
XX 23-OCT-2002; 2002JP-00308855.  
PR  
XX (OOSA-) ZH OOSAKA SANGYO SHINKO KIKO.  
XX (OSAP ) OSAKA PREFECTURE.  
PA  
XX  
XX WPI; 2004-382668/36.  
DR  
XX  
XX Novel LRR8 protein useful as marker for congenital non-gamma globulin  
PT blood disease, or for screening B-cell associated disease therapeutic  
PT agent or immunosuppressive agent.  
XX  
XX Disclosure; SEQ ID NO 12; 46pp; Japanese.

PS  
XX  
XX The invention relates to a novel LRR8 protein comprising a fully defined  
CC sequence as given in the specification, or a receptor protein in which  
CC one or more amino acid residues are substituted, added or deleted, that  
CC expresses on the B-cell surface membrane of a non-gamma globulin diseased  
CC patient. The polypeptide of the invention demonstrates immunosuppressive  
CC activity and may be useful for screening a B-cell-associated disease  
CC therapeutic agent or immunosuppressive agent, as a marker for congenital



CC non-gamma globulin blood disease or as an agent for maturation of human  
CC or mouse B-cells. The current sequence is that of the RT-PCR primer 2 of  
CC the invention which is related to the human LRRC8 mutant that is  
CC generated by a translocation between chromosomes 9 and 20.

XX Sequence 28 BP; 7 A; 7 C; 7 T; 0 U; 0 Other;

Query Match 2.4%; Score 23.4; DB 1; Length 28;  
Best Local Similarity 96.0%; Pred. No. 9.7e+02;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1018 TCAGCCTCCCAAGCAGCTGGATTA 1042  
DB 1 TCAGCCTCCCAAGTACTGGATTA 25

RESULT 335  
AAA04010/C  
ID AAA04010 standard; DNA; 29 BP.

XX AAA04010;  
XX 22-MAY-2000 (first entry)

DE Polymorphic fragment of hypertension associated gene APOC4.

KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;  
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;  
KW Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;  
KW polycystic kidney disease; von Willebrand disease; forensic; human;  
KW tubercous sclerosis; hereditary hemorrhagica telangiectasia;  
KW familial colonic polyposis; osteogenesis imperfecta; porphyria;  
KW Ehlers-Danlos syndrome; ss.

KW Homo sapiens.

XX EP955382-A2.

XX 10-NOV-1999.

XX 07-MAY-1999; 99EP-00250150.

XX 07-MAY-1998; 98US-0084641P.

XX 03-MAY-1999; 99US-00304232.

XX (AFY-) AFRYMETRIX INC.

XX (UYCA-) UNIV CASE WESTERN RESERVE.

XX Fan JB, Chakravarti A, Haluska MK;

XX WPI; 2000-107928/10.

XX Novel nucleic acids containing polymorphisms used in the diagnosis of  
XX hypertension.

PS Claim 1; Page 22; 53pp; English.  
XX The invention provides polymorphic fragments of genes associated with  
XX hypertension. The nucleic acids including the polymorphic sites can be  
XX used as probes or primers for expressing variant proteins. Detection of  
XX the polymorphisms is useful in designing prophylactic and therapeutic  
XX regimens customized to underlying abnormalities. The polymorphisms can be  
XX used for association studies for hypertension, and in hypertension  
XX diagnostic assays. Where the polymorphisms have strong correlation with  
XX hypertension, within a gene, they are likely to have a causative role in  
XX hypertension. This information can be used to find the precise role of a  
XX polymorphism in the disease, and this can be used to identify potential  
XX drugs which combat the disease. The polymorphisms can be tested for  
XX association with other diseases e.g. agammaglobulinemia, diabetes  
XX insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich  
XX syndrome, Fabry's disease, familial hypercholesterolemia, polycystic  
XX kidney disease, hereditary spherocytosis, von Willebrand disease,  
XX tubercous sclerosis, hereditary hemorrhagica telangiectasia, familial

CC colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and  
CC acute intermittent porphyria. The polymorphic forms can also be used in  
CC forensics to identify individuals

XX Sequence 29 BP; 5 A; 9 C; 8 G; 6 T; 0 U; 1 Other;

Query Match 2.4%; Score 23.4; DB 1; Length 29;  
Best Local Similarity 88.9%; Pred. No. 9.9e+02;  
Matches 24; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 721 GCCTCTGAGTAGTGTGGACTACAGGC 747  
DB 29 GCCTCCCAAGTACGCGATTACAGGC 3

RESULT 336  
AAH91473/C  
ID AAH91473 standard; DNA; 29 BP.

XX AAH91473;  
XX 09-OCT-2001 (first entry)

DE Human inflammatory bowel disease associated polymorphic site #548.

KW Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;  
KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;  
KW chromosome 5q31-33; forensic test; gene therapy; de.

XX Homo sapiens.

XX Key Location/Qualifiers

FT misc\_feature 16 /tag= a

FT /note= "SNP, optionally A or G at this position"

XX WO200142511-A2.

XX 14-JUN-2001.

XX 11-DEC-2000; 2000MO-US033632.

XX 10-DEC-1999; 99US-0170257P.

XX 10-APR-2000; 2000US-0196046P.

XX (WHD) WHITEHEAD INST BIOMEDICAL RES.

XX (ELL-) ELLIPSIS BIOTHERAPEUTICS CORP.

XX Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;

XX WPI; 2001-367874/38.

XX Testing for the presence of polymorphisms associated with inflammatory  
XX bowel disease, using a hybridization assay.

XX Claim 1; Page 61; 463pp; English.

XX The present invention describes a method for detecting the presence of  
XX polymorphisms associated with inflammatory bowel diseases such as  
XX ulcerative colitis and Crohn's disease. The methods can be used to detect  
XX the presence of genetic polymorphisms associated with inflammatory bowel  
XX disease and correlating their occurrence with disease states. They may be  
XX used in this way for phenotypic correlations, forensics, paternity  
XX testing, medicine and genetic analysis. The present sequence is a  
XX polymorphic site described in the exemplification of the invention

XX Sequence 29 BP; 9 A; 8 C; 7 G; 4 T; 0 U; 1 Other;

Query Match 2.3%; Score 23.2; DB 1; Length 29;  
Best Local Similarity 86.2%; Pred. No. 1e+03;  
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1014 TGTCTAGCCTCCCAAGCAGCTGGATTA 1042

[illegible]

XX	PCR primer F1209 used to sequence human LDLR DNA.
DE	
KW	discriminant function coefficient; DC; ethnic affiliation; haplotype;
KW	descent predictor; forensic analysis; Alu repeat; hot spot; diversity;
KW	human; low density lipoprotein receptor; LDLR; ss; primer; PCR; F1209.
XX	
OS	Homo sapiens.
PN	
PN	US6544730-B1.
PD	
PD	08-APR-2003.
PF	
PF	27-OCT-1997; 97US-00958009.
PR	
PR	27-OCT-1997; 97US-00958009.
XX	
XX	(DEIN/) DEININGER P.
PA	(KASS/) KASS D.
PA	
P1	Deininger P, Kass D;
DR	
DR	WPI; 2003-566586/53.
PT	
PT	Determining discriminant function coefficient for ethnic affiliation,
PT	comprises comparing haplotypes from donors of known ethnic origin with
PT	expected haplotype frequency and estimating coefficient from obtained
XX	discrepancies.
XX	
PS	Example 2; Col 19; 25pp; English.
XX	
XX	The invention relates to a method which comprises determining
CC	discriminant function coefficient (DC) for ethnic affiliation. This is
CC	achieved via obtaining haplotypes from specific DNA sequence analysis and
CC	comparing haplotypes from human donors of known ethnic origin with
CC	expected haplotype frequency. The DC is used as an ethnic descent
CC	predictor. The method of the invention may be useful for determining a DC
CC	for ethnic affiliation and thus for estimating ethnic affiliation, as
CC	well as for determining an ethnic specific haplotype, estimating genetic
CC	affiliation and during forensic analysis. The 3' A-rich region of the Alu
CC	repeat used within the method is a 'hot spot' for diversity making this
CC	region very useful for forensic analysis. The current sequence is that of
CC	the PCR primer F1209 of the invention which was used to sequence the
XX	human LDLR DNA.
XX	
SO	Sequence 23 BP; 5 A; 10 C; 3 G; 5 T; 0 U; 0 Other;
XX	
XX	Query Match 2.3%; Score 23; DB 1; Length 23;
XX	Best Local Similarity 100.0%; Pred. No. 8.9e+02;
XX	Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	861 AGTGGTGGATTACAGGCGTGAG 863
DB	23 AGTCTGGGATTACAGGCGTGAG 1
XX	
XX	RESULT 339
XX	AAH91561/c
ID	AAH91561 standard; DNA; 24 BP.
XX	
XX	AAH91561;
XX	
DT	09-OCT-2001 (first entry)
XX	
DE	Human inflammatory bowel disease associated polymorphic site #636.
XX	
KW	Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW	single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
KW	chromosome 5q31-33; forensic test; gene therapy; ds.
XX	
OS	Homo sapiens.
XX	
XX	
PH	Key Location/Qualifiers

```

FT misc_feature 12
FT /*tag= a
FT /note= "SNP, optionally T or C at this position"
PN
PN WO200142511-A2.
PD 14-JUN-2001.
PF 11-DEC-2000; 2000WO-US033632.
PR 10-DEC-1999; 99US-0170257P.
PR 10-APR-2000; 2000US-0196046P.
XX
PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.
PI Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;
XX WPI; 2001-367874/38.
XX
XX Testing for the presence of polymorphisms associated with inflammatory
PT bowel disease, using a hybridization assay.
XX
XX Claim 1; Page 65; 463pp; English.
XX
XX The present invention describes a method for detecting the presence of
CC polymorphisms associated with inflammatory bowel diseases such as
CC ulcerative colitis and Crohn's disease. The methods can be used to detect
CC the presence of genetic polymorphisms associated with inflammatory bowel
CC disease and correlating their occurrence with disease states. They may be
CC used in this way for phenotypic correlations, forensics, paternity
CC testing, medicine and genetic analysis. The present sequence is a
CC polymorphic site described in the exemplification of the invention
XX
XX Sequence 24 BP; 5 A; 4 C; 11 G; 3 T; 0 U; 1 Other;
SQ
Query Match 2.3%; Score 23; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 9.1e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0.
OY 839 TCTGCTGTGCTCGGCTCCCAAG 862
Db 24 TCTGCTGTGCTCGGCTCCCAAG 1
RESULT 340
AAQ14732
ID AAQ14732 standard; DNA; 26 BP.
XX
XX AAQ14732;
AC
XX
XX 19-DEC-1991 (first entry)
DT
XX
XX X-T-D oligonucleotide.
DE
XX
XX Branch migration; linker; displacer; target; ss.
XX
XX Synthetic.
OS
XX
XX EP450370-A.
PN
XX
XX 09-OCT-1991.
PD
XX
XX 15-MAR-1991; 91EP-00104066.
PF
XX
XX 26-MAR-1990; 90US-00499938.
PR
XX
XX (ENZO-) ENZO BIOCHEM INC.
PA
XX
XX Wetmur JG, Quartin RS, Engelhardt DL;
PI WPI; 1991-297200/41.
XX
XX

```

PT	Branch migration of nucleotide(s) - using one strand of recipient poly-deoxy-nucleotide sequence and displacer sequence of single-stranded DNA.
XX	
XX	Disclosure; Page 15; 34pp; English.
PS	
CC	The sequences represented in AAQ14004-32 and AAQ14728-33 are used in the
CC	examples of the specification, illustrating the method of the invention.
CC	Oligonucleotides AAQ14016-29 and AAQ14728-33 are linkers, displacers and
CC	targets. Nomenclature: X=XmaI restriction site T=taget D=polarity;
CC	displacer side
XX	
SO	Sequence 26 BP; 3 A; 12 C; 5 G; 6 T; 0 U; 0 Other;
XX	
Query Match	2.3%; Score 22.8; DB 1; Length 26;
Best Local Similarity	92.3%; Pred. No. 9.8e+02;
Matches	24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy	968 TCTGGCTCACTGCACCTCTGCCTC 993
Db	1 TCTGGCTCACTGCACCTCTGCCTC 26
RESULT 341	
AAQ71189/C	
ID	AAQ71189 standard; DNA; 26 BP.
XX	
AC	AAQ71189;
XX	
DT	25-MAR-2003 (revised)
DT	29-MAR-1995 (first entry)
XX	
DE	Inter-Alu region primer 614.
XX	
KW	Vector; p9lox5; turbo cloning; lox; lox/Cre recombinase; pUC9;
KW	inter-Alu region; polymerase chain reaction; PCR; primer; amplification;
KW	human chromosome-11; CHO; Chinese hamster ovary; 88.
OS	Synthetic.
XX	
PN	WO9418333-A1.
XX	
PD	18-AUG-1994.
XX	
PF	11-FEB-1994; 94WO-GB000272.
XX	
PR	12-FEB-1993; 93GB-00002798.
XX	
PA	(MEDT-) MEDICAL RES COUNCIL.
PI	Boyd AC;
XX	
DR	WPI; 1994-279754/34.
XX	
PT	Cloning of DNA molecules - by ligating with a vector contg a lox site,
PT	cyclisation with Cre protein and dissociation.
XX	
PS	Disclosure; Page 7; 36pp; English.
XX	
CC	To obtain vector p9lox5, a SalI cohesive-ended duplex containing a lox
CC	sequence from the phage P1 lox/Cre recombinase system was made by
CC	annealing oligos B16 (AAQ71187) and B17 (AAQ71188) and cloning into SalI-
CC	cleaved pUC9. Primer 614 (AAQ71189), designed from a consensus Alu repeat
CC	sequence, was used to prime amplification of the inter-Alu region of
CC	genomic DNA from line B2.13, which contains human chromosome-11 in a CHO
CC	background. The product was ligated to p9lox5 by turbo cloning. (Updated
CC	on 25-MAR-2003 to correct PN field.)
XX	
SQ	Sequence 26 BP; 5 A; 9 C; 8 G; 4 T; 0 U; 0 Other;
XX	
Query Match	2.3%; Score 22.8; DB 1; Length 26;
Best Local Similarity	92.3%; Pred. No. 9.8e+02;
Matches	24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;



KW haematopoietic disorder; dyslipidaemia; chronic disease; probe; RTQ-PCR;  
 KW real time quantitative PCR.  
 OS Homo sapiens.  
 XX US2004043382-A1.  
 XX  
 PD 04-MAR-2004.  
 XX  
 PF 07-MAR-2002; 2002US-00092900.  
 XX  
 XX 08-MAR-2001; 2001US-0274191P.  
 PR 08-MAR-2001; 2001US-0274194P.  
 PR 08-MAR-2001; 2001US-0274281P.  
 PR 08-MAR-2001; 2001US-0274322P.  
 PR 09-MAR-2001; 2001US-0274849P.  
 PR 12-MAR-2001; 2001US-0275235P.  
 PR 13-MAR-2001; 2001US-0275378P.  
 PR 13-MAR-2001; 2001US-0275579P.  
 PR 13-MAR-2001; 2001US-0275601P.  
 PR 14-MAR-2001; 2001US-0276000P.  
 PR 16-MAR-2001; 2001US-0276776P.  
 PR 19-MAR-2001; 2001US-0276994P.  
 PR 20-MAR-2001; 2001US-0277239P.  
 PR 20-MAR-2001; 2001US-0277321P.  
 PR 20-MAR-2001; 2001US-0277327P.  
 PR 21-MAR-2001; 2001US-0277388P.  
 PR 21-MAR-2001; 2001US-0277791P.  
 PR 22-MAR-2001; 2001US-0277833P.  
 PR 23-MAR-2001; 2001US-0278152P.  
 PR 26-MAR-2001; 2001US-0278894P.  
 PR 27-MAR-2001; 2001US-0278999P.  
 PR 27-MAR-2001; 2001US-0279036P.  
 PR 28-MAR-2001; 2001US-0279344P.  
 PR 30-MAR-2001; 2001US-0279995P.  
 PR 30-MAR-2001; 2001US-0280233P.  
 PR 02-APR-2001; 2001US-0280802P.  
 PR 02-APR-2001; 2001US-0280822P.  
 PR 02-APR-2001; 2001US-0280900P.  
 PR 04-APR-2001; 2001US-0281444P.  
 PR 13-APR-2001; 2001US-0283675P.  
 PR 30-APR-2001; 2001US-0287424P.  
 PR 02-MAY-2001; 2001US-0288066P.  
 PR 03-MAY-2001; 2001US-0288342P.  
 PR 03-MAY-2001; 2001US-0288528P.  
 PR 15-MAY-2001; 2001US-0291190P.  
 PR 16-MAY-2001; 2001US-0291099P.  
 PR 16-MAY-2001; 2001US-0291240P.  
 PR 30-MAY-2001; 2001US-0294485P.  
 PR 31-MAY-2001; 2001US-0294899P.  
 PR 31-MAY-2001; 2001US-0294899P.  
 PR 18-JUN-2001; 2001US-0299027P.  
 PR 19-JUN-2001; 2001US-0299303P.  
 PR 19-JUN-2001; 2001US-0299310P.  
 PR 10-JUL-2001; 2001US-0304354P.  
 PR 31-JUL-2001; 2001US-0309198P.  
 PR 16-AUG-2001; 2001US-0312903P.  
 PR 10-SEP-2001; 2001US-0318462P.  
 PR 12-SEP-2001; 2001US-0318770P.  
 PR 27-SEP-2001; 2001US-0325430P.  
 PR 27-SEP-2001; 2001US-0325681P.  
 PR 18-OCT-2001; 2001US-0330380P.  
 PR 31-OCT-2001; 2001US-0335301P.  
 PR 14-NOV-2001; 2001US-0332122P.  
 PR 14-NOV-2001; 2001US-0332271P.  
 PR 14-NOV-2001; 2001US-0332272P.  
 PR 14-NOV-2001; 2001US-0333184P.  
 PR 21-NOV-2001; 2001US-0332094P.  
 PR 03-DEC-2001; 2001US-0337426P.  
 PR 03-DEC-2001; 2001US-0338092P.  
 PR 04-DEC-2001; 2001US-0337185P.  
 PR 03-JAN-2002; 2002US-0345705P.

XX  
 PA (PADJ/) PADIGARU M.  
 PA (SPYT/) SPYTEK K A.  
 PA (SHEN/) SHENOY S G.  
 PA (TAUP/) TAUPIER R J.  
 PA (PENNA/) PENNA C E A.  
 PA (LILL/) LI L.  
 PA (ZERH/) ZERHUSEN B D.  
 PA (GUSE/) GUSEV V Y.  
 PA (JIMW/) JI W.  
 PA (GORM/) GORMAN L.  
 PA (MILL/) MILLER C E.  
 PA (KEKU/) KEKUDA R.  
 PA (PATT/) PATTUPAJAN M.  
 PA (GANG/) GANGOLLI E A.  
 PA (VERN/) VERNET C A M.  
 PA (GUOX/) GUO X S.  
 PA (TCHH/) TCHERNY V T.  
 PA (PERN/) FERNANDES E R.  
 PA (CASW/) CASMAN S J.  
 PA (MALY/) MALYANKAR U M.  
 PA (GERL/) GERLACH V.  
 PA (LIUY/) LIU Y.  
 PA (ANDR/) ANDERSON D W.  
 PA (SPAD/) SPADERNA S K.  
 PA (CATT/) CATTERTON E.  
 PA (LEIT/) LEITE M W.  
 PA (ZHON/) ZHONG H.  
 PA (ALSO/) ALSOBROOK J P.  
 PA (LEPL/) LEPLEY D M.  
 PA (RIEG/) RIEGER D K.  
 PA (BURG/) BURGESS C E.  
 XX  
 XX Padigaru M, Spytek KA, Shenoy SG, Taupier RJ, Pena CE, Li L,  
 PI Zehusen BD, Gusev VY, Ji W, Gorman L, Miller CE, Kekuda R;  
 PI Patturajan M, Gangolli EA, Vernet CM, Guo XS, Tcherny VT;  
 PI Fernandes ER, Casman SJ, Malyankar UM, Gerlach V, Liu Y;  
 PI Andrews DW, Spaderna SK, Catterton E, Leite MW, Zhong H;  
 PI Alsobrook JP, Lepley DM, Rieger DK, Burgess CE;  
 XX  
 DR MPI; 2004-225693/21.  
 XX  
 PT New NOVX polypeptides and nucleic acid molecules useful for diagnosing,  
 PT preventing or treating NOVX-associated disorders, e.g. cancer, diabetes,  
 PT infection or obesity, and in chromosome mapping, tissue typing or  
 PT pharmacogenomics.  
 XX  
 PS Example C; SEQ ID NO 464; 786bp; English.  
 XX  
 XX The invention relates to an isolated polypeptide (designated NOVX, or  
 CC NOV1-NOV127) comprising a sequence selected from 178 fully defined amino  
 CC acid sequences (and their mature forms, variants and fragments). Also  
 CC included are an isolated nucleic acid molecule encoding NOVX, a vector  
 CC comprising the nucleic acid, a cell comprising the vector, methods for  
 CC determining the presence or amount of the polypeptide or the nucleic acid  
 CC molecule in a sample, methods for determining the presence of or  
 CC predisposition to a disease associated with altered levels of expression  
 CC of the above polypeptide or nucleic acid molecule in a first mammalian  
 CC subject, a method for identifying an agent that binds to the above  
 CC polypeptide, a method for identifying a potential therapeutic agent for  
 CC use in the treatment of a pathology that is related to aberrant  
 CC expression or physiological interactions of the polypeptide, a method of  
 CC screening for a modulator of activity or of latency or predisposition to  
 CC a pathology associated with the polypeptide and a method for modulating  
 CC the activity of the polypeptide cited above. The composition and methods  
 CC are useful for diagnosing, preventing or treating diseases such as  
 CC diabetes, obesity, infectious diseases, anorexia, cancer-associated  
 CC cachexia, cancer, neurodegenerative disorders like Alzheimer's disease or  
 CC Parkinson's disease, immune disorders, haematopoietic disorders,  
 CC dyslipidaemias, and other chronic diseases. These may also be used in  
 CC chromosome mapping, tissue typing, preventive medicine and  
 CC pharmacogenomics. The polypeptides are also useful as vaccines. The  
 CC present sequence is an RTQ-PCR (real time quantitative PCR) probe used to

CC assay tissue specific expression of a NOVX mRNA.  
 XX Sequence 26 BP; 6 A; 9 C; 3 G; 8 T; 0 U; 0 Other;  
 SQ Sequence 26 BP; 6 A; 9 C; 3 G; 8 T; 0 U; 0 Other;  
 CC Query Match 2.3%; Score 22.8; DB 1; Length 26;  
 CC Best Local Similarity 92.3%; Pred. No. 9.8e+02;  
 CC Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 OY 573 ATGCACCACTACCTGGCTAATTT 598  
 DB 1 ATGCACCACTACCTGGCTAATTT 26  
 RESULT 344  
 AAH38083  
 ID AAH38083 standard; DNA; 27 BP.  
 AC AAH38083;  
 XX 14-AUG-2001 (first entry)  
 DT 14-AUG-2001 (first entry)  
 XX SNP specific SNPE primer SEQ ID 879.  
 DE SNP specific SNPE primer SEQ ID 879.  
 XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
 KW SNP; genotyping; agammaglobulinemia; diabetes insipidus; cancer;  
 KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;  
 KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
 KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
 KW inflammation; forensic investigation; paternity analysis; primer; ss.  
 OS Homo sapiens.  
 XX Homo sapiens.  
 PN WO200129262-A2.  
 XX 26-APR-2001.  
 PD 13-OCT-2000; 2000WO-US028436.  
 XX 15-OCT-1999; 99US-0160096P.  
 PR (ORCH-) ORCHID BIOSCIENCES INC.  
 XX (ORCH-) ORCHID BIOSCIENCES INC.  
 PI Picoult-Newburg L, Pohl M;  
 DR WPI; 2001-290930/30.  
 PT New genotyping oligonucleotide, useful for detecting the presence,  
 PT absence or identity of single polynucleotide polymorphism in a nucleic  
 PT acid sample.  
 PS Claim 1; Page 54; 83pp; English.  
 XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
 CC primer extension (SNPE) primers, and the sequences of regions flanking  
 CC sites of single nucleotide polymorphisms SNPs. The present invention  
 CC includes kits for determining the presence or absence of a SNP, using the  
 CC oligonucleotides of the invention. The PCR primers are used to amplify a  
 CC SNP flanking sequence, the SNPs primer is used as a genotyping primer.  
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by  
 CC performing a single-nucleotide primer extension reaction. The  
 CC oligonucleotides are useful for determining the presence, absence or  
 CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
 CC assess by association analysis the genotype of an individual or group of  
 CC individuals, having a pathological phenotypic trait suspected of being  
 CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
 CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular  
 CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,  
 CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
 CC traits also include symptoms of or susceptibility to multifactorial  
 CC disease of which a component is or may be genetic such as autoimmune  
 CC diseases, including, rheumatoid arthritis, multiple sclerosis,  
 CC inflammation, cancer, nervous system diseases and infection by pathogenic  
 CC microorganism. The method is also useful in forensic investigations and

CC paternity analysis. The present sequence represents a single nucleotide  
 CC primer extension (SNPE) primer specific for a human SNP containing DNA  
 CC sequence  
 XX Sequence 27 BP; 5 A; 10 C; 3 G; 8 T; 0 U; 1 Other;  
 SQ Sequence 27 BP; 5 A; 10 C; 3 G; 8 T; 0 U; 1 Other;  
 CC Query Match 2.3%; Score 22.8; DB 1; Length 27;  
 CC Best Local Similarity 88.9%; Pred. No. 1e+03;  
 CC Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 OY 699 TTCAGTATTTCTCTGCCCCAGCCTC 725  
 DB 1 TTCAGTATTTCTCTGCCCCAGCCTC 27  
 RESULT 345  
 AAH40487  
 ID AAH40487 standard; DNA; 27 BP.  
 AC AAH40487;  
 XX 14-AUG-2001 (first entry)  
 DT 14-AUG-2001 (first entry)  
 XX SNP specific SNPE primer SEQ ID 3283.  
 DE SNP specific SNPE primer SEQ ID 3283.  
 XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
 KW SNP; genotyping; agammaglobulinemia; diabetes insipidus; cancer;  
 KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;  
 KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
 KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
 KW inflammation; forensic investigation; paternity analysis; primer; ss.  
 OS Homo sapiens.  
 XX Homo sapiens.  
 PN WO200129262-A2.  
 XX 26-APR-2001.  
 PD 13-OCT-2000; 2000WO-US028436.  
 XX 15-OCT-1999; 99US-0160096P.  
 PR (ORCH-) ORCHID BIOSCIENCES INC.  
 XX (ORCH-) ORCHID BIOSCIENCES INC.  
 PI Picoult-Newburg L, Pohl M;  
 DR WPI; 2001-290930/30.  
 PT New genotyping oligonucleotide, useful for detecting the presence,  
 PT absence or identity of single polynucleotide polymorphism in a nucleic  
 PT acid sample.  
 PS Claim 1; Page 66; 83pp; English.  
 XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
 CC primer extension (SNPE) primers, and the sequences of regions flanking  
 CC sites of single nucleotide polymorphisms SNPs. The present invention  
 CC includes kits for determining the presence or absence of a SNP, using the  
 CC oligonucleotides of the invention. The PCR primers are used to amplify a  
 CC SNP flanking sequence, the SNPs primer is used as a genotyping primer.  
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by  
 CC performing a single-nucleotide primer extension reaction. The  
 CC oligonucleotides are useful for determining the presence, absence or  
 CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
 CC assess by association analysis the genotype of an individual or group of  
 CC individuals, having a pathological phenotypic trait suspected of being  
 CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
 CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular  
 CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,  
 CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
 CC traits also include symptoms of or susceptibility to multifactorial  
 CC disease of which a component is or may be genetic such as autoimmune  
 CC diseases, including, rheumatoid arthritis, multiple sclerosis,

CC inflammation, cancer, nervous system diseases and infection by pathogenic  
CC microorganism. The method is also useful in forensic investigations and  
CC paternity analysis. The present sequence represents a single nucleotide  
CC primer extension (SNPE) primer specific for a human SNP containing DNA  
CC sequence

XX Sequence 27 BP; 5 A; 7 C; 7 G; 7 T; 0 U; 1 Other;

Query Match 2.3%; Score 22.8; DB 1; Length 27;  
Best Local Similarity 88.9%; Pred. No. 1e+03;  
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 849 TCGGCTCCCAAGTGTGGATTACA 875

DB 1 TTGGCTCNCACAGTGTGGATTACA 27

#### RESULT 346

AAH40803

ID AAH40803 standard; DNA; 27 BP.

AC AAH40803;

DT 14-AUG-2001. (first entry)

DE SNP specific SNPE primer SEQ ID 3599.

XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
XX SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;  
XX Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolemia;  
XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
XX inflammation; forensic investigation; paternity analysis; primer; ss.

OS Homo sapiens.

PN WO200129262-A2.

XX 26-APR-2001.

XX 13-OCT-2000; 2000MO-US028436.

XX 15-OCT-1999; 99US-0160096P.

XX (ORCH-) ORCHID BIOSCIENCES INC.

PI Picoult-Newburg L, Pohl M;

DR WPI; 2001-290930/30.

PT New genotyping oligonucleotide, useful for detecting the presence,  
PT absence or identity of single polynucleotide polymorphism in a nucleic  
PT acid sample.

XX Claim 1; Page 68; 83pp; English.

XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
CC primer extension (SNPE) primers, and the sequences of regions flanking  
CC sites of single nucleotide polymorphisms SNPs. The present invention  
CC includes kits for determining the presence or absence of a SNP, using the  
CC oligonucleotides of the invention. The PCR primers are used to amplify a  
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.  
CC The oligonucleotides are useful for genotyping a nucleic acid sample by  
CC performing a single-nucleotide primer extension reaction. The  
CC oligonucleotides are useful for determining the presence, absence or  
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
CC assess by association analysis the genotype of an individual or group of  
CC individuals, having a pathological phenotypic trait suspected of being  
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular  
CC dystrophy, familial hypercholesterolemia, polycystic kidney disease,  
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
CC traits also include symptoms of or susceptibility to multifactorial

CC disease of which a component is or may be genetic such as autoimmune  
CC diseases, including, rheumatoid arthritis, multiple sclerosis,  
CC inflammation, cancer, nervous system diseases and infection by pathogenic  
CC microorganism. The method is also useful in forensic investigations and  
CC paternity analysis. The present sequence represents a single nucleotide  
CC primer extension (SNPE) primer specific for a human SNP containing DNA  
CC sequence

XX Sequence 27 BP; 8 A; 6 C; 7 G; 5 T; 0 U; 1 Other;

Query Match 2.3%; Score 22.8; DB 1; Length 27;  
Best Local Similarity 88.9%; Pred. No. 1e+03;  
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 861 AGTGCTGAGATTACAGCGCTGAGCCAC 887

DB 1 AGTGCTGAATTATACAGCGTGAAGCCAC 27

#### RESULT 347

AAH91322/c

ID AAH91322 standard; DNA; 27 BP.

XX AAH91322;

DT 09-OCT-2001 (first entry)

DE Human inflammatory bowel disease associated polymorphic site #397.

XX Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;  
XX single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;  
XX chromosome 5q31-33; forensic test; gene therapy; ds.

XX Homo sapiens.

OS Homo sapiens.

PN Key Location/Qualifiers

XX misc\_feature 16

XX /\*tag= a

XX /note= "SNP, optionally A or G at this position"

XX WO200142511-A2.

XX 14-JUN-2001.

XX 11-DEC-2000; 2000MO-US033632.

XX 10-DEC-1999; 99US-0170257P.

XX 10-APR-2000; 2000US-0196046P.

XX (WHEED ) WHITEHEAD INST BIOMEDICAL RES.

XX (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.

XX Dally M, Hudson TJ, Lander ES, Rouns J, Simionovitch K;

DR WPI; 2001-367874/38.

PT Testing for the presence of polymorphisms associated with inflammatory

PT bowel disease, using a hybridization assay.

XX Claim 1; Page 55; 463pp; English.

XX The present invention describes a method for detecting the presence of  
CC polymorphisms associated with inflammatory bowel diseases such as  
CC ulcerative colitis and Crohn's disease. The methods can be used to detect  
CC the presence of genetic polymorphisms associated with inflammatory bowel  
CC disease and correlating their occurrence with disease states. They may be  
CC used in this way for phenotypic correlations, forensics, paternity  
CC testing, medicine and genetic analysis. The present sequence is a  
CC polymorphic site described in the exemplification of the invention

XX Sequence 27 BP; 6 A; 4 C; 11 G; 5 T; 0 U; 1 Other;

Query Match 2.3%; Score 22.8; DB 1; Length 27;

Best Local Similarity 88.9%; Pred. No. 1e+03;  
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1003 AGCGATTCTCTCTCTCAGCTCCCA 1029

DB 27 AGCGATTCTCTCTCAGCTCCCA 1

RESULT 348

AAF92843 ID AAF92843 standard; DNA; 24 BP.

XX AAF92843;

XX 17-MAY-2001 (first entry)

DE Human ABC1 transcription factor binding site #6.

KW High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1, ds.

XX Homo sapiens.

XX WO200115676-A2.

XX 08-MAR-2001.

PD 01-SEP-2000; 2000WO-IB001492.

XX 01-SEP-1999; 99US-0151977P.

PR 15-MAR-2000; 2000US-00526193.

PR 23-JUN-2000; 2000US-0213958P.

XX (UYBR-) UNIV BRITISH COLUMBIA.

PA (XENON-) XENON GENETICS INC.

PI Hayden MR, Brooks-Wilson AR, Pimstone SN, Clee SM;

XX WPI; 2001-244356/25.

XX WPI; 2001-244356/25.

PT Treating a lower than normal high density lipoprotein-cholesterol (HDL-C)

PT level, a higher than normal triglyceride level, or a cardiovascular

PT disease, by administering a compound that modulates LXR- or RXR-mediated

PT transcriptional activity.

PS Disclosure; Fig 3; 317pp; English.

XX The present invention relates to a method for treating a patient

CC diagnosed as having a lower than normal high density lipoprotein-

CC cholesterol (HDL-C) level, a higher than normal triglyceride level, or a

CC cardiovascular disease, involving administering a compound that modulates

CC LXR- or RXR-mediated transcriptional activity or ABC1 expression or

CC activity. The LXR gene product may be used in an assay to identify

CC compounds useful for the treatment of a disease or condition selected a

CC lower than normal HDL cholesterol level, a higher than normal

CC triglyceride level, and a cardiovascular disease

CC Sequence 24 BP; 4 A; 8 C; 6 G; 6 T; 0 U; 0 Other;

XX Query Match 2.3%; Score 22.4; DB 1; Length 24;

XX Best Local Similarity 95.8%; Pred. No. 9.7e+02;

XX Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 208 AGCGTGTCTGGAAGTCCGACCT 231

DB 1 AGCGTGTCTGGAAGTCCGACCT 24

XX AGCGTGTCTGGAAGTCCGACCT 24

XX AAI69885; standard; DNA; 24 BP.

XX AAI69885;

XX AAI69885;

DT 14-DEC-2001 (first entry)

XX Human transglutaminase 12 PCR primer #1.

XX Human, transglutaminase 12; cytostatic; virucidal; immunomodulatory;

KW antiinflammatory; haemostatic; gene therapy; malignant tumour;

KW haemopathy; HIV infection; immunological disease; inflammation;

XX PCR primer; ss.

XX Homo sapiens.

XX WO200170787-A1.

XX 27-SEP-2001.

PF 26-FEB-2001; 2001WO-CN000243.

XX 10-MAR-2000; 2000CN-0011967.

XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.

XX Mao Y, Xie Y;

XX WPI; 2001-61474/70.

XX Human transglutaminase 12 and encoded polynucleotide, used in diagnosis

PT and treatment of malignant tumors, hemopathy, human immunodeficiency

PT virus infection, immunological diseases and inflammation.

PS Example 2; Page 17; 37pp; Chinese.

XX The present invention relates to human transglutaminase 12 (see

CC AAG7882). The transglutaminase and its coding sequence are useful in the

CC diagnosis and treatment of malignant tumors, haemopathy, HIV infection,

CC immunological diseases and various inflammations. The present sequence is

CC a PCR primer which was used in an example from the present invention

XX Sequence 24 BP; 5 A; 8 C; 4 G; 7 T; 0 U; 0 Other;

XX Query Match 2.3%; Score 22.4; DB 1; Length 24;

XX Best Local Similarity 95.8%; Pred. No. 9.7e+02;

XX Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 388 CAAAGTGTGAGTACAGCGTG 411

DB 24 CAAAGTGTGAGTACAGCGTG 1

XX CAAAGTGTGAGTACAGCGTG 411

XX AAS00333 standard; DNA; 24 BP.

XX AAS00333;

XX 17-MAY-2001 (first entry)

XX PCR primer #2, used to amplify human RAD51 gene at position -2339.

XX Human, RAD51; breast cancer; BRCA1; BRCA2; PCR primer; ss.

XX Homo sapiens.

XX WO200118254-A2.

XX 15-MAR-2001.

XX 08-SEP-2000; 2000WO-US024786.

XX 10-SEP-1999; 99US-0153288P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Wang WW, Struwing JP;



XX  
DR WPI; 2001-235217/24.

XX  
PT New nucleic acids comprising a mutant of the RAD51 gene, useful for  
diagnosing genetic predisposition or susceptibility to breast cancer.

XX  
PS Disclosure; Page 42; 42pp; English.

XX  
CC The sequence represents PCR primer #2, used to amplify human RAD51 gene  
at position -2339 upstream of the transcription start site of human RAD51  
gene. The RAD51 gene is useful in diagnosing genetic predisposition or  
susceptibility to breast cancer in an individual using the following  
steps: (1) detecting a mutation in the RAD51 gene in a human subject,  
comprising analysing a sample from the subject to detect the mutation;  
(2) assessing the risk of developing breast cancer, comprising: (a)  
analysing a sample from the subject for the presence of BRCA1 and/or  
BRCA2 mutations; and (b) if (a) is positive, analysing the sample for a  
mutation in the RAD51 gene, where the presence of the RAD51 mutation  
indicates an increased risk in developing breast cancer in the subject as  
compared to a subject having at least one of the BRCA mutations and a  
wild-type RAD51 gene. Primers derived from the sequence can be used in a  
kit for detecting a mutation in the RAD51 gene of a subject, which is  
associated with a predisposition to breast cancer, comprising at least 2  
nucleic acid primers derived from the RAD51 gene sequence

XX  
SQ Sequence 24 BP; 5 A; 10 C; 4 G; 5 T; 0 U; 0 Other;

XX  
Query Match 2.3%; Score 22.4; DB 1; Length 24;

XX  
Best Local Similarity 95.8%; Pred. No. 9.7e+02;  
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 538 CTGCTCAGCGCTCCCAAGTAGCTG 561

DB 1 CTGCTCAGCGCTCCCAAGTAGCTG 24

RESULT 351

ABZ21100/c

ID ABZ21100 standard; DNA; 24 BP.

XX  
AC ABZ21100;

XX  
DT 25-MAR-2003 (first entry)

XX  
DE Zinc finger protein 54.67 PCR primer #2.

XX  
KW Zinc finger protein 54.67; tumour; inflammation; immunological disease;  
haemopathy; HIV infection; cytostatic; anti-HIV; PCR; primer; ss.

XX  
OS Unidentified.

XX  
PN CN1352015-A.

XX  
PD 05-JUN-2002.

XX  
PF 06-NOV-2000; 2000CN-00127270.

XX  
PR 06-NOV-2000; 2000CN-00127270.

XX  
PA (BODE-) BODE GENE DEV CO LTD.

XX  
PI Mao Y, Xie Y;

XX  
DR WPI; 2002-699446/76.

XX  
PT New zinc finger protein 54.67 polypeptide for treating malignant tumors,  
inflammations, immunological diseases, hemopathy and human  
immunodeficiency virus infection.

XX  
PS Example 2; Page 16 (Disclosure); 34pp; Chinese.

XX  
CC The present invention relates to zinc finger protein 54.67 (ABZ98889).

CC  
CC The zinc finger protein can be used for treating various diseases, such

CC  
CC as malignant tumors, inflammations, immunological diseases, haemopathy  
and HIV infection. The present sequence is a PCR primer, which was used  
in an example from the invention

XX  
SQ Sequence 24 BP; 4 A; 7 C; 8 G; 5 T; 0 U; 0 Other;

XX  
Query Match 2.3%; Score 22.4; DB 1; Length 24;

XX  
Best Local Similarity 95.8%; Pred. No. 9.7e+02;  
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 721 GCCTCCTAGTAGCTGGAGACTACA 744

DB 24 GCCTCCTAGTAGCTGGAGACTACA 1

RESULT 352  
ABA96912/c

ID ABA96912 standard; DNA; 24 BP.

XX  
AC ABA96912;

XX  
DT 15-MAY-2002 (first entry)

XX  
DE Human arginase 9 RT-PCR primer, SEQ ID NO:3 version #1.

XX  
KW Human; arginase 9; recombinant production; arginaemia;

XX  
KW arginine metabolism disorder; urea metabolism disorder;

XX  
KW developmental disorder; malignant tumor; cancer; gene therapy;

XX  
KW immune disorder; inflammatory condition; cytostatic; antiinflammatory;

XX  
KW immunomodulator; reverse transcription-PCR; RT-PCR; primer; ss.

OS Homo sapiens.

XX  
PN WO200198502-A1.

XX  
PD 27-DEC-2001.

XX  
PF 14-MAY-2001; 2001WO-CN000788.

XX  
PR 19-MAY-2000; 2000CN-00115753.

XX  
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.

XX  
PI Mao Y, Xie Y;

XX  
DR WPI; 2002-090440/12.

XX  
PT Human arginase 9 and encoding polynucleotide, used in diagnosis and  
treatment of malignant tumors, hemopathy, human immunodeficiency virus  
infection, immunological diseases and inflammation.

XX  
PS Example 3; Page 29; 33pp; Chinese.

XX  
CC The invention relates to human arginase 9 (AAM49102), nucleic acids  
encoding it (ABA96911), and a method for the recombinant production of  
argininase 9. The protein has a molecular weight of 9 kD and has homology  
over a 60 amino acid stretch to the protein fragment shown in AAM49105.

XX  
CC The present invention additionally discloses an antagonist of arginase  
9 for therapeutic use, and an antibody which specifically binds to  
argininase 9. Arginase 9, and nucleotides which encode it may be used  
for treating a variety of diseases, such as arginemia, disorders of  
arginine or urea metabolism, developmental disorders, malignant tumors,  
immune disorders and inflammatory conditions. The protein may also be  
used to screen for modulators of its activity or for peptide  
fingerprinting identification. The polynucleotide can be used as a primer  
for nucleic acid amplification reactions or as a probe for hybridisation  
reactions, or in producing gene chips or microarrays. Sequences ABA96912-  
ABA96913 represent reverse transcription-PCR (RT-PCR) primers used in an  
exemplification of the invention to isolate human arginase 9 cDNA.

XX  
CC Note: The present sequence differs from the sequence also designated SEQ  
ID NO:3 (ABA96914) which is given on page 12 of the specification

XX  
SQ Sequence 24 BP; 3 A; 9 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 2.3%; Score 22.4; DB 1; Length 24;  
Best Local Similarity 95.8%; Pred. No. 9.7e+02;  
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 868 GGATTACAGCGGTGAGCCACG 891  
DB 24 GGATTACAGCGGTGAGCCACGCG 1

RESULT 353  
ABO83933/C  
ID ABO83933 standard; DNA; 24 BP.

XX ABO83933;  
XX  
XX 04-FEB-2003 (first entry)  
XX  
XX Human breast susceptible gene protein 10.45 PCR primer 2 SEQ ID NO:4.  
XX  
XX Human; breast susceptible gene coded protein 10.45; tumour;  
XX  
XX embryonic development deformity; PCR primer; ss.

XX Homo sapiens.  
XX  
XX CN1342702-A.  
XX  
XX 03-APR-2002.  
XX  
XX 12-SEP-2000; 2000CN-00125173.  
XX  
XX 12-SEP-2000; 2000CN-00125173.  
XX  
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.

XX Mao Y, Xie Y;  
XX  
XX WPI; 2002-529778/57.  
XX  
XX

PT A novel human breast susceptible gene coded protein 10.45 polypeptide,  
PT and the polynucleotide encoding it, useful for treating several diseases  
PT e.g. embryonic development deformity and tumors.

XX Example 2; Page 18 (Disclosure); 34pp; Chinese.

CC The present invention describes human breast susceptible gene coded  
CC protein 10.45 (I). Also described is a process for preparing (I) using  
CC DNA recombination techniques. (I) can be used for treating several  
CC diseases e.g. embryonic development deformity and tumours. The present  
CC sequence represents a PCR primer for (I), which is used in an example  
CC from the present invention

XX Sequence 24 BP; 9 A; 7 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 2.3%; Score 22.4; DB 1; Length 24;  
Best Local Similarity 95.8%; Pred. No. 9.7e+02;  
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 192 TTTCATGTTGTCAGGCTGCT 215  
DB 24 TTTCATGTTGTCAGGCTGCT 1

RESULT 354  
ABT08420  
ID ABT08420 standard; DNA; 24 BP.

XX ABT08420;  
XX  
XX 27-NOV-2002 (first entry)  
XX  
XX Human PSF promoter PCR primer SEQ ID NO: 55.  
XX

KW Human; cyclin-dependent kinase; CDK; cyclin-dependent kinase inhibitor;  
KW inhibitor; cancer; age-related disease; promoter; atherosclerosis;  
KW cytosolic; antiarteriosclerotic; neurotropic; neuroprotective;  
KW nephrotropic; antiarthritic; arthritis; renal disease;  
KW Alzheimer's disease; amyloidosis; PCR; primer; ss.

XX Homo sapiens.  
XX  
XX WO200266681-A2.  
XX  
XX 25-AUG-2002.  
XX  
XX

XX 01-FEB-2002; 2002WO-US002784.  
XX  
XX  
XX 01-FEB-2001; 2001US-0265840P.  
XX  
XX 21-MAY-2001; 2001US-00861925.  
XX  
XX (UNIT) UNIV ILLINOIS FOUND.

XX Poole J, Robinson IB, Chang B;  
XX  
XX WPI; 2002-674960/72.  
XX  
XX

PT New recombinant expression construct, useful for identifying compounds  
PT that inhibit the induction of genes induced by cyclin-dependent kinase  
PT inhibitors for preventing or treating cancer, renal failure or  
PT Alzheimer's disease.  
XX  
XX Example 8; Page 130; 137pp; English.

CC The present invention relates to a recombinant expression construct  
CC encoding a reporter gene operably linked to a promoter from a mammalian  
CC gene induced by a cyclin-dependent kinase (CDK) inhibitor. The construct  
CC is useful for identifying compounds that inhibit the induction of genes  
CC induced by CDK inhibitors. The compounds are useful for preventing or  
CC treating a disease caused by CDK inhibitor induced gene expression, e.g.  
CC cancer other than colon cancer, renal failure, Alzheimer's disease,  
CC amyloidosis, age-related diseases, atherosclerosis or arthritis. The  
CC present sequence is a PCR primer used to amplify a human promoter  
CC suitable for use in the construct of the invention

XX Sequence 24 BP; 7 A; 2 C; 10 G; 5 T; 0 U; 0 Other;

Query Match 2.3%; Score 22.4; DB 1; Length 24;  
Best Local Similarity 95.8%; Pred. No. 9.7e+02;  
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 859 AAAGTCTGGATTACAGCGTGA 882  
DB 1 AAAGTCTGGATTACAGCGTGA 24

RESULT 355  
ACF05122/C  
ID ACF05122 standard; DNA; 24 BP.

XX ACF05122;  
XX  
XX 06-NOV-2003 (first entry)  
XX  
XX Human genomic DNA primer Alu.  
XX  
XX Human; aliphoid; immunodeficiency virus; HIV; anti-HIV; latency; PCR;  
XX primer; ss.

XX Homo sapiens.  
XX  
XX WO2003054160-A2.  
XX  
XX 03-JUL-2003.  
XX  
XX 18-DEC-2002; 2002WO-US040698.  
XX

XX 19-DEC-2001; 2001US-0341727P.  
XX (REGC ) UNIV CALIFORNIA.  
XX Verdin E, Jordan A;  
XX WPI; 2003-577369/54.  
XX Novel isolated cells that comprise transcription competent  
XX immunodeficiency virus e.g. HIV-1, or immunodeficiency virus-based  
XX retroviral vector integrated into its genome, useful for identifying  
XX latent HIV activators.  
XX  
XX Example 1; Page 33; 71pp; English.  
XX The present sequence is that of primer Alu (EVI255) for human genomic  
XX DNA. This primer was used with primer A (see ACC05121) in alipoid PCR  
XX amplifications that demonstrated preferential HIV integration in or near  
XX alipoid DNA in latently infected Jurkat cells. The invention provides  
XX isolated cells that harbour a latent immunodeficiency virus that is  
XX transcription competent, that can be reactivated, and that is an in vitro  
XX model for latent HIV infection in vivo. The cells are useful for  
XX investigating the nature of latency, and also in drug screening assays to  
XX identify agents that activate latent HIV. Such agents are useful for  
XX reducing the reservoir of latent HIV. Methods are provided of treating an  
XX immunodeficiency virus infection  
XX  
XX Sequence 24 BP; 4 A; 7 C; 9 G; 4 T; 0 U; 0 Other;  
XX  
XX Query Match 2.3%; Score 22.4; DB 1; Length 24;  
XX Best Local Similarity 95.8%; Pred. No. 9.7e+02;  
XX Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX 541 CCTGACCTCCCAAGTAGCTGGGA 564  
XX 24 CCTGACCTCCCAAGTAGCTGGGA 1  
XX  
XX RESULT 356  
XX ACP35685/C  
XX ID ACP35685 standard; DNA; 24 BP.  
XX AC ACP35685;  
XX DT 13-OCT-2003 (first entry)  
XX DE Human TGNP promoter amplifying forward primer.  
XX XX Trans-Golgi network integral membrane protein; TGNP; chromosome 2p11.2;  
XX KM cytosolic; antiinflammatory; immunomodulator; neuroprotective; human;  
XX KM neurotropic; gene therapy; PCR; primer; ss.  
XX OS Homo sapiens.  
XX PN WO2003050302-A2.  
XX PD 19-JUN-2003.  
XX PF 13-DEC-2002; 2002WO-GB005670.  
XX PR 13-DEC-2001; 2001GB-00029846.  
XX PA (EIRX-) EIRX THERAPEUTICS LTD.  
XX PI Hayes I, Cotter T, Murphy F, Seery L,  
XX WPI; 2003-532920/50.  
XX Detecting apoptosis in a cell, useful for treating cancer, an  
XX inflammatory disease, an autoimmune disease or a neurodegenerative  
XX disease, comprises detecting a decrease in TGNP activity or expression.  
XX Example 11; Page 80; 110pp; English.

XX The invention relates to detecting apoptosis in a cell. The method  
XX involves detecting a decrease in trans-Golgi network integral membrane  
XX protein (TGNP) activity or expression by detecting the decrease in TGNP  
XX polypeptide or its homologue, a nucleic acid encoding the polypeptide, a  
XX nucleic acid that hybridizes under stringent conditions to the  
XX aforementioned nucleic acid, or their complements. The method,  
XX polypeptides, nucleic acids and modulators are useful for treating  
XX cancer, an inflammatory disease, an autoimmune disease or a PCR primer  
XX for amplifying the human TGNP promoter  
XX  
XX Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;  
XX  
XX Query Match 2.3%; Score 22.4; DB 1; Length 24;  
XX Best Local Similarity 95.8%; Pred. No. 9.7e+02;  
XX Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX 635 CCTGTGACCCAGGCTGAGTGA 658  
XX 24 CCTGTGACCCAGGCTGAGTGA 1  
XX  
XX RESULT 357  
XX ADG28972  
XX ID ADG28972 standard; DNA; 24 BP.  
XX AC ADG28972;  
XX DT 26-FEB-2004 (first entry)  
XX DE PCR primer SEQ ID 55 used to amplify human PSF promoter DNA.  
XX XX recombinant expression construct; cyclin-dependent kinase inhibitor; CDK;  
XX KM viruslike; cytosolic; neuroprotective; neurotropic; antiarteriosclerotic;  
XX KM antiarthritic; nephrotropic; viral infection; cancer; renal;  
XX KM age-related disease; Alzheimer's; atherosclerosis; arthritis;  
XX KM gene therapy; human; ss; PCR; primer; PSF promoter.  
XX OS Homo sapiens.  
XX PN WO2003073062-A2.  
XX PD 04-SEP-2003.  
XX PF 29-AUG-2002; 2002WO-US027584.  
XX PR 29-AUG-2001; 2001US-0315791P.  
XX XX (UNIT ) UNIV ILLINOIS FOUND.  
XX PA Robinson IB, Poole J;  
XX PI Robinson IB, Poole J;  
XX WPI; 2003-731624/69.  
XX New recombinant expression construct for identifying and modulating  
XX expression of genes regulated by cyclin-dependent kinase inhibitors, such  
XX as genes involved in viral infection, cancer, renal diseases or age-  
XX related diseases.  
XX Example 8; SEQ ID NO 55; 143pp; English.  
XX The invention relates to a novel recombinant expression construct  
XX encoding a reporter gene operably linked to a promoter from a mammalian  
XX viral or cellular gene induced by a cyclin-dependent kinase (CDK)  
XX inhibitor. The construct of the invention demonstrates viruslike,  
XX cytosolic, neuroprotective, neurotropic, antiarteriosclerotic,  
XX antiarthritic and nephrotropic activities and may be useful in  
XX identifying compounds that inhibit the induction of genes involved in  
XX viral infection, cancer, renal diseases or age-related diseases including  
XX Alzheimer's disease, atherosclerosis or arthritis, such genes being  
XX induced by cyclin-dependent kinase inhibitors. Furthermore, the construct  
XX may have gene therapy applications. The current sequence is that of the

CC PCR primer which was used in the exemplification of the invention.  
XX Sequence 24 BP; 7 A; 2 C; 10 G; 5 T; 0 U; 0 Other;  
SQ

Query Match 2.3%; Score 22.4; DB 1; Length 24;  
Best Local Similarity 95.8%; Pred. No. 9.7e+02;  
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 859 AAAGTCTGGATTACAGCGCTGA 882  
DB 1 AAAGTCTGGATTACAGCGCTGA 24

RESULT 358  
ADQ30417/C  
ID ADQ30417 standard; DNA; 24 BP.  
XX  
XX ADQ30417;  
AC  
XX  
XX 09-SEP-2004 (first entry)  
DT  
XX  
XX Human VRI exon 1d transcription factor binding fragment #136.  
DE  
XX  
XX de; VRI receptor; vanilloid receptor type 1; modulator;  
KW pain transmission; primary sensory neuron; transcription factor;  
KW detection; MZFI; NKkappaB; NFAT; GATM; sensitivity disorder; analgesia;  
KW hyperalgesia; hyperalgesia; neuralgia; myalgia; human.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO2004053120-A2.  
PN  
XX  
XX 24-JUN-2004.  
PD  
XX  
XX 01-DEC-2003; 2003WO-EP013522.  
PF  
XX  
XX 09-DEC-2002; 2002DE-01057421.  
PR  
XX  
XX (CHEP) GRENENTHAL GMBH.  
PA  
XX  
XX weine E, Biebler A, Schaefer MKH;  
PI  
XX  
XX WPI; 2004-468868/44.  
DR  
XX  
XX New nucleic acid that modulates expression of the vanilloid receptor-1,  
PT useful for control of pain or sensitivity disorders, comprises sequences  
PT from control regions of the receptor gene.  
PS  
XX  
XX Disclosure; Page 54; 68pp; German.  
XX  
XX This invention describes a novel nucleic acid containing a specific  
CC segment having at least one region that modulates expression of the VRI  
CC (vanilloid receptor type 1) receptor, or a functional derivative, allele  
CC or fragment of this region, or a sequence that hybridizes to it under  
CC standard conditions. The VRI modulator is derived from one or more of  
CC positions 221931-22344 of Genbank AF670399, 31673-36359 of AF63116, or  
CC 44731-43231 or 36616-33151 of AF16787 and is involved in transmission of  
CC pain, particularly in primary sensory neurons. The invention also  
CC describes a vector that contains the VRI modulator, host cells containing  
CC this vector (other than human germ or embryonal stem cells) and a method  
CC for modulating expression of the VRI receptor by introducing the  
CC modulator or the vector into a cell that contains the VRI gene. The  
CC products of the invention are used for detecting a transcription factor  
CC from its binding to a regulatory sequence (or a double-stranded  
CC oligonucleotide fragment of it), e.g. by Western blotting or enzyme-  
CC linked immunosorbent assay, particularly for diagnosis of diseases  
CC associated with overexpression or underexpression of the transcription  
CC factor. The region that modulates VRI receptor expression includes a  
CC binding site for a transcription factor, e.g. MZFI, NKkappaB, NFAT or  
CC GATM. The nucleic acids of the invention, or vectors containing them,  
CC are used for prevention or treatment of pain, also for treating  
CC sensitivity disorders, e.g. analgesia, hyperalgesia or hyperalgesia, also  
CC neuralgia and myalgia, that are associated with activity of the VRI

CC receptor. This sequence represents a fragment of human VRI exon 1d DNA  
CC which is capable of binding to a transcription factor.  
XX  
XX Sequence 24 BP; 5 A; 8 C; 6 G; 5 T; 0 U; 0 Other;  
SQ

Query Match 2.3%; Score 22.4; DB 1; Length 24;  
Best Local Similarity 95.8%; Pred. No. 9.7e+02;  
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 387 CCAAGTCTGGATTACAGCGCT 410  
DB 24 CCAAGTCTGGATTACAGCGCT 1

RESULT 359  
ABX15537  
ID ABX15537 standard; DNA; 25 BP.  
XX  
XX ABX15537;  
AC  
XX  
XX 11-APR-2003 (first entry)  
DT  
XX  
XX Human IL-1 genotyping marker g251g26 primer #1.  
DE  
XX  
XX Human; ss; PCR; primer; interleukin-1; IL-1; marker g251g26; nephropathy;  
KW inflammatory disease; Systemic Inflammatory Response; SIRS; genotyping;  
KW Alzheimer's disease; arthritis; acute joint inflammation; ophthalmopathy;  
KW juvenile chronic arthritis; asthma; bronchial asthma; pulmonary disease;  
KW chronic obstructive airways disease; cardiovascular disease; thyroiditis;  
KW atherosclerosis; autoimmune carditis; cardiomyopathy; ulcerative colitis;  
KW cardiac cell dysfunction; aortic smooth muscle cell activation; trauma;  
KW inflammatory bowel disease; gastrointestinal inflammation; cerebral trauma;  
KW Kawasaki's syndrome; cervical lymphadenopathy; diabetic nephropathy;  
KW glomerulonephritis; diabetic retinopathy; Grave's ophthalmopathy;  
KW osteoporosis; bone loss; otitis media; pancreatitis; periodontal disease;  
KW chronic lung disease; chronic sinusitis; chronic lymphocytic thyroiditis;  
KW urinary tract infection; chronic prostatitis; immunological disorder;  
KW chronic pelvic pain syndrome; alopecia areata; Grave's disease;  
KW thyroid disease; goiter; struma lymphomatosa; sleep disorder; neoplasia;  
KW chronic fatigue syndrome; obesity; infectious disease; Leishmaniasis;  
KW Leprosy; myocardial dysfunction; breast cancer; organ transplant;  
KW Hodgkin's disease; hormonal regulation; fertility; septicemia.  
XX  
XX Homo sapiens.  
OS  
XX  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
XX modified\_base 1..25  
FT FT /\*tag= a  
FT FT /mod\_base= OTHER  
FT FT /note= "OTHER= FAM labelled"  
FT misc\_difference 5  
FT FT /\*tag= b  
FT FT /note= "Given in the specification as the number 7."  
XX  
XX US2002146700-A1.  
PN  
XX  
XX 10-OCT-2002.  
PD  
XX  
XX 27-APR-2001; 2001US-00845129.  
PF  
XX  
XX 29-MAY-1997; 97GB-00011040.  
PR 30-JUN-1999; 99US-00345217.  
XX  
XX (INTE-) INTERLEUKIN GENETICS INC.  
PA  
XX  
XX Duff GW, Cox A, Camp NJ, Di Giovine FS;  
PI  
XX  
XX WPI; 1999-080814/07.  
DR  
XX  
XX New method of determining a patient's susceptibility to inflammatory  
PT disorders - by detecting the presence of an IL-1 (44112332) haplotype,  
PT

PT useful in designing treatment strategies that modulate the activity of  
PT proteins produced by the IL-1 gene cluster.

XX Claim 5, Page 19; 42pp; English.

CC The invention relates to a method for determining whether a subject has  
CC or is predisposed to developing a disease or condition that is associated  
CC with an IL-1 inflammatory haplotype. The method involves detecting at  
CC least one allele of the haplotype, where the presence of the allele  
CC indicates that the subject is predisposed to the development of or has the  
CC disease or condition. The invention allows the determination of an  
CC individual's likelihood for developing a particular disease or condition  
CC associated with interleukin 1 (IL-1) polymorphisms without necessarily  
CC determining or characterizing the causative genetic variation. Diseases  
CC such as inflammatory disease e.g. Systemic Inflammatory Response (SIRS),  
CC Alzheimer's disease; arthritis e.g. acute joint inflammation, juvenile  
CC chronic arthritis; asthma e.g. bronchial asthma, chronic obstructive  
CC airways disease; cardiovascular diseases e.g. atherosclerosis, autoimmune  
CC arthritis; cardiomyopathy and cardiac cell apoptosis; gastrointestinal  
CC muscle cell activation, cardiac cell apoptosis; gastroenteritis  
CC inflammation e.g. inflammatory bowel disease, ulcerative colitis; HIV  
CC infection; Kawasaki's syndrome e.g. cervical lymphadenopathy, coronary  
CC artery lesions; nephropathies e.g. diabetic nephropathy,  
CC glomerulonephritis; opthalmopathies e.g. diabetic retinopathy, Grave's  
CC opthalmopathy; osteoporosis e.g. bone loss, osteitis media; pancreatitis;  
CC periodontal disease; pulmonary diseases e.g. chronic lung disease,  
CC chronic sinusitis; thyroiditis e.g. chronic lymphocytic thyroiditis;  
CC urinary tract infections e.g. chronic prostatitis, chronic pelvic pain  
CC syndrome; immunological disorders e.g. alopecia areata, Graves disease;  
CC thyroid diseases e.g. goiter, struma lymphomatosa; sleep disorders;  
CC chronic fatigue syndrome; obesity; infectious diseases e.g. leprosy,  
CC leishmaniasis; trauma e.g. cerebral trauma, myocardial dysfunction;  
CC neoplasias e.g. breast cancer, Hodgkin's disease; hormonal regulation e.g.  
CC fertility, septicemia; organ transplants. This allows for a more  
CC customized approach to preventing the onset or progression of the disease  
CC or condition, e.g. a clinician can more effectively prescribe a therapy  
CC that will address the molecular basis of the disease or condition. The  
CC present sequence represents the sequence of the human IL-1 genotyping  
CC marker g251g26 primer #1

XX Sequence 25 BP; 5 A; 7 C; 10 G; 2 T; 0 U; 1 Other;

Query Match 2.3%; Score 22.4; DB 1; Length 25;  
Best Local Similarity 92.0%; Pred. NO. 1e+03;

Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 867 GGGATTACAGCGCTGAGCCACG 891

DB 1 GGGANTACAGCGCTGAGCCACGCG 25

RESULT 360

AAH38447/C

ID AAH38447 standard; DNA; 25 BP.

XX AAH38447;

AC 14-ANG-2001 (first entry)

DT 14-ANG-2001 (first entry)

DE SNP specific SNPE primer SEQ ID 1243.

XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;

XX SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;

XX Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;

XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;

XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;

XX inflammation; forensic investigation; paternity analysis; primer; ss.

XX Homo sapiens.

XX MO200129262-A2.

XX 26-APR-2001.

PD

XX 13-OCT-2000; 2000MO-US028436.

XX 15-OCT-1999; 99US-0160096P.

XX (ORCH-) ORCHID BIOSCIENCES INC.

XX Picoult-Newburg L, Pohl M;

XX WPI; 2001-290930/30.

PT New genotyping oligonucleotide, useful for detecting the presence,  
PT absence or identity of single polynucleotide polymorphism in a nucleic  
PT acid sample.

PS Claim 1; Page 56; 83pp; English.

CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
CC primer extension (SNPE) primers, and the sequences of regions flanking  
CC sites of single nucleotide polymorphisms SNPs. The present invention  
CC includes kits for determining the presence or absence of a SNP, using the  
CC oligonucleotides of the invention. The PCR primers are used to amplify a  
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.  
CC The oligonucleotides are useful for genotyping a nucleic acid sample by  
CC performing a single-nucleotide primer extension reaction. The  
CC oligonucleotides are useful for determining the presence, absence or  
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
CC assess by association analysis the genotype of an individual or group of  
CC individuals, having a pathological phenotypic trait suspected of being  
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular  
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,  
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
CC traits also include symptoms of or susceptibility to multifactorial  
CC disease of which a component is or may be genetic such as autoimmune  
CC diseases, including, rheumatoid arthritis, multiple sclerosis,  
CC inflammation, cancer, nervous system diseases and infection by pathogenic  
CC microorganism. The method is also useful in forensic investigations and  
CC paternity analysis. The present sequence represents a single nucleotide  
CC primer extension (SNPE) primer specific for a human SNP containing DNA  
CC sequence

XX Sequence 25 BP; 6 A; 2 C; 13 G; 4 T; 0 U; 0 Other;

Query Match 2.3%; Score 22.4; DB 1; Length 25;  
Best Local Similarity 95.8%; Pred. NO. 1e+03;

Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 531 CATCTCTCTGCTCCCTCCCA 554

DB 24 CATCTCTCTGCTCCCTCCCA 1

RESULT 361

ADB04744

ID ADB04744 standard; DNA; 25 BP.

XX ADB04744;

AC 20-NOV-2003 (first entry)

DT 20-NOV-2003 (first entry)

DE Human MD27 scanning oligonucleotide SEQ ID 5730.

XX Cytostatic; immunostimulant; gene therapy; vaccine; human;

XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;

XX developmental disorder; ss.

XX Homo sapiens.

XX EPI281758-A2.

XX 05-FEB-2003.

XX 05-FEB-2003.

PD

```
XX 30-JUL-2002; 2002EP-00016874.
XX
XX 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M, Gu Y, Nguyen C;
XX
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 5730; 103pp; English.
XX
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
XX
XX Sequence 25 BP; 5 A; 1 C; 9 G; 10 T; 0 U; 0 Other;
XX
XX Query Match 2.3%; Score 22.4; DB 1; Length 25;
XX Best Local Similarity 95.8%; Pred. No. 1e+03;
XX Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 771 TTTGTAATTTTGTAGTAGAGCGGG 794
XX |||||
XX 1 TTTGTAATTTTGTAGTAGAGCGGG 24
XX
XX DB
XX
XX RESULT 362
XX ADB04742
XX ID ADB04742 standard; DNA; 25 BP.
XX
XX ADB04742;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human MD27 scanning oligonucleotide SEQ ID 5728.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX
XX Homo sapiens.
XX
XX EP1281758-A2.
XX
XX 05-FEB-2003.
XX
XX 30-JUL-2002; 2002EP-00016874.
XX
XX 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M, Gu Y, Nguyen C;
XX
XX PI
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XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 5728; 103pp; English.
XX
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
XX
XX Sequence 25 BP; 6 A; 1 C; 7 G; 11 T; 0 U; 0 Other;
XX
XX Query Match 2.3%; Score 22.4; DB 1; Length 25;
XX Best Local Similarity 95.8%; Pred. No. 1e+03;
XX Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 770 TTTTGTATTTTGTAGTAGAGCGG 793
XX |||||
XX 2 TTTTGTATTTTGTAGTAGAGCGG 25
XX
XX DB
XX
XX RESULT 363
XX ADO12082/c
XX ID ADO12082 standard; DNA; 27 BP.
XX
XX ADO12082;
XX
XX 15-JUL-2004 (first entry)
XX
XX Single multiplex PCR primer #1454.
XX
XX ss; primer; simultaneous amplification;
XX single multiplex polymerase chain reaction; multifactorial disease;
XX genetic alteration; pharmacogenetic reaction; genotyping; polymorphism;
XX gene expression profiling.
XX
XX Synthetic.
XX
XX WO2004033649-A2.
XX
XX 22-APR-2004.
XX
XX 07-OCT-2003; 2003WO-US031874.
XX
XX 07-OCT-2002; 2002US-0417009P.
XX
XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX
XX Li H, Li J;
XX
XX WPI; 2004-340914/31.
XX
XX Designing primers for simultaneous amplification of target DNA fragments
XX in a single multiplex polymerase chain reaction, for high throughput
XX multiplex DNA sequence amplification, comprises aligning two primers.
XX
XX Disclosure; Page 39; 120pp; English.
XX
XX PS
```

XX The invention relates to a method of designing primers for simultaneous  
CC amplification of target DNA fragments in a single multiplex polymerase  
CC chain reaction by aligning a first primer and a second primer. The method  
CC comprises: (a) aligning a first primer and a second primer; and (b)  
CC selecting the first primer where the first primer at its 3' end does not  
CC contain four or more bases that are perfectly matching to the 3' end  
CC sequence of the first primer or a second primer, the first primer at its  
CC 3' end does not contain seven or more bases that are perfectly matching  
CC except one mismatch to the 3' end sequence of the first primer or the  
CC second primer, the first primer at its 3' end does not contain six or  
CC more bases that are perfectly matching to a sequence anywhere of the  
CC first primer or the second primer, and the first primer at its 3' end  
CC does not contain eleven or more bases that are perfectly matching except  
CC one mismatch to a sequence anywhere of the first primer or the second  
CC primer. The method is useful for designing primers for simultaneous  
CC amplification of target DNA fragments in a single multiplex polymerase  
CC chain reaction. It is also useful in the identification of multiple genes  
CC related to multifactorial diseases, the genome-scale detection of genetic  
CC alterations, the studies in pharmacogenetic reactions, the genotyping  
CC genetic polymorphisms in a large population, the gene expression  
CC profiling in various samples and high throughput genotyping technologies.  
CC This sequence corresponds to an example of a primer of the invention.  
XX  
SQ Sequence 27 BP; 5 A; 6 C; 11 G; 5 T; 0 U; 0 Other;  
Query Match 2.2%; Score 22.2; DB 1; Length 27;  
Best Local Similarity 88.9%; Pred. No. 1.1e+03;  
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 661 GGGCGAATCTTGGCTCAGTCAACCTC 687  
Db 27 GGGCGACTCTCGGCTCAGTCAACCTC 1  
ID ADO12035 standard; DNA; 27 BP.  
XX  
AC ADO12035;  
XX  
DT 15-JUL-2004 (first entry)  
XX  
DE Single multiplex PCR primer #1407.  
XX  
KW ss; primer; simultaneous amplification;  
KW single multiplex polymerase chain reaction; multifactorial diseases;  
KW genetic alteration; pharmacogenetic reaction; genotyping; polymorphism;  
KW gene expression profiling.  
XX  
OS Synthetic.  
XX  
PN WO2004033649-A2.  
XX  
PD 22-APR-2004.  
XX  
PF 07-OCT-2003; 2003WO-US031874.  
XX  
PR 07-OCT-2002; 2002US-0417009P.  
XX  
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.  
XX  
PI L4 H, L4 J;  
XX  
PI WPI; 2004-340914/31.  
XX  
PT Designing primers for simultaneous amplification of target DNA fragments  
PT in a single multiplex polymerase chain reaction, for high throughput  
PT multiplex DNA sequence amplification, comprises aligning two primers.  
XX  
PS Disclosure; Page 39; 120pp; English.  
XX  
CC The invention relates to a method of designing primers for simultaneous

CC amplification of target DNA fragments in a single multiplex polymerase  
CC chain reaction by aligning a first primer and a second primer. The method  
CC comprises: (a) aligning a first primer and a second primer; and (b)  
CC selecting the first primer where the first primer at its 3' end does not  
CC contain four or more bases that are perfectly matching to the 3' end  
CC sequence of the first primer or a second primer, the first primer at its  
CC 3' end does not contain seven or more bases that are perfectly matching  
CC except one mismatch to the 3' end sequence of the first primer or the  
CC second primer, the first primer at its 3' end does not contain six or  
CC more bases that are perfectly matching to a sequence anywhere of the  
CC first primer or the second primer, and the first primer at its 3' end  
CC does not contain eleven or more bases that are perfectly matching except  
CC one mismatch to a sequence anywhere of the first primer or the second  
CC primer. The method is useful for designing primers for simultaneous  
CC amplification of target DNA fragments in a single multiplex polymerase  
CC chain reaction. It is also useful in the identification of multiple genes  
CC related to multifactorial diseases, the genome-scale detection of genetic  
CC alterations, the studies in pharmacogenetic reactions, the genotyping  
CC genetic polymorphisms in a large population, the gene expression  
CC profiling in various samples and high throughput genotyping technologies.  
CC This sequence corresponds to an example of a primer of the invention.  
XX  
SQ Sequence 27 BP; 5 A; 11 C; 6 G; 5 T; 0 U; 0 Other;  
Query Match 2.2%; Score 22.2; DB 1; Length 27;  
Best Local Similarity 88.9%; Pred. No. 1.1e+03;  
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 661 GGGCGAATCTTGGCTCAGTCAACCTC 687  
Db 1 GGGCGACTCTCGGCTCAGTCAACCTC 27  
ID AAV29285 standard; cDNA; 22 BP.  
XX  
AC AAV29285;  
XX  
DT 21-AUG-1998 (first entry)  
XX  
DE Nucleotide sequence of PCR primer P2.  
XX  
KW Human; tumorigenesis gene; T-gene; PLAG2; PLAG1; CTNMB1; antibody;  
KW benign tumour; malignant tumour; leukaemia; lymphoma; cancer; inhibition;  
KW PCR; amplification; primer; ss.  
XX  
OS Synthetic.  
XX  
OS Homo sapiens.  
XX  
PN EP825198-A1.  
XX  
PD 25-FEB-1998.  
XX  
PF 17-JAN-1997; 97EP-00200130.  
XX  
PR 22-AUG-1996; 96EP-00202339.  
XX  
PA (KULR-) KU LEUVEN RES & DEV.  
XX  
PA (UYGO-) UNIV GOETTERBORGS HOLDINGBOUAGET AB.  
XX  
PI Van De Ven WJM, Stenman KGD, Kas KP, Voz ML;  
XX  
PI WPI; 1998-132252/13.  
XX  
PT New tumorigenesis T-genes and proteins - useful for, e.g. preparing  
PT antibodies for clinically diagnosing cells having non-physiological  
PT proliferative capacity such as lipoblastomas.  
XX  
PS Example 1; Page 6; 71pp; English.  
XX  
CC This is the nucleotide sequence of the PCR primer P2 used for  
CC amplification in the method of the invention, which involves isolation of

CC the tumorigenesis genes (T-gene), in the form of PLAG1, PLAG2, and  
 CC CTNNB1 genes. Their proteins can be used as a starting point for  
 CC preparing antibodies for clinically/medically diagnosing cells having a  
 CC non-physiological proliferative capacity as compared to wild type cells,  
 CC where the former cells are selected from both benign and malignant  
 CC tumours, as well as leukaemia and lymphomas. Derivatives of the T-gene  
 CC are also used in the diagnosis and preparation of therapeutical  
 CC compositions for the treatment of cancers, such as nucleic acid  
 CC derivatives, and antibodies. The T-gene may be used as a starting point  
 CC for designing suitable expression-modulating compounds or techniques for  
 CC the treatment of non-physiological proliferation phenomena in humans or  
 CC animals. Expression inhibitors of the T-gene can be used in the treatment  
 CC of diseases involving benign or malignant tumours

CC Sequence 22 BP; 6 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

SO

Query Match 2.2%; Score 22; DB 1; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 9.6e+02;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 385 TCCCAAGTGTGGATTACAG 406  
 1 TCCCAAGTGTGGATTACAG 22

Db

RESULT 366  
 AA207500  
 ID AA207500 standard; DNA; 22 BP.  
 AC AA207500;  
 XX  
 DT 26-NOV-1999 (first entry)  
 DE AHRCASEPO transgene specific primer 220.  
 XX  
 DE Erythropoietin; EPO; mammalian milk; transgenic animal; lactation;  
 KW ectopic expression; growth factor; cytokine; enzyme; transgene; human;  
 KW PCR primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN USS959171-A.  
 XX  
 PD 28-SEP-1999.  
 XX  
 PF 17-AUG-1994; 94US-00291074.  
 XX  
 PR 17-AUG-1994; 94US-00291074.  
 XX  
 PA (PHAR-) PHARMING BV.  
 XX  
 PI Jaenne J, Hyttinen J, Korhonen V;  
 XX  
 DR WPI; 1999-561081/47.  
 XX  
 PT Producing biologically active polypeptides in mammalian milk.  
 XX  
 PS Example 1; Col 7; 10pp; English.

CC The invention relates to a new process for producing biologically active  
 CC polypeptides (e.g. erythropoietin (EPO)) in mammalian milk as fusion  
 CC proteins that are less active (or non-active) than the free polypeptides.  
 CC The process may be used for the recombinant expression of proteins  
 CC (especially EPO) in the milk of transgenic animals such as sheep and  
 CC cows. The protein is expressed and secreted into the milk as a fusion  
 CC protein that has reduced biological activity. The animal is then milked  
 CC and the fusion protein is then cleaved (chemically or enzymatically) to  
 CC release the desired active protein which may then be isolated and  
 CC utilized. The use of to recombinantly produce polypeptides in milk  
 CC minimizes health problems in the animal and prevents side effects  
 CC associated with ectopic expression or leakage of the protein into  
 CC surrounding tissues and the circulation. These side effects are a  
 CC particular risk when producing potent polypeptides such as growth

CC factors, cytokines and enzymes. This means the transgenic animal remains  
 CC healthy, viable and able to lactate for longer. Sequences AA207499-500  
 CC represent AHRCASEPO transgene specific primers used for screening GO  
 CC mice. AHRCASEPO is a gene construct designed to secrete biologically  
 CC active free human EPO in transgenic mouse milk

CC Sequence 22 BP; 4 A; 4 C; 8 G; 6 T; 0 U; 0 Other;

SO

Query Match 2.2%; Score 22; DB 1; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 9.6e+02;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 480 GTGCAGTGTGTGATCACAGCT 501  
 1 GTGCAGTGTGTGATCACAGCT 22

Db

RESULT 367  
 AAC87596  
 ID AAC87596 standard; DNA; 22 BP.  
 AC AAC87596;  
 XX  
 DT 16-MAR-2001 (first entry)  
 DE Human Alu sequence PCR primer, CL1.  
 XX  
 DE Human; keratinocyte growth factor; KGF; chromosome 9p11; abnormality;  
 KW cancer; miscarriage; spontaneous abortion; genetic susceptibility;  
 KW diagnosis; Alu sequence; PCR primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN JP2000287684-A.  
 XX  
 PD 17-OCT-2000.  
 XX  
 PF 31-JAN-2000; 2000JP-00022688.  
 XX  
 PR 05-FEB-1999; 99JP-00028705.  
 XX  
 PA (ASAK) ASAKI BREWERIES LTD.  
 XX  
 DR WPI; 2001-065570/08.  
 XX  
 PT The base sequence of 9p11 chromosomal region participating to cancer and  
 XX abortion.  
 XX  
 PS Example 3; Page 5; 88pp; Japanese.

CC The invention relates to human chromosomal region 9p11 (AAC87588).  
 CC Abnormalities in this region of the short arm of chromosome 9 is thought  
 CC to be associated with miscarriage and cancer, as an ovarian cancer  
 CC patient with a history of miscarriage was found to have a chromosomal  
 CC inversion inv(9) (p11;q13). The 9p11 region contains the gene encoding  
 CC keratinocyte growth factor (KGF), and the invention also specifically  
 CC claims the KGF PCR primers AAC87589 and AAC87590 for use in detecting all  
 CC or part of the KGF gene. The nucleic acid sequences can be used to detect  
 CC abnormalities in chromosomal region 9p11 and thus give an indication of  
 CC an individual's risk of developing a 9p11-associated condition. Sequences  
 CC AAC87596-C87597 represent human Alu sequence PCR primers used in an  
 CC exemplification to the invention

CC Sequence 22 BP; 6 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

SO

Query Match 2.2%; Score 22; DB 1; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 9.6e+02;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 385 TCCCAAGTGTGGATTACAG 406  
 1 TCCCAAGTGTGGATTACAG 22

Db



```
RESULT 368
AAF88160
ID AAF88160 standard; DNA; 22 BP.
XX
XX AAF88160;
AC
XX 17-JUL-2001 (first entry)
DT
XX
XX Human thyroid malfunction-associated protein RITA PCR primer #1.
DE
XX KRAB domain; hyperplasia; thyroid; tumor; zinc finger motif; primer;
KW cystostatic; antithyroid; gene therapy; chromosome 19; 19q13; ss.
XX
XX Homo sapiens.
OS
XX W0200127265-A1.
PN
XX 19-APR-2001.
PD
XX 11-OCT-2000; 2000WO-DE003600.
PF
XX 12-OCT-1999; 99DB-01049179.
PR
XX (UYBR-) UNITV BREMEN.
PA
XX Bullerdielk J, Rippe V, Melboom M, Belge G;
PI WPI; 2001-290723/30.
DR
XX
XX New nucleic acid useful for the diagnosis and treatment of thyroid
PT disorders, e.g. tumors.
XX
XX Example 8; Page 29; 59pp; German.
PS
XX This invention describes a novel nucleic acid (N1) encoding a polypeptide
CC which comprises a KRAB-domain and/or at least one zinc finger motif. The
CC products of the invention have cytosstatic and antithyroid activity and
CC can be used in gene therapy. Nucleic acids, polypeptides, and antibodies
CC of the invention may be used in the diagnosis and/or the therapy of the
CC malfunction of the thyroid and/or hyperplasias of the thyroid and/or
CC thyroid tumors. They may also be used in the production of medicaments.
CC (N1) can also be used to diagnose thyroid tumors which are located on
CC chromosome 19 at band 19q13. This sequence represents a PCR primer used
CC in the isolation of the thyroid malfunction-associated protein, RITA
CC which is described in the method of the invention
XX
XX Sequence 22 BP; 6 A; 5 C; 6 G; 5 T; 0 U; 0 Other;
SQ
Query Match 2.2%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 385 TCCCAAGTCTGGGATTACAG 406
DB 1 TCCCAAGTCTGGGATTACAG 22
RESULT 369
ACC84464
ID ACC84464 standard; DNA; 22 BP.
XX
XX ACC84464;
AC
XX 28-AUG-2003 (first entry)
DT
XX
XX NTP peptide encoding sequence #11.
DE
XX
XX Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;
KW neural thread protein; NTP; tumour; ds.
XX
XX Unidentified.
XX
```

```
PN W02003008443-A2.
XX
XX 30-JAN-2003.
PD
XX
XX 19-JUL-2002; 2002WO-CA001105.
PF
XX
XX 19-JUL-2001; 2001US-0306150P.
PR 19-JUL-2001; 2001US-0306161P.
PR 16-NOV-2001; 2001US-0331477P.
XX
XX (NYMO-) NYMOX CORP.
PA
XX
XX Averbach PA;
PI
XX
XX WPI; 2003-247999/24.
DR
XX P-PSDB; ABR63259.
PT
XX
XX Novel neural thread protein peptide, referred as cell death peptide,
PT useful for treating prostatic hyperplasia, psoriasis, eczema, dermatosis,
PT atherosclerosis, cosmetic modification to skin, throat, mouth, muscle.
XX
XX Disclosure; Page 18; 77pp; English.
PS
XX
XX The present invention relates to a neural thread protein (NTP) peptide
CC referred to as cell death peptide. Thought to be cytosstatic,
CC antibacterial, immunosuppressive and antiinflammatory. It is useful for
CC treating a condition in a patient requiring removal or destruction of
CC cells, for treating a condition such as benign or malignant tumor,
CC inflammatory disease, autoimmune disease and infectious disease. The
CC peptide useful for treatment is derived from the amino acid sequence for
CC a pancreatic thread protein. The peptide is conjugated, linked or bound
CC to a molecule chosen from antibody or its fragment, antibody-like binding
CC molecule, where the molecule has a higher affinity for binding to a tumor
CC or other target than binding to other cells. Treatment using NTP peptides
CC can remove benign tumors with less risk and fewer of the undesirable side
CC effects of surgery. The present sequence is an NTP encoding sequence
XX
XX Sequence 22 BP; 5 A; 5 C; 9 G; 3 T; 0 U; 0 Other;
SQ
Query Match 2.2%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 728 GAGTACTGGGACTACAGGCGC 749
DB 1 GAGTACTGGGACTACAGGCGC 22
RESULT 370
AAH44054/c
ID AAH44054 standard; DNA; 24 BP.
XX
XX AAH44054;
AC
XX 11-SEP-2001 (first entry)
DT
XX
XX Mouse SMN 5' untranslated region PCR primer SEQ ID NO:5.
DE
XX
XX Mouse; survival motor neuron; SMN; knockout; spinal muscular atrophy;
KW SMA; diagnosis; detection; PCR primer; ss.
XX
XX Mus sp.
OS
XX
XX U66245963-B1.
PN
XX
XX 12-JUN-2001.
PD
XX
XX 25-MAY-2000; 2000US-00578656.
PF
XX
XX 28-MAY-1999; 99US-0136520P.
PR
XX
XX (SINI-) ACAD SINICA.
PA
XX
```

PI Li H, Hsieh-Li H, Chang J;  
XX MPI; 2001-380517/40.  
XX  
PT New transgenic mouse having a genome comprising a homozygous disruption  
PT of an Smn gene, useful e.g. as a model for human spinal muscular atrophy,  
PT or for testing the efficacy of present or future treatments for spinal  
XX muscular atrophy.  
XX PS Disclosure; Col 7; 12pp; English.  
XX  
CC The present invention describes a transgenic mouse whose genome comprises  
CC a homozygous disruption of an Smn (Survival motor neuron) gene which does  
CC not produce functional Smn protein. The mouse genome additionally  
CC comprises a DNA sequence encoding human SMN protein, where expression of  
CC the DNA sequence encoding the human SMN protein makes the mouse viable.  
CC The mouse shows one or more neurological defects similar to the  
CC pathological features of an SMN patient. The transgenic mouse is useful  
CC as a model for human spinal muscular atrophy (SMA); in developing and  
CC evaluating methods for diagnosing and treating SMA; for testing the  
CC accuracy and sensitivity of diagnostic methods for SMA; for testing the  
CC efficacy of various present and future therapeutic methods for SMA; and  
CC as a convenient positive control necessary for developing and testing any  
CC diagnostic methods for SMA. The present sequence represents a PCR primer  
CC which is used in the identification of transgenic mice by probing the 5'  
CC untranslated region of Smn  
XX  
SQ Sequence 24 BP; 7 A; 8 C; 5 G; 4 T; 0 U; 0 Other;  
  
Query Match 2.2%; Score 22; DB 1; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 202 TTGTCAGGCTGCTCGAACT 223  
DB 23 TTGTCAGGCTGCTCGAACT 2  
  
RESULT 371  
AAH38407  
ID AAH38407 standard; DNA; 25 BP.  
XX  
AC AAH38407;  
XX  
DT 14-AUG-2001 (first entry)  
XX  
DE SNP specific SNPE primer SEQ ID 1203.  
XX  
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
KW SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;  
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;  
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
KW inflammation; forensic investigation; paternity analysis; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN MO200129262-A2.  
XX  
PD 26-APR-2001.  
XX  
PF 13-OCT-2000; 2000WO-US028436.  
XX  
PR 15-OCT-1999; 99US-0160096P.  
XX  
PA (ORCH-) ORCHID BIOSCIENCES INC.  
XX  
PI Picoult-Newburg L, Pohl M;  
XX  
DR MPI; 2001-290930/30.  
XX  
PT New genotyping oligonucleotide, useful for detecting the presence,  
PT absence or identity of single polynucleotide polymorphism in a nucleic

PT acid sample.  
XX  
XX Claim 1; Page 56; 83pp; English.  
XX  
CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
CC primer extension (SNPE) primers, and the sequences of regions flanking  
CC sites of single nucleotide polymorphism SNPs. The present invention  
CC includes kits for determining the presence or absence of a SNP, using the  
CC oligonucleotides of the invention. The PCR primers are used to amplify a  
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.  
CC The oligonucleotides are useful for genotyping a nucleic acid sample by  
CC performing a single-nucleotide primer extension reaction. The  
CC oligonucleotides are useful for determining the presence, absence or  
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
CC assess by association analysis the genotype of an individual or group of  
CC individuals, having a pathological phenotypic trait suspected of being  
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular  
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,  
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
CC traits also include symptoms of or susceptibility to multifactorial  
CC diseases of which a component is or may be genetic such as autoimmune  
CC diseases, including, rheumatoid arthritis, multiple sclerosis,  
CC inflammation, cancer, nervous system diseases and infection by pathogenic  
CC microorganism. The method is also useful in forensic investigations and  
CC paternity analysis. The present sequence represents a single nucleotide  
CC primer extension (SNPE) primer specific for a human SNP containing DNA  
CC sequence  
XX  
SQ Sequence 25 BP; 6 A; 5 C; 7 G; 6 T; 0 U; 1 Other;  
  
Query Match 2.2%; Score 22; DB 1; Length 25;  
Best Local Similarity 91.7%; Pred. No. 1e+03;  
Matches 22; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 724 TCCTGAGTACTGGGACTACAGGC 747  
DB 1 TCCTGAGTACTGGGACTACAGGC 24  
  
RESULT 372  
ADB04745  
ID ADB04745 standard; DNA; 25 BP.  
XX  
AC ADB04745;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Human MD27 scanning oligonucleotide SEQ ID 5731.  
XX  
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;  
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;  
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
KW developmental disorder; ss.  
XX  
OS Homo sapiens.  
XX  
PN EP1281758-A2.  
XX  
PD 05-FEB-2003.  
XX  
PF 30-JUL-2002; 2002EP-00016874.  
XX  
PR 02-AUG-2001; 2001US-00922181.  
XX  
PA (AEOM-) AEOMICA INC.  
XX  
PI Shannon M, Gu Y, Nguyen C;  
XX  
DR MPI; 2003-423107/40.  
XX  
PT New zinc finger-containing proteins and nucleic acids, useful in  
PT manufacturing a medicament for treating or preventing a disorder

PT associated with decreased or increased expression or activity of MDZ3,  
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.  
XX  
PS Example 8; SEQ ID NO 5731; 103pp; English.  
XX  
CC The present invention relates to novel human zinc finger-containing  
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is  
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,  
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome  
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,  
CC or in manufacturing a medicament for treating or preventing a disorder  
CC associated with decreased or increased expression or activity of MDZ3,  
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic  
CC acids and proteins are also useful for diagnosing or monitoring a disease  
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic  
CC acids can also be used as probes to detect and characterize gross  
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are  
CC useful in constructing microarrays for measuring gene expression. The  
CC proteins are useful as therapeutic agents for gene therapy or as  
CC vaccines. The present sequence was used to illustrate the invention.  
XX  
SQ Sequence 25 BP; 5 A; 1 C; 9 G; 10 T; 0 U; 0 Other;  
XX  
Query Match 2.2%; Score 21.8; DB 1; Length 25;  
Best Local Similarity 92.0%; Pred. No. 1.1e+03;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 772 TTGTATTTTGTAGAGATGGGCTT 796  
DB 1 TTGTATTTTGTAGAGACGGGGT 25  
XX  
RESULT 373  
ADB04579  
ID ADB04579 standard; DNA; 25 BP.  
XX  
XX ADB04579;  
AC  
XX  
XX 20-NOV-2003 (first entry)  
DT  
XX  
DE Human MDZ7 scanning oligonucleotide SEQ ID 5565.  
XX  
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;  
XX zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;  
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
XX developmental disorder; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX EP1281758-A2.  
PN  
XX  
XX 05-FEB-2003.  
PD  
XX  
XX 30-JUL-2002; 2002EP-00016874.  
PF  
XX  
XX 02-AUG-2001; 2001US-00922181.  
PR  
XX  
XX (AEOM-) AEOMICA INC.  
PA  
XX  
XX Shannon M, Gu Y, Nguyen C;  
PI  
XX  
XX WPI; 2003-423107/40.  
DR  
XX  
XX New zinc finger-containing proteins and nucleic acids, useful in  
PT manufacturing a medicament for treating or preventing a disorder  
PT associated with decreased or increased expression or activity of MDZ3,  
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.  
XX  
XX Example 8; SEQ ID NO 5565; 103pp; English.  
XX  
XX The present invention relates to novel human zinc finger-containing  
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is  
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,

CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome  
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,  
CC or in manufacturing a medicament for treating or preventing a disorder  
CC associated with decreased or increased expression or activity of MDZ3,  
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic  
CC acids and proteins are also useful for diagnosing or monitoring a disease  
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic  
CC acids can also be used as probes to detect and characterize gross  
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are  
CC useful in constructing microarrays for measuring gene expression. The  
CC proteins are useful as therapeutic agents for gene therapy or as  
CC vaccines. The present sequence was used to illustrate the invention.  
XX  
SQ Sequence 25 BP; 4 A; 2 C; 4 G; 15 T; 0 U; 0 Other;  
XX  
Query Match 2.2%; Score 21.8; DB 1; Length 25;  
Best Local Similarity 92.0%; Pred. No. 1.1e+03;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 607 TTTTATTTTGTGACAGACTCT 631  
DB 1 TTTTATTTTGTGACAGACTCT 25  
XX  
RESULT 374  
ADB04741  
ID ADB04741 standard; DNA; 25 BP.  
XX  
XX ADB04741;  
AC  
XX  
XX 20-NOV-2003 (first entry)  
DT  
XX  
DE Human MDZ7 scanning oligonucleotide SEQ ID 5727.  
XX  
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;  
XX zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;  
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
XX developmental disorder; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX EP1281758-A2.  
PN  
XX  
XX 05-FEB-2003.  
PD  
XX  
XX 30-JUL-2002; 2002EP-00016874.  
PF  
XX  
XX 02-AUG-2001; 2001US-00922181.  
PR  
XX  
XX (AEOM-) AEOMICA INC.  
PA  
XX  
XX Shannon M, Gu Y, Nguyen C;  
PI  
XX  
XX WPI; 2003-423107/40.  
DR  
XX  
XX New zinc finger-containing proteins and nucleic acids, useful in  
PT manufacturing a medicament for treating or preventing a disorder  
PT associated with decreased or increased expression or activity of MDZ3,  
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.  
XX  
XX Example 8; SEQ ID NO 5727; 103pp; English.  
XX  
XX The present invention relates to novel human zinc finger-containing  
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is  
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,  
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome  
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,  
CC or in manufacturing a medicament for treating or preventing a disorder  
CC associated with decreased or increased expression or activity of MDZ3,  
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic  
CC acids and proteins are also useful for diagnosing or monitoring a disease  
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic  
CC acids can also be used as probes to detect and characterize gross



XX Sequence 26 BP; 6 A; 4 C; 9 G; 6 T; 0 U; 1 Other;  
SQ  
Query Match 2.2%; Score 21.8; DB 1; Length 26;  
Best Local Similarity 88.5%; Pred. No. 1.1e+03;  
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 862 GTGCTGGATTACAGCGCTGAGCCAC 887  
DB 1 GTGCTGGATTACAGCGCTGAGCCAC 26  
RESULT 377  
AAH91096/C  
ID AAH91096 standard; DNA; 26 BP.  
XX AAH91096;  
AC  
XX  
XX 09-OCT-2001 (first entry)  
XX  
XX Human inflammatory bowel disease associated polymorphic site #171.  
DE  
XX  
XX Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;  
KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;  
KW chromosome 5q31-33; forensic test; gene therapy; ds.  
XX  
XX Homo sapiens.  
OS  
XX  
XX Key Location/Qualifiers  
FH misc\_feature 12  
FT /tag= a  
FT /note= "SNP, optionally C or T at this position"  
XX  
XX WO200142511-A2.  
XX  
XX 14-JUN-2001.  
XX  
XX 11-DEC-2000; 2000WO-US033632.  
XX  
XX 10-DEC-1999; 99US-0170257P.  
PR 10-APR-2000; 2000US-0196046P.  
XX  
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.  
XX PA (ELI-) ELIPSIS BIOTHERAPEUTICS CORP.  
XX  
XX Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;  
XX WPI; 2001-367874/38.  
XX  
XX Testing for the presence of polymorphisms associated with inflammatory  
PT bowel disease, using a hybridization assay.  
XX  
XX Claim 1; Page 46; 463pp; English.  
XX  
XX The present invention describes a method for detecting the presence of  
CC polymorphisms associated with inflammatory bowel diseases such as  
CC ulcerative colitis and Crohn's disease. The methods can be used to detect  
CC the presence of genetic polymorphisms associated with inflammatory bowel  
CC disease and correlating their occurrence with disease states. They may be  
CC used in this way for phenotypic correlations, forensics, paternity  
CC testing, medicine and genetic analysis. The present sequence is a  
CC polymorphic site described in the exemplification of the invention  
XX  
SQ Sequence 26 BP; 6 A; 10 C; 5 G; 4 T; 0 U; 1 Other;  
Query Match 2.2%; Score 21.8; DB 1; Length 26;  
Best Local Similarity 88.5%; Pred. No. 1.1e+03;  
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 862 GTGCTGGATTACAGCGCTGAGCCAC 887  
DB 26 GTGCTGGATTACAGCGCTGAGCCAC 1

RESULT 378  
AAH38507/C  
ID AAH38507 standard; DNA; 27 BP.  
XX  
XX AAH38507;  
AC  
XX  
XX 14-AUG-2001 (first entry)  
XX  
XX SNP specific SNPE primer SEQ ID 1303.  
DE  
XX  
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
KW SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;  
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;  
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
KW inflammation; forensic investigation; paternity analysis; primer; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200129262-A2.  
XX  
XX 26-APR-2001.  
PD  
XX  
XX 13-OCT-2000; 2000WO-US028436.  
PF  
XX  
XX 15-OCT-1999; 99US-0160096P.  
PR  
XX  
XX (ORCH-) ORCHID BIOSCIENCES INC.  
XX  
XX Picoult-Newburg L, Pohl M;  
XX WPI; 2001-290930/30.  
XX  
XX New genotyping oligonucleotide, useful for detecting the presence,  
PT absence or identity of single polymorphic polymorphism in a nucleic  
PT acid sample.  
XX  
XX Claim 1; Page 56; 83pp; English.  
XX  
XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
CC primer extension (SNPE) primers, and the sequences of regions flanking  
CC sites of single nucleotide polymorphisms SNPs. The present invention  
CC includes kits for determining the presence or absence of a SNP, using the  
CC oligonucleotides of the invention. The PCR primers are used to amplify a  
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.  
CC The oligonucleotides are useful for genotyping a nucleic acid sample by  
CC performing a single-nucleotide primer extension reaction. The  
CC oligonucleotides are useful for determining the presence, absence or  
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
CC assess by association analysis the genotype of an individual or group of  
CC individuals, having a pathological phenotypic trait suspected of being  
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular  
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,  
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
CC traits also include symptoms of or susceptibility to multifactorial  
CC disease of which a component is or may be genetic such as autoimmune  
CC diseases, including, rheumatoid arthritis, multiple sclerosis,  
CC inflammation, cancer, nervous system diseases and infection by pathogenic  
CC microorganism. The method is also useful in forensic investigations and  
CC paternity analysis. The present sequence represents a single nucleotide  
CC primer extension (SNPE) primer specific for a human SNP containing DNA  
XX  
SQ Sequence 27 BP; 8 A; 6 C; 8 G; 3 T; 0 U; 2 Other;  
Query Match 2.2%; Score 21.8; DB 1; Length 27;  
Best Local Similarity 85.2%; Pred. No. 1.1e+03;  
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
OY 671 TGGCTCACTGCAACCTCTGCTCCCG 697  
DB TGGCTCACTGCAACCTCTGCTCCCG 1

```
Db      27 TGGCTCACTGNAACCTGACTGCTGG 1
RESULT 379
AAH37975/C
ID      AAH37975 standard; DNA; 27 BP.
XX
XX
AC      AAH37975;
XX
XX
DT      14-AUG-2001 (first entry)
XX
XX
DE      SNP specific SNPE primer SEQ ID 771.
XX
XX
DE      Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW      SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
KW      Leisch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW      polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW      acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW      inflammation; forensic investigation; paternity analysis; primer; ss.
XX
XX
OS      Homo sapiens.
XX
XX
PN      WO200129262-A2.
XX
XX
PD      26-APR-2001.
XX
XX
PF      13-OCT-2000; 2000WO-US028436.
XX
XX
PR      15-OCT-1999; 99US-0160096P.
XX
XX
PA      (ORCH-) ORCHID BIOSCIENCES INC.
XX
XX
PI      Picoult-Newburg L, Pohl M;
XX
XX
DR      WPI; 2001-290930/30.
XX
XX
PT      New genotyping oligonucleotide, useful for detecting the presence,
PT      absence or identity of single polynucleotide polymorphism in a nucleic
PT      acid sample.
XX
XX
PS      Claim 1; Page 53; 83pp; English.
XX
XX
CC      Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC      primer extension (SNPE) primers, and the sequences of regions flanking
CC      sites of single nucleotide polymorphisms SNPs. The present invention
CC      includes kits for determining the presence or absence of a SNP, using the
CC      oligonucleotides of the invention. The PCR primers are used to amplify a
CC      SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC      The oligonucleotides are useful for genotyping a nucleic acid sample by
CC      performing a single-nucleotide primer extension reaction. The
CC      oligonucleotides are useful for determining the presence, absence or
CC      identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC      assess by association analysis the genotype of an individual or group of
CC      individuals, having a pathological phenotypic trait suspected of being
CC      caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC      agammaglobulinaemia, diabetes insipidus, Leisch-Nyhan syndrome, muscular
CC      dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC      osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC      traits also include symptoms of or susceptibility to multifactorial
CC      disease of which a component is or may be genetic such as autoimmune
CC      diseases, including, rheumatoid arthritis, multiple sclerosis,
CC      inflammation, cancer, nervous system diseases and infection by pathogenic
CC      microorganism. The method is also useful in forensic investigations and
CC      paternity analysis. The present sequence represents a single nucleotide
CC      primer extension (SNPE) primer specific for a human SNP containing DNA
CC      sequence
XX
SQ      Sequence 27 BP; 6 A; 6 C; 8 G; 5 T; 0 U; 2 Other;
```

```
Query Match      2.2%; Score 21.8; DB 1; Length 27;
Best Local Similarity 85.2%; Pred. No. 1.1e+03;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
OY      485 GTGGTGTGATCAGCTGCTACTGCAGCC 511
Db      27 GTGGTGTGATCAGCTGCTACTGNAACC 1
RESULT 380
AAH91552
ID      AAH91552 standard; DNA; 27 BP.
XX
XX
AC      AAH91552;
XX
XX
DT      09-OCT-2001 (first entry)
XX
XX
DE      Human inflammatory bowel disease associated polymorphic site #627.
XX
XX
KW      Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW      single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
KW      chromosome 5q31-33; forensic test; gene therapy; ds.
XX
XX
OS      Homo sapiens.
XX
XX
FH      Key Location/Qualifiers
FT      misc_feature 15
FT      /tag= a
FT      /note= "SNP, optionally T or C at this position"
XX
XX
PN      WO200142511-A2.
XX
XX
PD      14-JUN-2001.
XX
XX
PF      11-DEC-2000; 2000WO-US033632.
XX
XX
PR      10-DEC-1999; 99US-0170257P.
XX
XX
PR      10-APR-2000; 2000US-0196046P.
XX
XX
PA      (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA      (ELLIP) ELLIPSIS BIOTHERAPEUTICS CORP.
XX
XX
PI      Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;
XX
XX
DR      WPI; 2001-367874/38.
XX
XX
PT      Testing for the presence of polymorphisms associated with inflammatory
PT      bowel disease, using a hybridization assay.
XX
XX
PS      Claim 1; Page 65; 463pp; English.
XX
XX
CC      The present invention describes a method for detecting the presence of
CC      polymorphisms associated with inflammatory bowel diseases such as
CC      ulcerative colitis and Crohn's disease. The methods can be used to detect
CC      the presence of genetic polymorphisms associated with inflammatory bowel
CC      disease and correlating their occurrence with disease states. They may be
CC      used in this way for phenotypic correlations, forensics, paternity
CC      testing, medicine and genetic analysis. The present sequence is a
CC      polymorphic site described in the exemplification of the invention
XX
XX
SQ      Sequence 27 BP; 7 A; 6 C; 7 G; 6 T; 0 U; 1 Other;
```

```
Query Match      2.2%; Score 21.8; DB 1; Length 27;
Best Local Similarity 88.5%; Pred. No. 1.1e+03;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
RESULT 381
AAH83037/C
ID      AAX83037 standard; DNA; 23 BP.
XX
XX
AC      AAX83037;
XX
```

DT 31-AUG-1999 (first entry)  
 XX Primer E2C to isolate human WRN gene 3' exons.  
 DE Human; WRN; Werner's syndrome; detection; diagnosis; autosomal;  
 XX recessive disorder; phenotype; primer; RT-PCR; amplification; ss.  
 KM Synthetic.  
 OS Homo sapiens.  
 XX MO9724435-A1.  
 PN 10-JUL-1997.  
 XX 30-DEC-1996; 96WO-US020785.  
 PD 29-DEC-1995; 95US-0009409P.  
 XX 29-DEC-1995; 95US-00580539.  
 PR 30-JAN-1996; 96US-0010835P.  
 PR 30-JAN-1996; 96US-00594242.  
 PR 12-APR-1996; 96US-00632175.  
 XX (DARW-) DARWIN MOLECULAR CORP.  
 PA Oshima J, Fu Y, Yu C, Mulligan J, Schellenberg GD;  
 PI WPI; 1997-363671/33.  
 DR Isolated nucleic acid molecule encoding the WRN gene product - useful for  
 PT detection and treatment of Werner's syndrome, and related diseases.  
 XX Example 2; Page 42; 153pp; English.  
 CC Primers AAX83008-X83064 were used to RT-PCR amplify exons from the 5' and  
 CC 3' ends of the human WRN gene (AAX83003) which encodes a protein related  
 CC to Werner's syndrome. The products can be used for the detection and  
 CC treatment of Werner's syndrome (WS), an autosomal recessive disorder with  
 CC a complex phenotype, as well as related diseases  
 CC Sequence 23 BP; 6 A; 5 C; 6 G; 6 T; 0 U; 0 Other;  
 SO  
 Query Match 2.2%; Score 21.4; DB 1; Length 23;  
 Best Local Similarity 95.7%; Pred. No. 1.1e+03;  
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 383 CCTCCCAAGTCTGGGATTACA 405  
 DB 23 CCTCCCAAGTGTGGGATTACA 1  
 RESULT 382  
 ID AAI65098 standard; DNA; 24 BP.  
 XX AAI65098;  
 AC 28-NOV-2001 (first entry)  
 XX Human zinc finger protein 15  
 DE Human zinc finger protein 15 PCR primer #1.  
 XX Human; zinc finger protein 15; cytosolic; viral; immunomodulatory;  
 KM anti-inflammatory; haemostatic; gene therapy; malignant neoplasm;  
 KM haemopathy; HIV infection; immunological disease inflammation;  
 KM PCR primer; ss.  
 XX Homo sapiens.  
 OS MO200168690-A1.  
 PN 20-SEP-2001.  
 PD 26-FEB-2001; 2001WO-CN000165.  
 PF  
 XX

PR 15-MAR-2000; 2000CN-00114909.  
 XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.  
 PA Mao Y, Xie Y;  
 XX WPI; 2001-570864/64.  
 DR Human zinc finger protein 15 and encoded polynucleotide, applicable in  
 XX diagnosis and treatment of malignant neoplasm, hemopathy, human  
 PT immunodeficiency virus infection, immunological diseases and  
 PT inflammation.  
 XX Example 2; Page 17; 39pp; Chinese.  
 PS The present invention relates to human zinc finger protein 15 (see  
 CC AAI65097 and AAG78828). The zinc finger protein and its coding sequence  
 CC are useful in the diagnosis and treatment of malignant neoplasm,  
 CC haemopathy, HIV infection, immunological diseases and various  
 CC inflammations. The present sequence is a PCR primer, which was used in an  
 CC example from the present invention  
 XX Sequence 24 BP; 5 A; 5 C; 9 G; 5 T; 0 U; 0 Other;  
 SO  
 Query Match 2.2%; Score 21.4; DB 1; Length 24;  
 Best Local Similarity 95.7%; Pred. No. 1.1e+03;  
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 866 TGGGATTACAGCGTGAGCCACC 888  
 DB 1 TGGGATTACAGTGTGAGCCACC 23  
 RESULT 383  
 ID ABS58183/C  
 XX ABS58183 standard; DNA; 24 BP.  
 AC ABS58183;  
 XX 26-FEB-2003 (first entry)  
 DT RT-PCR primer #1 for cDNA encoding human zinc finger protein 10.01.  
 XX Human; zinc finger protein 10.01; malignant tumour; haemopathy;  
 KM human immunodeficiency virus infection; HIV infection; inflammation;  
 KM immunological disease; RT-PCR; primer; reverse transcriptase-PCR; ss.  
 XX Homo sapiens.  
 OS CN1352110-A.  
 PN 05-JUN-2002.  
 PD 06-NOV-2000; 2000CN-00127241.  
 PF 06-NOV-2000; 2000CN-00127241.  
 XX 06-NOV-2000; 2000CN-00127241.  
 PR (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
 PA Mao Y, Xie Y;  
 XX WPI; 2002-692406/75.  
 DR New human zinc finger protein 10.01 polypeptide for treating malignant  
 XX tumors, hemopathy, human immunodeficiency virus infection, immunological  
 PT diseases and various inflammations.  
 PT Example 2; Page 17 (disclosure); 33pp; Chinese.  
 PS The present invention relates to the isolation of human zinc finger  
 CC protein 10.01, and the polynucleotide sequence encoding it. Also  
 CC described is the process for preparing the protein by DNA recombination  
 CC and the application of the polypeptide and polynucleotide in treating

CC various diseases such as malignant tumours, haemopathy, human  
CC immunodeficiency virus (HIV) infection, immunological diseases, and  
CC various inflammations. The present sequence represents a reverse  
CC transcriptase (RT)-PCR primer used to isolate cDNA encoding human zinc  
CC finger protein 10.01  
XX  
SQ Sequence 24 BP; 3 A; 8 C; 7 G; 6 T; 0 U; 0 Other;  
Query Match 2.2%; Score 21.4; DB 1; Length 24;  
Best Local Similarity 95.7%; Pred. No. 1.1e+03;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 868 GGATTACAGCGGTGAGCCACCAC 890  
Db 24 GGATTACAGCGGTGAGCCACCAC 2  
RESULT 384  
ABS58184/C  
ID ABS58184 standard; DNA; 24 BP.  
XX  
AC ABS58184;  
XX  
DT 26-FEB-2003 (first entry)  
XX  
DE RT-PCR primer #2 for cDNA encoding human zinc finger protein 10.01.  
XX  
KW Human; zinc finger protein 10.01; malignant tumour; haemopathy;  
KW human immunodeficiency virus infection; HIV infection; inflammation;  
KW immunological disease; RT-PCR; primer; reverse transcriptase-PCR; ss.  
XX  
OS Homo sapiens.  
XX  
PN CN1352110-A.  
XX  
PD 05-JUN-2002.  
XX  
PF 06-NOV-2000; 2000CN-00127241.  
XX  
PR 06-NOV-2000; 2000CN-00127241.  
XX  
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
XX  
PI Mao Y, Xie Y;  
XX  
DR WPI; 2002-692406/75.  
XX  
PT New human zinc finger protein 10.01 polypeptide for treating malignant  
PT tumour; haemopathy, human immunodeficiency virus infection, immunological  
PT diseases and various inflammations.  
XX  
PS Example 2; Page 17 (disclosure); 33pp; Chinese.  
XX  
CC The present invention relates to the isolation of human zinc finger  
CC protein 10.01, and the polynucleotide sequence encoding it. Also  
CC described is the process for preparing the protein by DNA recombination  
CC and the application of the polypeptide and polynucleotide in treating  
CC various diseases such as malignant tumours, haemopathy, human  
CC immunodeficiency virus (HIV) infection, immunological diseases, and  
CC various inflammations. The present sequence represents a reverse  
CC transcriptase (RT)-PCR primer used to isolate cDNA encoding human zinc  
CC finger protein 10.01  
XX  
SQ Sequence 24 BP; 6 A; 5 C; 9 G; 4 T; 0 U; 0 Other;  
Query Match 2.2%; Score 21.4; DB 1; Length 24;  
Best Local Similarity 95.7%; Pred. No. 1.1e+03;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 997 GGCTCAGCGATTCTCTGCTC 1019  
Db 23 GGCTCAGCGATTCTCTGCTC 1

RESULT 385  
ABA04737  
ID ABA04737 standard; DNA; 24 BP.  
XX  
AC ABA04737;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Human alkylation DNA protein cysteine methyltransferase 11 PCR primer #2.  
XX  
KW Human; alkylation DNA protein cysteine methyltransferase 11; cytosolic;  
KW haemostatic; virucide; immunomodulatory; antiinflammatory; gene therapy;  
KW tumour; haemopathy; HIV infection; immunological disease; inflammation;  
KW PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200188146-A1.  
XX  
PD 22-NOV-2001.  
XX  
PE 26-MAR-2001; 2001WO-CN000464.  
XX  
PR 28-MAR-2000; 2000CN-00115226.  
XX  
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.  
XX  
PI Mao Y, Xie Y;  
XX  
DR WPI; 2002-055701/07.  
XX  
PT Human alkylation-DNA-protein cysteine methyltransferase and encoding  
PT polynucleotide, used in diagnosis and treatment of malignant tumors,  
PT haemopathy, human immunodeficiency virus infection, immunological diseases  
PT and inflammation.  
XX  
PS Example 2; Page 19; 40pp; Chinese.  
XX  
CC The present invention relates to human alkylation-DNA-protein cysteine  
CC methyltransferase (see AM47739). The protein and its coding sequence are  
CC useful in the diagnosis and treatment of malignant tumours, haemopathy,  
CC HIV infection, immunological diseases and various inflammations. The  
CC present sequence is a PCR primer, which was used in an example from the  
CC present invention  
XX  
SQ Sequence 24 BP; 4 A; 0 C; 4 G; 16 T; 0 U; 0 Other;  
Query Match 2.2%; Score 21.4; DB 1; Length 24;  
Best Local Similarity 95.7%; Pred. No. 1.1e+03;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 767 TTTTGTGATTTTGTAGTGA 789  
Db 2 TTTTGTGATTTTGTAGTGA 24  
RESULT 386  
AAL45771/C  
ID AAL45771 standard; DNA; 24 BP.  
XX  
AC AAL45771;  
XX  
DT 28-JUN-2002 (first entry)  
XX  
DE Human acid phosphatase family protein 11 cDNA PCR primer #2.  
XX  
KW Human; acid phosphatase family protein 11; cancer; haemopathy;  
KW cytosolic; haemostatic; virucide; immunomodulatory; antiinflammatory;  
KW immune disease; HIV infection; phlogosis; gene therapy; PCR; primer; ss.  
XX  
OS Homo sapiens.  
XX



PN WO200220579-A1.  
XX  
PD 14-MAR-2002.  
XX  
XX 19-JUN-2001; 2001WO-CN001011.  
PF  
XX 21-JUN-2000; 2000CN-00116667.  
XX  
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.  
PI Mao Y, Xie Y;  
XX  
DR WPI; 2002-329869/36.  
XX  
PT Homo acid phosphatase family protein 11 and encoding polynucleotide, used  
PT in diagnosis and treatment of malignant tumors, hemopathy, human  
PT immunodeficiency virus infection, immunological diseases and  
PT inflammation.  
XX  
PS Example 2; Page 12; 39pp; Chinese.  
XX  
CC The present invention provides the protein and coding sequences of human  
CC acid phosphatase family protein 11. The sequences can be used in the  
CC treatment of cancer, haemopathy, HIV infection, immune diseases and  
CC phlogosis. The present sequence is a PCR primer for the coding sequence  
CC of the invention  
XX  
SQ Sequence 24 BP; 5 A; 3 C; 11 G; 5 T; 0 U; 0 Other;  
XX  
Query Match 2.2%; Score 21.4; DB 1; Length 24;  
Best Local Similarity 95.7%; Pred. No. 1.1e+03;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 675 TCACCTGCACCTCTGCTCCCGG 697  
DB 24 TCACCTGCACCTCTGCTCCCGG 2  
XX  
RESULT 387  
AAD50373/C  
ID AAD50373 standard; DNA; 24 BP.  
XX  
AC AAD50373;  
XX  
DT 24-MAR-2003 (first entry)  
XX  
DE PCR primer #1 used to illustrate the method of the invention.  
XX  
XX Stutter reduction; microsatellite amplification; genetic analysis; PCR;  
XX primer; ss.  
XX  
XX Unidentified.  
XX  
XX WO200290562-A2.  
XX  
XX 14-NOV-2002.  
XX  
XX 06-MAY-2002; 2002WO-US014189.  
XX  
XX 07-MAY-2001; 2001US-00850514.  
XX  
XX (BIOW) APPLIED BIOSYSTEMS INC.  
XX  
XX  
XX Coticone SR, Bloch W;  
XX  
XX WPI; 2003-111983/10.  
XX  
XX  
XX Reducing stutter in the amplification of a microsatellite for genetic  
XX analysis by contacting the sample comprising a microsatellite with an  
XX enzyme with nucleic acid polymerase activity and incubating the sample  
XX with the enzyme.  
XX  
PS Disclosure; Page 29; 60pp; English.

XX  
CC The present invention relates to a method of reducing stutter in the  
CC amplification of a microsatellite. The method involves providing a sample  
CC comprising a microsatellite of interest; contacting the sample with at  
CC least one enzyme having nucleic acid polymerase activity and incubating  
CC the sample with the enzyme for amplifying the microsatellite. The method  
CC is useful for reducing stutter in the amplification of a microsatellite  
CC for genetic analysis. The present sequence is a PCR primer used to  
CC illustrate the method of the invention  
XX  
SQ Sequence 24 BP; 7 A; 3 C; 9 G; 5 T; 0 U; 0 Other;  
XX  
Query Match 2.2%; Score 21.4; DB 1; Length 24;  
Best Local Similarity 95.7%; Pred. No. 1.1e+03;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 966 AATCTGGCTCACTGCACTCT 988  
DB 23 AATCTGGCTCACTGCACTCT 1  
XX  
RESULT 388  
ADL06343/C  
ID ADL06343 standard; DNA; 24 BP.  
XX  
AC ADL06343;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE RT-PCR primer #1 for cDNA encoding human protein-13.2.  
XX  
XX Human; protein-13.2; site-specific recombinase;  
XX growth development disorder; tumour; reverse transcriptase-PCR; RT-PCR;  
XX primer; ss.  
XX  
XX Homo sapiens.  
XX  
XX CN1393548-A.  
XX  
XX 29-JAN-2003.  
XX  
XX 29-JUN-2001; 2001CN-00113178.  
XX  
XX 29-JUN-2001; 2001CN-00113178.  
XX  
XX (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.  
XX  
XX Mao Y, Xie Y;  
XX  
XX WPI; 2003-422181/40.  
XX  
XX Polypeptide-human protein-13.2 containing site specific recombinase  
XX characteristic sequence fragment and polynucleotide for coding it.  
XX  
XX Example 3; SEQ ID NO 3; 32pp; Chinese.  
XX  
XX The present invention relates to the isolation of human protein-13.2  
XX containing a site-specific recombinase characteristic sequence fragment,  
XX and the polynucleotide sequence encoding it. Also disclosed is a process  
XX for preparing the polypeptide by a DNA recombination technique and  
XX application of the polypeptide and polynucleotide in treating diseases  
XX such as growth development disorders and tumours. The present sequence  
XX represents a reverse transcriptase-PCR primer used in the examples of the  
XX present invention.  
XX  
SQ Sequence 24 BP; 6 A; 4 C; 12 G; 2 T; 0 U; 0 Other;  
XX  
Query Match 2.2%; Score 21.4; DB 1; Length 24;  
Best Local Similarity 95.7%; Pred. No. 1.1e+03;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1005 CGATTCTCGTGTCCAGCTCC 1027  
XXXXXXXXXXXXXXXXXXXX

DB 24 CGATTCTCTGCTCAGCCTCCC 2  
 RESULT 389  
 AAH38671 standard; DNA, 25 BP.  
 ID AAH38671  
 AC AAH38671;  
 DT 14-AUG-2001 (first entry)  
 DE SNP specific SNPE primer SEQ ID 1467.  
 XX  
 XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
 KW SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;  
 KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;  
 KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
 KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
 KW inflammation; forensic investigation; paternity analysis; primer; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 PN MO200129262-A2.  
 PD 26-APR-2001.  
 XX  
 XX 13-OCT-2000; 2000WO-US028436.  
 PF  
 XX 15-OCT-1999; 99US-0160096P.  
 PR  
 XX (ORCH-) ORCHID BIOSCIENCES INC.  
 XX  
 XX Picoult-Newburg L, Pohl M;  
 PI  
 XX WPI; 2001-290930/30.  
 DR  
 XX  
 XX New genotyping oligonucleotide, useful for detecting the presence,  
 PT absence or identity of single polynucleotide polymorphism in a nucleic  
 PT acid sample.  
 PT  
 XX  
 PS Claim 1; Page 57; 83pp; English.  
 XX  
 XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
 CC primer extension (SNPE) primers, and the sequences of regions flanking  
 CC sites of single nucleotide polymorphisms SNPs. The present invention  
 CC includes kits for determining the presence or absence of a SNP, using the  
 CC oligonucleotides of the invention. The PCR primers are used to amplify a  
 CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.  
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by  
 CC performing a single-nucleotide primer extension reaction. The  
 CC oligonucleotides are useful for determining the presence, absence or  
 CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
 CC assess by association analysis the genotype of an individual or group of  
 CC individuals, having a pathological phenotypic trait suspected of being  
 CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
 CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular  
 CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,  
 CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
 CC traits also include symptoms of or susceptibility to multifactorial  
 CC disease of which a component is or may be genetic such as autoimmune  
 CC diseases, including, rheumatoid arthritis, multiple sclerosis,  
 CC inflammation, cancer, nervous system diseases and infection by pathogenic  
 CC microorganism. The method is also useful in forensic investigations and  
 CC paternity analysis. The present sequence represents a single nucleotide  
 CC primer extension (SNPE) primer specific for a human SNP containing DNA  
 CC sequence  
 XX  
 SQ Sequence 25 BP; 7 A; 1 C; 5 G; 12 T; 0 U; 0 Other;

Query Match 2.2%; Score 21.4; DB 1; Length 25;  
 Best Local Similarity 95.7%; Pred. No. 1.1e+03;  
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 769 TTTTGTATTTTAGTAGAGATG 791  
 DB 3 TTTTGTATTTTAGTAGAGACG 25  
 RESULT 390  
 AAH38231  
 ID AAH38231 standard; DNA, 25 BP.  
 AC AAH38231;  
 DT 14-AUG-2001 (first entry)  
 DE SNP specific SNPE primer SEQ ID 1027.  
 XX  
 XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
 KW SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;  
 KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;  
 KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
 KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
 KW inflammation; forensic investigation; paternity analysis; primer; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 PN MO200129262-A2.  
 PD 26-APR-2001.  
 XX  
 XX 13-OCT-2000; 2000WO-US028436.  
 PF  
 XX 15-OCT-1999; 99US-0160096P.  
 PR  
 XX (ORCH-) ORCHID BIOSCIENCES INC.  
 XX  
 XX Picoult-Newburg L, Pohl M;  
 PI  
 XX WPI; 2001-290930/30.  
 DR  
 XX  
 XX New genotyping oligonucleotide, useful for detecting the presence,  
 PT absence or identity of single polynucleotide polymorphism in a nucleic  
 PT acid sample.  
 PT  
 XX  
 PS Claim 1; Page 55; 83pp; English.  
 XX  
 XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
 CC primer extension (SNPE) primers, and the sequences of regions flanking  
 CC sites of single nucleotide polymorphisms SNPs. The present invention  
 CC includes kits for determining the presence or absence of a SNP, using the  
 CC oligonucleotides of the invention. The PCR primers are used to amplify a  
 CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.  
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by  
 CC performing a single-nucleotide primer extension reaction. The  
 CC oligonucleotides are useful for determining the presence, absence or  
 CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
 CC assess by association analysis the genotype of an individual or group of  
 CC individuals, having a pathological phenotypic trait suspected of being  
 CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
 CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular  
 CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,  
 CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
 CC traits also include symptoms of or susceptibility to multifactorial  
 CC disease of which a component is or may be genetic such as autoimmune  
 CC diseases, including, rheumatoid arthritis, multiple sclerosis,  
 CC inflammation, cancer, nervous system diseases and infection by pathogenic  
 CC microorganism. The method is also useful in forensic investigations and  
 CC paternity analysis. The present sequence represents a single nucleotide  
 CC primer extension (SNPE) primer specific for a human SNP containing DNA  
 CC sequence  
 XX  
 SQ Sequence 25 BP; 7 A; 1 C; 5 G; 12 T; 0 U; 0 Other;

Query Match 2.2%; Score 21.4; DB 1; Length 25;  
 Best Local Similarity 95.7%; Pred. No. 1.1e+03;

Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 769 TTTTGTATTTTGTAGAGAG 791  
 |||||  
 DB 3 TTTTGTATTTTGTAGAGAG 25  
 |||||

RESULT 391  
 AAZ45143/C  
 ID AAZ45143 standard; DNA; 26 BP.  
 XX  
 AC AAZ45143;  
 XX  
 DT 28-FEB-2000 (first entry)  
 XX  
 DE Oligonucleotide used to determine the function of MMP-9 polymorphism.  
 XX  
 XX Matrix metalloproteinase-9; MMP-9; polymorphism; endopeptidase; detect;  
 KW inflammatory disease; diagnose; atherosclerosis; tumour; metastasis;  
 KW neurological disease; multiple sclerosis; arthritis; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO9597315-A2.  
 XX  
 PD 11-NOV-1999.  
 XX  
 PF 07-MAY-1999; 99WO-GB001447.  
 XX  
 PR 07-MAY-1998; 98GB-00009764.  
 XX  
 PA (ISIS-) ISIS INNOVATION LTD.  
 XX  
 PI Zhang BP, Ye S, Henney A;  
 PI  
 DR WPI; 2000-052977/04.  
 XX  
 PT Detection of matrix metalloproteinase 9 gene polymorphisms for diagnosis or  
 PT prognosis of diseases characterized by metalloproteinase mediated  
 PT remodelling.  
 PT  
 PS Example 3; Page 14; 29pp; English.  
 XX  
 CC Oligonucleotides AAZ45143-Z45144 are used to determine the function of  
 CC the matrix metalloproteinase-9 (MMP-9) gene -1562 (C/T) polymorphic site.  
 CC MMP-9 is a zinc-dependent endopeptidase, and is located on chromosome 20.  
 CC MMP activity is associated with inflammatory diseases and MMP-9 is  
 CC implicated in the pathology of multiple sclerosis. Certain polymorphic  
 CC sequences in the MMP-9 promoter, coding sequence and 3' untranslated  
 CC region of the human MMP-9 gene (see AAZ45145) can affect the severity of  
 CC atherosclerosis. The invention relates to the presence or absence of one  
 CC variant form of a MMP-9 gene polymorphism (-1562 Cytosine/Threonine),  
 CC detection of this polymorphism using oligonucleotides AAZ45137-Z45140 can  
 CC be used for disease prognosis. The invention shows that the MMP-9 C-1562T  
 CC polymorphism is a regulatory functional polymorphism. The methods and  
 CC oligonucleotides are used to detect polymorphisms in the MMP-9 gene. They  
 CC are useful for the diagnosis and prognosis of diseases characterized by  
 CC metalloproteinase mediated remodelling, such as atherosclerosis, tumour  
 CC invasion and metastasis, inflammatory disease, and neurological diseases,  
 CC particularly those involving demyelination such as multiple sclerosis,  
 CC and arthritic disease. Proteins encoded by the MMP-9 gene variants may be  
 CC used for screening compounds that bind specifically to a molecule encoded  
 CC by one variant of a polymorphic sequence, thus identifying compounds  
 CC which modulate the activity of the enzyme. Such compounds can then be  
 CC used for rational drug design  
 CC  
 SQ Sequence 26 BP; 5 A; 7 C; 9 G; 5 T; 0 U; 0 Other;

Query Match 2.1%; Score 21.2; DB 1; Length 26;  
 Best Local Similarity 88.5%; Pred. No. 1.2e+03;  
 Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 870 ATTACAGCGTGAGCCACGCGCG 895  
 |||||  
 DB 26 ATTATAGCGTGCGCCACGCGCTG 1  
 |||||

RESULT 392  
 ABK61474/C  
 ID ABK61474 standard; DNA; 26 BP.  
 XX  
 AC ABK61474;  
 XX  
 DT 18-JUN-2002 (first entry)  
 XX  
 DE Human NOV3 Exon linking PCR primer #2.  
 XX  
 XX Human; ss; NOVX; gene therapy; cardiomyopathy; atherosclerosis;  
 KW cell signal processing disorder; metabolic pathway modulation disorder;  
 KW diabetes; cancer; adenocarcinoma; lymphoma; prostate cancer; primer;  
 KW uterus cancer; immune response; graft-versus-host disease; Exon linking;  
 KW acquired immunodeficiency syndrome; AIDS; asthma; Crohn's disease;  
 KW hypertension; congenital heart defects; multiple sclerosis; inflammation;  
 KW Albright hereditary osteodystrophy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200216599-A2.  
 XX  
 PD 28-FEB-2002.  
 XX  
 PF 27-AUG-2001; 2001WO-US026510.  
 XX  
 PR 25-AUG-2000; 2000US-0228191P.  
 PR 08-FEB-2001; 2001US-0267300P.  
 PR 20-FEB-2001; 2001US-0269961P.  
 PR 20-MAR-2001; 2001US-0277337P.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 PA (CORR-) COR THERAPEUTICS INC.  
 PI Burgess CE, Conley PB, Grose WM, Hart M, Kekuda R, Shinkets RA;  
 PI Spytek KA, Szekeres ES, Tomlinson JE, Topper JN, Yang R;  
 PI  
 DR WPI; 2002-280937/32.  
 XX  
 PT New polypeptides for treating or preventing a disorder associated with  
 PT them, in humans, e.g. cardiomyopathy, atherosclerosis or cancers.  
 PT  
 PS Example 1; Page 204; 263pp; English.  
 XX  
 CC The invention relates to an isolated polypeptide (NOVX) a mature form of  
 CC NOVX, a NOVX variant (differing by no more than 15%), the nucleotide  
 CC encoding NOVX (or its complement, fragment or variant). NOVX is NOV1-14,  
 CC 15a, 15b, 16a, and 16b. The NOVX polypeptide, nucleic acid encoding it  
 CC and antibody against it, are useful for treating or preventing (e.g. by  
 CC gene therapy) a NOVX-associated disorder in humans, e.g. cardiomyopathy,  
 CC atherosclerosis, a disorder related to cell signal processing and  
 CC metabolic pathway modulation, diabetes or cancers. The NOVX polypeptide  
 CC and nucleic acids are also useful for determining the presence of  
 CC predisposition to the diseases. The NOVX nucleic acid and polypeptide are  
 CC especially useful in therapeutic or prophylactic applications for  
 CC disorders associated with aberrant NOVX expression or activity, e.g.  
 CC cancers (e.g. adenocarcinoma, lymphoma, prostate cancer or uterus  
 CC cancer), immune response, graft-versus-host disease, acquired  
 CC immunodeficiency syndrome (AIDS), asthma, Crohn's disease, hypertension,  
 CC congenital heart defects, multiple sclerosis, inflammation or Albright  
 CC hereditary osteodystrophy and many other diseases listed in the  
 CC specification. The DNA encoding the protein is useful in gene therapy for  
 CC treating the conditions. This is also useful in detection assays,  
 CC chromosome mapping, tissue typing, diagnostic or prognostic assays, or  
 CC for developing a powerful assay system for functional analysis of various  
 CC human disorders, as well as in diagnostic applications. The present  
 CC sequence is a primer used to isolate DNA encoding a NOVX protein by the  
 CC technique of exon linking

XX SQ Sequence 26 BP; 7 A; 5 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 2.1%; Score 21.2; DB 1; Length 26;  
Best Local Similarity 88.5%; Pred. No. 1.2e+03;  
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 535 CTCCTGCTCAGCTCCCAAGTAGCT 560  
DB 26 CTCCTGCTCAGCTCCCAAGTAGCT 1

RESULT 393

ABK67128  
ID ABK67128 standard; DNA; 26 BP.

XX AC ABK67128;

XX DT 02-JUL-2002 (first entry)

XX DE Human gene specific PCR primer #1216.

XX KW Primer; ss; DNA microarray; differential expression analysis; human.

XX OS Homo sapiens.

XX PN US6352829-B1.

XX PD 05-MAR-2002.

XX PF 05-JAN-1999; 99US-00225928.

XX PR 21-MAY-1997; 97US-00859998.

XX PA (CLON-) CLONTECH LAB INC.

XX PI Chenchik A, Jokhadze G, Bibilashvili R;

XX DR WPI; 2002-314699/35.

PT Producing sub-population of labeled nucleic acids, useful for analyzing  
PT differences in RNA profiles between several different physiological  
PT sources, using set of distinct gene specific primers.

XX PS Example 3; SEQ ID NO 1216; 11pp; English.

XX CC The invention relates to producing a sub-population of labeled nucleic  
XX acids (NAs) comprising contacting a NA sample from a physiological  
XX source, with a pool of 50 distinct gene specific primers under suitable  
XX conditions to enzymatically generate sub-population of NAs, where each  
XX gene specific primer has a sequence complementary to a distinct mRNA, and  
XX each labeled NA is generated using a single gene specific primer. The  
XX method is useful for producing a sub-population of labeled NAs which is  
XX useful for analyzing the differences in the RNA profiles between several  
XX different physiological sources, where the method comprises producing  
XX subpopulation of labeled NAs for the different physiological sources,  
XX comprising the populations for each physiological source to identify  
XX differences in the population, where the comparison is preferably  
XX performed by hybridizing the labeled NAs for each of the distinct  
XX physiological sources to an array of probe NAs stably associated with the  
XX surface of a substrate to produce a hybridisation pattern for each of the  
XX sources, and comparing the patterns for each of the sources, where  
XX differential gene expression assays are utilised in differential  
XX expression analysis of diseased a normal tissue e.g. neoplastic a normal  
XX tissue, or different tissue or sub-tissue types. The present sequence is a  
XX human gene specific PCR primer used in the method of the invention. Note:  
XX The sequence data for this patent did not form part of the printed  
XX specification, but was obtained in electronic format directly from USPTO  
XX at <http://wipo.segdata.uspto.gov/sequence.htm?docID=6352829B1>

XX SQ Sequence 26 BP; 7 A; 5 C; 9 G; 5 T; 0 U; 0 Other;

Query Match 2.1%; Score 21.2; DB 1; Length 26;

Best Local Similarity 88.5%; Pred. No. 1.2e+03;  
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 867 GGGATTACAGCGTGAGCCACCACGC 892  
DB 1 GGGATTACAGCGTGAGCCACCACGC 26

RESULT 394

ABZ22656/C  
ID ABZ22656 standard; DNA; 26 BP.

XX AC ABZ22656;

XX DT 31-MAR-2003 (first entry)

XX DE Human PEPT1 PCR primer PEPT1#1 R.

XX KW Human; PEPT1; PEPT2; intestinal peptide transporter; transport;  
KW transporter; PCR primer; ss.

XX OS Homo sapiens.

XX PN WO2002100172-A1.

XX PD 19-DEC-2002.

XX PF 11-JUN-2002; 2002WO-US018686.

XX PR 11-JUN-2001; 2001US-0297732P.

XX PR 01-MAR-2002; 2002US-0361002P.

XX PA (XENO-) XENOPORT INC.

XX PI Zerangue N, Dias T, Dower WJ;

XX DR WPI; 2003-148722/14.

PT Screening for agents, conjugates or their moieties for transport by PEPT2  
PT transporter, by contacting cell expressing transporter with the agent,  
PT and detecting their passage pass into and/or through the transporter.

XX PS Example; Page 23; 43pp; English.

XX CC The present invention describes a method (M1) of screening for agents,  
XX conjugates or conjugate moieties (I), for transport by PEPT2 (an  
XX intestinal peptide transporter) transporter (II), comprising providing a  
XX cell expressing (II), contacting the cell with (I), and determining if  
XX (I) passes into and/or through the cell by the way of (II). Also  
XX described: (1) a conjugate (III), comprising an agent linked to a  
XX conjugate moiety that is a substrate for (II), where the conjugate shows  
XX a Vmax of at least 1 % of Gly-Sar for (II), where the agent has a  
XX pharmaceutical activity without the conjugate moiety, and the conjugate  
XX has a greater Vmax for PEPT2 than the agent without the conjugate moiety;  
XX and (2) manufacturing (M2) a pharmaceutical composition, by linking an  
XX agent to a conjugate moiety to form a conjugate, where the conjugate is  
XX transported by (II) with a Vmax of at least 1 % of the Vmax of the  
XX substrate Gly-Sar, and formulating the conjugate with a carrier as a  
XX pharmaceutical composition. (III) is useful for treatment, by orally  
XX administering (III) to a patient, where the agent exerts a  
XX pharmacological effect in the patient who is free of a disease of brain,  
XX kidney, lung or spleen. The present sequence represents a PCR primer for  
XX human PEPT1, which is used in an example from the present invention

XX SQ Sequence 26 BP; 5 A; 9 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 2.1%; Score 21.2; DB 1; Length 26;  
Best Local Similarity 88.5%; Pred. No. 1.2e+03;  
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 867 GGGATTACAGCGTGAGCCACCACGC 892

DB 26 GGGATTACAGCGTGAGCCACCACGC 1

RESULT 395  
AD112547/C  
ID AD112547 standard; DNA; 26 BP.  
XX  
XX AD112547;  
XX  
XX  
XX  
XX 22-APR-2004 (first entry)  
XX  
XX  
XX Mutant human BRCA1 genomic DNA resulting from deletion 4 Segid 30.  
XX  
XX  
XX ds; cancer; human; tumour suppressor;  
XX breast cancer susceptibility gene 1; BRCA1; repetitive Alu;  
XX ovarian cancer; recombination; mutant.  
XX  
XX Homo sapiens.  
XX  
XX WO2003104474-A2.  
XX  
XX 18-DEC-2003.  
XX  
XX 09-JUN-2003; 2003WO-US018098.  
XX  
XX 07-JUN-2002; 2002US-0387132P.  
XX  
XX 09-AUG-2002; 2002US-0402430P.  
XX  
XX (MYRI-) MYRIAD GENETICS INC.  
XX  
XX Scholl T, Hendrickson EC, Ward B, Pruss D;  
XX  
XX WPI; 2004-062369/06.  
XX  
XX  
XX Predicting a predisposition to cancer in a patient comprising detecting a  
XX deletion in the BRCA1 gene that results from the unequal crossover  
XX between a pair of repetitive sequences in the BRCA1 gene.  
XX  
XX  
XX Disclosure; SEQ ID NO 30; 59pp; English.  
XX  
XX This invention relates to a novel method for predicting a predisposition  
XX to cancer in a patient by detecting large deletions in the human tumour  
XX suppressor gene identified as the breast cancer susceptibility gene 1  
XX (BRCA1). Specifically, it refers to deletions that result from the  
XX unequal crossover between a pair of repetitive Alu sequences in the BRCA1  
XX gene, such that the recombined nucleotide sequence containing the  
XX deletion indicates a predisposition to breast and ovarian cancer. The  
XX present invention describes newly discovered deletion mutations that are  
XX believed to be deleterious and cause significant alterations in the  
XX structure or biochemical function of BRCA1. Accordingly, it provides  
XX methods for detecting such mutants, as well as identifying and screening  
XX for cytostatic compounds useful for treating or preventing cancers  
XX associated with a BRCA1 genetic variant. This polynucleotide is a mutant  
XX human BRCA1 genomic DNA fragment that arises as a result of a  
XX recombination event (deletion 4), which causes the omission of exons 16  
XX and 17, given in an exemplification of the invention.  
XX  
XX Sequence 26 BP; 7 A; 6 C; 8 G; 5 T; 0 U; 0 Other;  
XX  
XX  
XX Query Match 2.1%; Score 21.2; DB 1; Length 26;  
XX Best Local Similarity 88.5%; Pred. No. 1.2e+03;  
XX Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

DT 11-JUN-1997 (first entry)  
XX  
XX Primer Alu-S binds Alu repeat sequence.  
XX  
XX  
XX Bubble; interspersed repetitive element; ligation; annealing; primer;  
XX PCR; polymerase chain reaction; amplification; chromosomal aberration;  
XX genetic disorder; ss.  
XX  
XX Synthetic.  
XX  
XX US5597694-A.  
XX  
XX 28-JAN-1997.  
XX  
XX 07-OCT-1993; 93US-00133629.  
XX  
XX 07-OCT-1993; 93US-00133629.  
XX  
XX (MASI ) MASSACHUSETTS INST TECHNOLOGY.  
XX  
XX Munroe DJ, Housman DE;  
XX  
XX WPI; 1997-108321/10.  
XX  
XX  
XX Amplification of nucleic acid having interspersed repetitive element -  
XX using bubble oligo:nucleotide.  
XX  
XX Disclosure; Col 17; 16pp; English.  
XX  
XX The invention relates to the amplification of region of DNA containing  
XX interspersed repetitive elements (IRE) such as the Alu repeat sequence  
XX (AAT62346). The method involves ligating a double stranded DNA structure  
XX with a non-complementary region, a 'bubble', in the centre (e.g. see  
XX AAT62343-4), to restriction digested fragments of regions containing  
XX IREs. The ligation results in a double stranded DNA molecule containing  
XX at least one 'bubble' at either end. After denaturing the structure,  
XX amplification of the IRE-containing region proceeds by PCR using primers  
XX targeted to the IRE sequence (e.g. AAT62347-50) and to the sequence in  
XX the 'bubble' region (e.g. see AAT62345). The primer presented here binds  
XX to nucleotides 216-236 of the Alu-S polymorphic repeat sequence. The  
XX method can be used to detect the presence or absence of a chromosomal  
XX aberration e.g. in a genetic disorder, in a test organism  
XX  
XX Sequence 21 BP; 5 A; 3 C; 9 G; 4 T; 0 U; 0 Other;  
XX  
XX  
XX Query Match 2.1%; Score 21; DB 1; Length 21;  
XX Best Local Similarity 100.0%; Pred. No. 1e+03;  
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 967 ATCTCGGCTCAGTCACTC 987  
Db 21 ATCTCGGCTCAGTCACTC 1

RESULT 397  
AAF95738  
ID AAF95738 standard; DNA; 21 BP.  
XX  
XX  
XX AAF95738;  
XX  
XX 06-JUN-2001 (first entry)  
XX  
XX  
XX Human gene single nucleotide polymorphism #499.  
XX  
XX Human; variant thrombospondin 1; variant thrombospondin 4; SNP;  
XX polymorphism; vascular disease; coronary artery disease; forensics;  
XX myocardial infarction; atherosclerosis; stroke; venous thromboembolism;  
XX pulmonary embolism; paternity test; ds.  
XX  
XX Homo sapiens.  
XX  
XX  
XX Key Location/Qualifiers  
XX FT Variation replace(11,C)

```
FT      /*tag= a
XX      /standard_name="single nucleotide polymorphism"
XX
XX
XX      WO200118250-A2.
XX
XX      15-MAR-2001.
XX
XX      07-SEP-2000; 2000WO-US024503.
XX
XX      10-SEP-1999; 99US-0153357P.
XX      26-JUL-2000; 2000US-0220947P.
XX      16-AUG-2000; 2000US-0225724P.
XX
XX      (MHED ) WHITEHEAD INST BIOMEDICAL RES.
XX      (MILL-) MILENNIUM PHARM INC.
XX
XX      Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ,
XX      WPI; 2001-226749/23.
XX
XX      Nucleic acids comprising single nucleotide polymorphisms, useful in
XX      applications such as forensics, paternity testing, medicine, genetic
XX      analysis and phenotype correlations to diseases such as diabetes and
XX      atherosclerosis.
XX
XX      Example; Page 83; 242pp; English.
XX
XX      The present invention provides a method of diagnosing a vascular disease
XX      in an individual, involving determining the sequence at various
XX      polymorphic sites within the human chromosome 1 and thrombospondin 4
XX      genes. The sequences at a number of polymorphic sites are also provided
XX      in the specification. In particular, the method can be used in the
XX      diagnosis of atherosclerosis, myocardial infarction, coronary heart
XX      disease, stroke, peripheral vascular diseases, venous thrombembolism and
XX      pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
XX      useful in forensics, paternity testing, genetic analysis and phenotype
XX      correlations to diseases. The present sequence is an example of one of
XX      the human gene SNPs shown in the specification
XX
XX      Sequence 21 BP; 5 A; 6 C; 5 G; 5 T; 0 U; 0 Other;
XX
XX      Query Match      2.1%; Score 21; DB 1; Length 21;
XX      Best Local Similarity 100.0%; Pred. No. 1e+03;
XX      Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY      383 CCTCCCAAGTGTGGGATTA 403
XX      |||||
XX      1 CCTCCCAAGTGTGGGATTA 21
XX
XX      RESULT 398
XX      AAH24567/c
XX      ID      AAH24567 standard; DNA; 21 BP.
XX
XX      AAH24567;
XX
XX      07-AUG-2001 (first entry)
XX
XX      Human Alu sequence-specific primer Alu-Sense.
XX
XX      Human; Alu; metastatic potential determination; cancer;
XX      chorioallantoic membrane; CAM; avian embryo; intravasation;
XX      cell migration; drug screening; PCR primer; ss.
XX
XX      Homo sapiens.
XX
XX      US6228345-B1.
XX
XX      08-MAY-2001.
XX
XX      04-AUG-1999; 99US-00366840.
XX
XX      04-AUG-1999; 99US-00366840.
XX
```

```
XX
XX      (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX
XX      Osowski L;
XX
XX      WPI; 2001-342659/36.
XX
XX      Determining the metastatic potential of cancer cells and measuring
XX      invasion, comprises introducing cancer cells into the upper
XX      chorioallantoic membrane (CAM) and detecting cancer cell migration from
XX      the upper CAM to the lower CAM.
XX
XX      Example; Col 11; 24pp; English.
XX
XX      The invention relates to a method for determining the metastatic
XX      potential of cancer cells derived from a subject with cancer. The method
XX      comprises introducing a cancer cell sample into the upper chorioallantoic
XX      membrane (CAM) of an avian embryo into which an artificially generated
XX      air pocket has been created, incubating the embryo for intravasation to
XX      occur, and detecting migration of the cancer cells from the upper CAM to
XX      the lower CAM. The present sequence was used to selectively amplify human
XX      specific Alu repeat sequences, which will be present in the cancer cell
XX      DNA but not in the DNA of the CAM. This procedure enables detection of
XX      the migration of inoculated cancer cells into the lower CAM. The method
XX      is useful for measuring the metastatic potential of cancer cells, for
XX      measuring the ability of the cancer cells to invade blood vessels, and as
XX      a drug screening assay for the identification of agents having anti-
XX      metastatic activity and thereby modulating the metastatic potential of
XX      cancer cells. The method may also be used to screen for agents capable of
XX      inhibiting cancer cell intravasation, and to detect phenotypic changes
XX      effected by genetic manipulation of cancer cells that result in changes
XX      in metastatic potential
XX
XX      Sequence 21 BP; 5 A; 8 C; 3 G; 5 T; 0 U; 0 Other;
XX
XX      Query Match      2.1%; Score 21; DB 1; Length 21;
XX      Best Local Similarity 100.0%; Pred. No. 1e+03;
XX      Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY      390 AAGTCTGGGATTACAGGCGT 410
XX      |||||
XX      21 AAGTCTGGGATTACAGGCGT 1
XX
XX      ABS98163 standard; DNA; 21 BP.
XX
XX      ABS98163;
XX
XX      23-DEC-2002 (first entry)
XX
XX      Human multidrug resistance gene polymorphic sequence #65.
XX
XX      Human; ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;
XX      cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;
XX      adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR112;
XX      aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
XX      cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
XX      epoxide hydrolase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
XX      glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
XX      HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
XX      NADPH quinone oxidoreductase 2; NQO2; sulfoxidoreductase thermolabile; STM;
XX      UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
XX      UGT2B7; UDP-glucuronosyl transferase; UGT2B15; uridine kinase receptor; URA;
XX      multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
XX      acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
XX      altered drug metabolism; pulmonary; cardiovascular function; colorectal tumour;
XX      central nervous system; pulmonary; immunological; SNP;
XX      single nucleotide polymorphism.
XX
XX      Homo sapiens.
XX
XX      OS
```

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XX WO200257410-A2.
XX
XX 25-JUL-2002.
XX
XX 28-NOV-2001; 2001WO-US044838.
XX
XX 28-NOV-2000; 2000US-00724389.
XX
XX (DNAS-) DNA SCI LAB INC.
XX
XX Guida M, Hall J;
XX
XX WPI; 2002-698522/75.
XX
XX Isolated nucleic acid molecules having polymorphisms in known human genes
XX e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers
XX for locating, identifying and characterizing the genes responsible for
XX disorder-related traits.
XX
XX Example 22; Page 144; 714p; English.
XX
XX This invention relates to the sequence of an isolated nucleic acid
XX molecule comprising at least one base variation from that of a known
XX human cytochrome P450 A1 (CYP450A1), cytochrome P450 A2 (CYP450A2),
XX cytochrome P450 02B1 (CYP45002B1), adrenergic receptor beta1 (ADRB1),
XX aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
XX (ARNT), cathepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding
XX inhibitor (DBI), epoxide hydrolase 2 (EPHX2), 5-lipoxygenase activating
XX protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
XX transferase (HNMT), NADPH quinone oxidoreductase 2 (NQO2),
XX sulfolactonase thermolabile (STM), UDP-glucuronosyl transferase 2B4
XX (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
XX transferase (UGT2B5), uronkinase receptor (UPR), multidrug resistance 1
XX (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
XX (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic
XX receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
XX The polymorphisms in the human genes cited in the invention are useful as
XX genetic linkage markers for locating and characterizing the genes that
XX are responsible for specific traits within the genome and eventually
XX identifying the genes responsible for a variety of disorder-related
XX traits as a result of their e.g., overexpression, constitutive
XX expression, mutation or underexpression, which may be used in diagnosing
XX and/or treating the disorders. The nucleic acid molecules comprising the
XX polymorphic sequences contained in CYP450A1, CYP450A2, CYP4502B1,
XX ANNT, EPHX2, GST12, NNMT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B5, AHR,
XX MDR1 and/or MDR3 are useful for screening individuals for altered drug
XX metabolism. The polymorphic sequences contained in CYP450A1, CYP450A2,
XX AHR, MDR1 and/or MDR3 may also be used to screen individuals for
XX susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
XX used to screen for altered cardiovascular function, in COX2 for altered
XX susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
XX nervous system function, in FLAP and HNMT for altered pulmonary,
XX immunological or haematological function, in KLR2 for altered serine
XX protease activity in the prostate, in LTF for altered immunological or
XX haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
XX peripheral nervous system function. The present sequence represents a
XX polymorphic DNA sequence of the invention.
XX
XX Sequence 21 BP; 5 A; 6 C; 7 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 2.1%; Score 21; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 1e+03;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 868 GGATTACAGCGCTGAGCCACC 888
XX |||||
XX 1 GGATTACAGCGCTGAGCCACC 21
XX
XX RESULT 400
XX ADF38789/c
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```
ID ADF38789 standard; DNA; 21 BP.
XX
XX ADF38789;
XX
XX 12-FEB-2004 (first entry)
XX
XX Human TNF-alpha induced apoptosis-related DNA - SEQ ID 17.
XX
XX tumour necrosis factor; TNF-alpha; apoptosis; antiapoptotic;
XX antisense gene therapy; human; ds.
XX
XX Homo sapiens.
XX
XX JP2003289866-A.
XX
XX 14-OCT-2003.
XX
XX 01-APR-2002; 2002JP-00098130.
XX
XX 01-APR-2002; 2002JP-00098130.
XX
XX (GENO-) GENO FUNCTION KK.
XX (DOKU-) DOKURITSU GYOSEI HOJIN SANGYO GIUTSU SO.
XX (TAHI/) TAHIRA K.
XX (KAWA/) KAWASAKI H.
XX
XX WPI; 2004-038428/04.
XX
XX Novel polynucleotide encoding protein involved in tumor necrosis factor
XX induced apoptosis, useful as probe to acquire perfect length cDNA of gene
XX related to TNF-alpha induced apoptosis.
XX
XX Claim 1; SEQ ID NO 17; 18p; Japanese.
XX
XX The invention relates to a novel polynucleotide which encodes a protein
XX involved in tumour necrosis factor (TNF)-alpha induced apoptosis. The
XX polynucleotide of the invention demonstrates antiapoptotic activity and
XX may be useful during gene therapy as an antisense polynucleotide for
XX suppressing the expression of the protein involved in TNF-alpha induced
XX apoptosis and for elucidating the mechanism of TNF-alpha induced
XX apoptosis. The current sequence is that of the human TNF-alpha induced
XX apoptosis-related DNA of the invention.
XX
XX Sequence 21 BP; 9 A; 7 C; 0 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 2.1%; Score 21; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 1e+03;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 776 ATTTTGTAGTACAGATGCGGTT 796
XX |||||
XX 21 ATTTTGTAGTACAGATGCGGTT 1
XX
XX RESULT 401
XX ADO55495
XX ID ADO55495 standard; DNA; 21 BP.
XX
XX ADO55495;
XX
XX 26-AUG-2004 (first entry)
XX
XX HIV gene expression analysis primer SB704 following siRNA inhibition.
XX sb; primer; anti-HIV; virucide; gene therapy; small interfering RNA;
XX siRNA; HIV; genome; diagnosis.
XX
XX Human immunodeficiency virus 1.
XX
XX WO2004047764-A2.
XX
XX 10-JUN-2004.
XX
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PF 24-NOV-2003; 2003WO-US037860.
XX
XX 22-NOV-2002; 2002US-0428631P.
PR 04-FEB-2003; 2003US-0444893P.
XX
XX (UTMA-) UNIV MASSACHUSETTS.
PA
XX Stevenson M, Jacque J;
XX
XX WPI; 2004-441081/41.
DR
XX
XX New small interfering RNA (siRNA) comprising a sequence complementary to
PT a portion of the HIV genome to mediate RNA interference (RNAi), useful
PT for diagnosing, preventing and/or treating HIV infections.
XX
XX Disclosure; SEQ ID NO 18; 59pp; English.
XX
XX The invention relates to a small interfering RNA (siRNA) comprising a
XX sequence complementary to a portion of the HIV genome to mediate RNA
XX interference (RNAi). The methods and compositions of the present
XX invention are useful for the diagnosis, prevention and/or treatment of
XX HIV infections. This sequence corresponds to a PCR primer to carry out
XX real time PCR to determine gene expression after expression interference
XX by the siRNAs of the invention.
XX
XX Sequence 21 BP; 4 A; 3 C; 9 G; 5 T; 0 U; 0 Other;
SQ
Query Match 2.1%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 863 TGCTGGATTACAGCGCTGAG 883
DB 1 TGCTGGATTACAGCGCTGAG 21
RESULT 402
ADH13395/C
ID ADH13395 standard; DNA; 23 BP.
XX
XX ADH13395;
AC
XX 11-MAR-2004 (first entry)
DT
XX Human malignant neoplasia-related PCR primer SeqID244.
DE
XX malignant neoplasia; cytostatic; breast cancer; ovarian cancer;
XX gastric cancer; colon cancer; oesophageal cancer; mesenchymal cancer;
XX bladder cancer; non-small cell lung cancer; human; PCR; primer; ss.
XX
XX Homo sapiens.
OS
XX
XX EPI165034-A2.
PN
XX 26-NOV-2003.
PD
XX 09-MAY-2003; 2003EP-00010447.
PF
XX 21-MAY-2002; 2002EP-00010291.
PR 13-FEB-2003; 2003EP-00003112.
XX
XX (FARB ) BAYER AG.
PA
XX
XX Wirtz R, Munnes M, Kallabis H;
PI
XX WPI; 2004-073279/08.
DR
XX
XX Predicting, diagnosing or prognosing malignant neoplasia by detecting at
PT least two markers, where the markers are genes from one or more
PT chromosomal regions altered in malignant neoplasia,.
XX
XX Disclosure; SEQ ID NO 244; 267pp; English.
XX
```

```
CC This invention relates to a novel method for the prediction, diagnosis,
CC or prognosis of malignant neoplasia by the detection of at least two
CC markers. The invention may also be useful for the development of
CC cytostatic compounds through the regulation of the expression of a gene
CC or activity of a protein associated with malignant neoplasia. The method
CC is useful for prediction, diagnosis or prognosis of malignant neoplasia
CC such as breast cancer, ovarian cancer, gastric cancer, colon cancer,
CC oesophageal cancer, mesenchymal cancer, bladder cancer or non-small cell
CC lung cancer. The polynucleotides and polypeptides defined in the
CC specification, antisense polynucleotides targeting the polynucleotides,
CC antibodies targeting either one of the polynucleotides or polypeptides,
CC and compounds identified by the screening methods are useful for
CC preventing or treating malignant neoplasia. The disease treated is
CC preferably breast cancer. The present sequence is that of a PCR primer
CC which was used in the exemplification of the invention.
XX
XX Sequence 23 BP; 6 A; 3 C; 9 G; 4 T; 0 U; 1 Other;
SQ
Query Match 2.1%; Score 21; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 667 ATCTTGCTCTCTGCAACCTC 687
DB 23 ATCTTGCTCTCTGCAACCTC 3
RESULT 403
AAV19046/C
ID AAV19046 standard; DNA; 24 BP.
XX
XX AAV19046;
AC
XX 28-JUL-1998 (first entry)
DT
XX
XX Alu PCR primer 3.
DE
XX
XX PCR; primer; amplification; Alu repeat sequence; vector;
XX circular yeast artificial chromosome; YAC; ss.
XX
XX Synthetic.
OS
XX Saccharomyces sp.
XX
XX WO9801573-A1.
PN
XX 15-JAN-1998.
PD
XX 09-JUL-1996; 96WO-US011478.
PF
XX 09-JUL-1996; 96WO-US011478.
PR
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Resnick MA, Lationov VL, Kouprina NY, Perkins EL;
XX WPI; 1998-110234/10.
DR
XX
XX Preparation of yeast artificial chromosomes - by in vivo recombination
PT using vector comprising yeast centromere, marker, yeast telomere and
PT nucleic acid for recombination.
XX
XX Example 2; Page 61; 117pp; English.
XX
XX This is the nucleotide sequence for the PCR primer used in the
XX amplification of the 3' fragment of the Alu repeat sequence, which is
XX used as a probe in the method of the invention. It involves the creation
XX and use of circular yeast artificial chromosome (YAC) to selectively
XX clone specific nucleic acids from a background of mixed nucleic acids by
XX introducing the vector(s) into E. coli cells. They can be used to rapidly
XX isolate human DNA where only a part of the sequence of DNA is known.
XX Using the methods large fragments of DNA can be easily cloned and
XX analysed
XX
```



Sequence 24 BP; 4 A; 6 C; 11 G; 3 T; 0 U; 0 Other;  
Query Match 2.1%; Score 20.8; DB 1; Length 24;  
Best Local Similarity 91.7%; Pred. No. 1.2e+03;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Db 675 TCACGTGCAACCTCTGCTCCCGGG 698  
24 TCACGTGCAAGCTCCGCTCCCGGG 1

RESULT 404  
AA27181  
ID AAA27181 standard; DNA; 24 BP.  
XX  
AC AAA27181;  
XX  
DT 11-SEP-2000 (first entry)  
XX  
DE Reverse primer P2 for target sequence human P2 gene.  
XX  
KW P2; CX5C chemokine; Chromosome 5q31; gene therapy; asthma; PCR primer;  
KW allergic rhinitis; urticaria; anaphylactic shock; hives; hay fever; human;  
KW ss.  
XX Homo sapiens.  
XX MO200029621-A2.  
XX  
XX 25-MAY-2000.  
XX  
XX 12-NOV-1999; 99MO-US026931.  
XX  
XX 16-NOV-1998; 98US-00193320.  
XX  
PA (GENE-) GENELABS TECHNOLOGIES INC.  
PA Dolganov G, Novikov A;  
PI WPI; 2000-387825/33.  
XX  
XX WPI; 2000-387825/33.  
XX  
PT Measuring target polynucleotide sequences in biological samples by  
PT contacting sequence-selective primer pairs, forming conjugates with  
PT adaptor molecules, polymerizing target-identifier dimers and quantifying  
PT them.  
XX  
XX Disclosure, Page 99; 103pp; English.  
XX  
XX A novel method for simultaneously determining the level of a number of  
XX target polynucleotides in a sample has been disclosed. The method  
XX involves forming double stranded copies of the target sequence in direct  
XX proportion to the target levels in the original sample. The target  
XX sequence is copied using primer pairs designed to flank a defined region  
XX in the target sequence. The double stranded copies are then cleaved and  
XX reacted with either first or second adaptor sequences. The first and  
XX second conjugate mixtures are then allowed to form dimers with each other  
XX through the target sequences. The adaptor sequences are then removed to  
XX leave target sequence dimers. These dimers are then polymerised to form  
XX dimer multimers. The relative abundances of target identifiers in the  
XX multimer allow expression levels to be determined. This method is useful  
XX for developing polynucleotide abundance level profiles for cells and  
XX tissues under various conditions, stages of development and disease  
XX states, particularly where the target polynucleotide is present at low  
XX levels. The method may also be used in the discovery and evaluation of  
XX candidate therapeutic agents and their effective dosage levels. In  
XX addition to the method described above, the invention also includes the  
XX polynucleotide and polypeptide of P2. P2 is thought to be a member of a  
XX novel chemokine family, denoted CX5C and may be associated with immune  
XX function. Compositions of the P2 polypeptide may be useful in the  
XX treatment of asthma, allergic rhinitis (hay fever), urticaria (hives),  
XX anaphylactic shock and conditions involving immune system  
XX hypersensitivity. The P2 polynucleotide to treat conditions using gene  
XX therapy. The human P2 gene has been localised to chromosome 5, within the

cytokine gene cluster at 5q31. The present sequence is the reverse primer  
P2 for target sequence human P2 gene  
Sequence 24 BP; 4 A; 6 C; 9 G; 5 T; 0 U; 0 Other;  
Query Match 2.1%; Score 20.8; DB 1; Length 24;  
Best Local Similarity 91.7%; Pred. No. 1.2e+03;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Db 636 TCTGTACCCAGGCTGTGAGTCAG 659  
1 TATGTACCCAGGCTGTGAGTCAG 24

RESULT 405  
AA165251  
ID AA165251 standard; DNA; 24 BP.  
XX  
AC AA165251;  
XX  
DT 29-NOV-2001 (first entry)  
XX  
DE Human dihydroorotase 15 PCR primer 2.  
XX  
XX Human; dihydroorotase 15; cytosolic; virucidal; immunomodulatory;  
KW antiinflammatory; haemostatic; anti-HIV; gene therapy; cancer;  
KW haemopathy; human immunodeficiency virus; HIV; infection;  
KW immunological disease; inflammatory disease; PCR primer; ss.  
XX  
XX Homo sapiens.  
XX MO200172979-A1.  
XX  
XX 04-OCT-2001.  
XX  
XX 26-MAR-2001; 2001MO-CN000439.  
XX  
XX 27-MAR-2000; 2000CN-00115187.  
XX  
PA (SHAN-) SHANGHAI BOWINDOW GENE DEV INC.  
PA Mao Y, Xie Y;  
PI WPI; 2001-597115/67.  
XX  
XX New human dihydroorotase 15 for diagnosing and treating malignant  
PT neoplasm, hemopathy, human immunodeficiency virus infection,  
PT immunological diseases and various inflammations.  
PT  
XX  
XX Example 2; Page 17; 36pp; Chinese.  
XX  
XX The invention relates to an isolated polypeptide of human dihydroorotase  
XX 15 comprising a sequence of 137 amino acids or its fragment, analogue or  
XX derivative. The polypeptide and the polynucleotide encoding it are useful  
XX in the diagnosis and treatment of malignant neoplasm, haemopathy, human  
XX immunodeficiency virus (HIV) infection, immunological diseases and  
XX various inflammatory diseases. The present sequence is a primer used to  
XX isolate a polynucleotide encoding the polypeptide of the invention  
XX

Sequence 24 BP; 4 A; 9 C; 6 G; 5 T; 0 U; 0 Other;  
Query Match 2.1%; Score 20.8; DB 1; Length 24;  
Best Local Similarity 91.7%; Pred. No. 1.2e+03;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Db 926 GGAATCTCACTCTGTATCCAGGC 949  
1 GGAATCTCACTCTGTATCCAGGC 24

RESULT 406  
AAF24627/c  
ID AAF24627 standard; DNA; 24 BP.

```
XX AC AAF24627;
XX XX
DT 20-APR-2001 (first entry)
XX XX
DE Primer for a polymorphism at base 1962 of HMG-CoA reductase gene.
XX XX
KM 3-hydroxy-3-methylglutaryl-coenzyme A reductase gene; dyslipidemia;
KW HMG-CoA reductase gene; genetic marker; cardiovascular disease;
XX myocardial infarction; stroke; PCR primer; ss.
XX OS Homo sapiens.
XX PN WO20079003-A1.
XX PD 28-DEC-2000.
XX PF 19-JUN-2000; 2000WO-GB002396.
XX PR 19-JUN-2000; 2000WO-GB002396.
XX PS 22-JUN-1999; 99GB-00014440.
XX PA (ASTR ) ASTRAZENECA UK LTD.
XX PI March RE, Thornton SM;
XX DR WPI; 2001-102732/11.
XX PT Novel polymorphisms in human 3-hydroxy-3-methylglutaryl-coenzyme A (HMG-
XX PT CoA) gene useful for diagnosis and treatment of HMG-CoA reductase-
XX PT mediated diseases such as dyslipidemia and other cardiovascular diseases.
XX PS Example 1; Page 31; 45pp; English.
XX XX
CC PCR primers AAF24627-28 were used to detect a polymorphism in the human 3
CC -hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA) reductase gene. The
CC polymorphism is present in the promoter region, exon 15, introns 2, 5, 15
CC or 18. HMG-CoA reductase polymorphisms are useful as genetic markers in
CC linkage studies. Detection of the presence of the polymorphisms is useful
CC for assessing the pharmacogenetics of therapeutic compounds in the
CC treatment of HMG-CoA reductase mediated diseases. The polymorphisms are
CC useful for diagnosis of HMG-CoA reductase mediated diseases such as
CC dyslipidemia and other cardiovascular diseases such as myocardial
CC infarction and stroke. HMG-CoA reductase antagonist drugs are used to
CC treat dyslipidemia and other cardiovascular diseases such as myocardial
CC infarction and stroke
XX SQ Sequence 24 BP; 5 A; 8 C; 8 G; 3 T; 0 U; 0 Other;
XX
Query Match 2.1%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.2e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 931 CTCACCTGCTTACCCAGGCTGAG 954
DB 24 CTCACCTGCTGAGCCAGGCTGAG 1
XX
RESULT 407
AAF24635/C
ID AAF24635 standard; DNA; 24 BP.
XX
AC AAF24635;
XX XX
DT 20-APR-2001 (first entry)
XX XX
DE Primer for polymorphism at base 37 of human HMG-CoA reductase gene.
XX XX
KM 3-hydroxy-3-methylglutaryl-coenzyme A reductase gene; dyslipidemia;
KW HMG-CoA reductase gene; genetic marker; cardiovascular disease;
XX myocardial infarction; stroke; PCR primer; ss.
XX OS Homo sapiens.
XX XX
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PN WO20079003-A1.
XX XX
PD 28-DEC-2000.
XX PF 19-JUN-2000; 2000WO-GB002396.
XX PR 22-JUN-1999; 99GB-00014440.
XX PS (ASTR ) ASTRAZENECA UK LTD.
XX PI March RE, Thornton SM;
XX DR WPI; 2001-102732/11.
XX PT Novel polymorphisms in human 3-hydroxy-3-methylglutaryl-coenzyme A (HMG-
XX PT CoA) gene useful for diagnosis and treatment of HMG-CoA reductase-
XX PT mediated diseases such as dyslipidemia and other cardiovascular diseases.
XX PS Example 1; Page 32; 45pp; English.
XX XX
CC PCR primers AAF24635-36 were used to detect a polymorphism in the human 3
CC -hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA) reductase gene. The
CC polymorphism is present in the promoter region, exon 15, introns 2, 5, 15
CC or 18. HMG-CoA reductase polymorphisms are useful as genetic markers in
CC linkage studies. Detection of the presence of the polymorphisms is useful
CC for assessing the pharmacogenetics of therapeutic compounds in the
CC treatment of HMG-CoA reductase mediated diseases. The polymorphisms are
CC useful for diagnosis of HMG-CoA reductase mediated diseases such as
CC dyslipidemia and other cardiovascular diseases such as myocardial
CC infarction and stroke. HMG-CoA reductase antagonist drugs are used to
CC treat dyslipidemia and other cardiovascular diseases such as myocardial
CC infarction and stroke
XX SQ Sequence 24 BP; 5 A; 8 C; 8 G; 3 T; 0 U; 0 Other;
XX
Query Match 2.1%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.2e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 931 CTCACCTGCTTACCCAGGCTGAG 954
DB 24 CTCACCTGCTGAGCCAGGCTGAG 1
XX
RESULT 408
AAH75870
ID AAH75870 standard; DNA; 24 BP.
XX
AC AAH75870;
XX XX
DT 26-OCT-2001 (first entry)
XX XX
DE Human reverse transcriptase 13 coding sequence PCR primer #2.
XX XX
KM Human; reverse transcriptase 13; cytosolic; virucide; immunomodulatory;
KW antiinflammatory; haemostatic; gene therapy; malignant tumour;
KW haemopathy; HIV infection; immunological disease; inflammation;
KW developmental disorder; PCR primer; ss.
XX OS Homo sapiens.
XX PN WO200164893-A1.
XX PD 07-SEP-2001.
XX PF 26-FEB-2001; 2001WO-CN000280.
XX PR 02-MAR-2000; 2000CN-00111806.
XX PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX PI Mao Y, Xie Y;
XX XX
```

DR WPI; 2001-550183/61.  
XX  
XX New human reverse transcriptase 13 for diagnosing and treating  
PT developmental disorders, malignant tumor, hemopathy, human  
PT immunodeficiency virus infection, immunological diseases and  
PT inflammations.  
XX  
XX Example 3; Page 12; 34pp; Chinese.  
XX  
XX The present invention relates to human reverse transcriptase 13 and its  
CC coding sequence (see AA175868 and AA66428). The reverse transcriptase  
CC and its coding sequence are useful in the diagnosis and treatment of  
CC malignant tumor, haemopathy, HIV infection, immunological diseases,  
CC various inflammations and developmental disorders. The present sequence  
CC is a PCR primer, which was used in an example from the present invention  
XX  
SQ Sequence 24 BP; 4 A; 9 C; 6 G; 5 T; 0 U; 0 Other;  
  
Query Match 2.1%; Score 20.8; DB 1; Length 24;  
Best Local Similarity 91.7%; Pred. No. 1.2e+03;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 926 GGAACTCACTCTGTTACCCAGGC 949  
DB 1 GGAGTCTCACTGTGACCCAGGC 24  
  
RESULT 409  
AA12447  
ID AA12447 standard; DNA; 24 BP.  
XX  
AC AA12447;  
XX  
DT 18-DEC-2001 (first entry)  
XX  
DE Ribosome s19e protein 11, RT-PCR primer #2.  
XX  
XX Human; ribosome s19e protein 11; cytosolic; virucidal; immunomodulatory;  
KM anti-inflammatory; haemostatic; malignant tumor; haemopathy; ss;  
KM human immunodeficiency virus; HIV; immunological disease; inflammation;  
KW PCR primer.  
XX  
OS Homo sapiens.  
XX  
PN WO200164866-A1.  
XX  
XX 07-SEP-2001.  
XX  
XX 26-FEB-2001; 2001WO-CN000219.  
XX  
XX 02-MAR-2000; 2000CN-00111831.  
XX  
XX (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.  
XX  
XX Mao Y, Xie Y;  
XX  
XX WPI; 2001-582156/65.  
XX  
XX Ribosome s19e protein 11 and encoded polynucleotide for diagnosis and  
PT treatment of malignant tumors, hemopathy, HIV infection, immunological  
PT diseases and inflammations.  
XX  
XX Example 2; Page 12; 34pp; Chinese.  
XX  
XX The invention relates to an isolated polypeptide of ribosome s19e protein  
CC 11 and its corresponding coding sequence. The polypeptide and encoded  
CC polynucleotide are applicable in diagnosis and treatment of malignant  
CC tumours, haemopathy, human immunodeficiency virus (HIV) infection,  
CC immunological diseases and various inflammations. The present sequence  
CC represents the reverse transcriptase (RT) PCR primer #2 used in analysis  
CC of ribosome s19e protein 11  
XX  
SQ Sequence 24 BP; 4 A; 4 C; 7 G; 9 T; 0 U; 0 Other;

Query Match 2.1%; Score 20.8; DB 1; Length 24;  
Best Local Similarity 91.7%; Pred. No. 1.2e+03;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 181 TAGAGATGAGTTCTCCATGTTG 204  
DB 1 TAGACATGGGGTTCTCCATGTTG 24  
  
RESULT 410  
AA16532  
ID AA16532 standard; DNA; 24 BP.  
XX  
AC AA16532;  
XX  
XX 11-DEC-2001 (first entry)  
XX  
XX Human pterin-molybdenum oxidoreductase 10 cDNA PCR primer #2.  
DE  
XX Human; pterin-molybdenum oxidoreductase 10; cancer; haemopathy;  
XX immunological disease; HIV infection; inflammation; gene therapy;  
KM PCR primer; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200172788-A1.  
XX  
XX 04-OCT-2001.  
XX  
XX 23-MAR-2001; 2001WO-CN000393.  
XX  
XX 24-MAR-2000; 2000CN-00115110.  
XX  
XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.  
XX  
XX Mao Y, Xie Y;  
XX  
XX WPI; 2001-602841/68.  
XX  
XX New polypeptide for the diagnosis and treatment of malignant neoplasm,  
PT hemopathy, HIV infection, immunological diseases and inflammations,  
PT comprises the human pterin-molybdenum oxidoreductase 10 protein.  
XX  
XX Example 2; Page 17; 36pp; Chinese.  
XX  
XX The present invention provides the protein and coding sequences of human  
CC pterin-molybdenum oxidoreductase 10. The sequences can be used in the  
CC treatment of cancer, haemopathy, HIV infection, immunological diseases  
CC and inflammation. The present sequence is a PCR primer for the coding  
CC sequence of the invention  
XX  
SQ Sequence 24 BP; 5 A; 5 C; 8 G; 6 T; 0 U; 0 Other;  
  
Query Match 2.1%; Score 20.8; DB 1; Length 24;  
Best Local Similarity 91.7%; Pred. No. 1.2e+03;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 638 TGTCAACCAGCTGAGTGACATG 661  
DB 1 TGTCAATCAGCTGAGTACATG 24  
  
RESULT 411  
AA171673/C  
ID AA171673 standard; DNA; 24 BP.  
XX  
XX AA171673;  
XX  
XX 15-JAN-2002 (first entry)  
XX  
XX Human myosin heavy chain 12-14 coding sequence PCR primer #1.  
DE

KW Human; myosin heavy chain 12-14; Prader Willi syndrome; PCR primer;  
KM Klinefelter syndrome; inflammation; kinetic illness; gene therapy; ss.  
XX Homo sapiens.  
OS  
FN WO200185752-A1.  
XX  
PD 15-NOV-2001.  
XX  
PF 28-APR-2001; 2001WO-CN000670.  
XX  
PR 29-APR-2000; 2000CN-00115544.  
XX  
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.  
XX  
PI Mao Y, Xie Y;  
XX  
DR WPI; 2001-648982/74.  
XX  
PT Peptide-human myosin heavy chain 12-14 and encoded polynucleotide, used  
PT in diagnosis and treatment of Prader Willi syndrome, and Klinefelters  
PT syndrome.  
XX  
PS Example 2; Page 17; 39pp; Chinese.  
XX  
CC The present invention provides the protein and coding sequences of human  
CC myosin heavy chain 12-14. The sequences can be used in the treatment of  
CC Prader Willi syndrome, Klinefelter syndrome, kinetic illnesses and  
CC inflammation. The present sequence is a PCR primer for the coding  
CC sequence of the invention  
XX  
SQ Sequence 24 BP; 5 A; 5 C; 11 G; 3 T; 0 U; 0 Other;  
XX  
Query Match 2.1%; Score 20.8; DB 1; Length 24;  
Best Local Similarity 91.7%; Pred. No. 1.2e+03;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 969 CTCGGCTCACTGCAACCTCTGCTT 992  
DB 24 CTCGGCTCACTGCAACCTCTGCTT 1  
XX  
RESULT 412  
AAF69722  
ID AAF69722 standard; DNA; 24 BP.  
XX  
AC AAF69722;  
XX  
DT 18-APR-2001 (first entry)  
XX  
DE Human IL4Ralpha gene PCR primer #58.  
XX  
KM Polymorphism; human; interleukin 4 receptor-alpha; IL4R-alpha;  
KM allergic disease; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200104270-A1.  
XX  
PD 18-JAN-2001.  
XX  
PF 13-JUL-2000; 2000WO-US019094.  
XX  
PR 13-JUL-1999; 99US-0143435P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Chew A, Denton RR, Duda A, Nandabalan K, Stephens JC;  
PI Windemuth AK;  
XX  
DR WPI; 2001-103078/11.  
XX  
PT New isolated polynucleotide useful for the identification of therapeutics

PT in allergic diseases is new.  
XX  
PS Example 1; Page 62; 188pp; English.  
XX  
CC The present invention relates to polymorphisms of the human interleukin 4  
CC receptor-alpha gene (IL4R-alpha; see AAF57718 for the reference  
CC sequence). Polynucleotides comprising polymorphic gene variants are  
CC useful for therapeutic purposes. For example, where a patient may benefit  
CC from expression of a particular IL4Ralpha protein isoform, an expression  
CC vector encoding the isoform may be administered to the patient. It may  
CC desirable to decrease or block expression of a particular IL4Ralpha  
CC isogene, which may be done by turning off by transforming a targeted  
CC organ, tissue or cell population with an expression vector that expresses  
CC high levels of untranslatable mRNA for the isogene. Specific therapeutics  
CC identified by these methods may be useful for allergic diseases. The  
CC present sequence is a PCR primer for human IL4R-alpha  
XX  
SQ Sequence 24 BP; 4 A; 9 C; 4 G; 7 T; 0 U; 0 Other;  
XX  
Query Match 2.1%; Score 20.8; DB 1; Length 24;  
Best Local Similarity 91.7%; Pred. No. 1.2e+03;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 1002 AAGGATTCTCTCTCTCAGCCTC 1025  
DB 1 AAGGATTCTCTCTCTCAGCCTC 24  
XX  
RESULT 413  
AAI68386  
ID AAI68386 standard; DNA; 24 BP.  
XX  
AC AAI68386;  
XX  
DT 03-JAN-2002 (first entry)  
XX  
DE Human ATP-dependent hydrolase serine 9 PCR primer SEQ ID NO 4.  
XX  
KM Human; ATP-dependent hydrolase serine 9; cytosolic; viral; viral;  
KM immunomodulatory; anti-inflammatory; haemostatic; malignant tumour; HIV;  
KM infection; human immunodeficiency virus; gene therapy;  
KM immunological disease; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200175042-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 26-MAR-2001; 2001WO-CN000434.  
XX  
PR 27-MAR-2000; 2000CN-00115164.  
XX  
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.  
XX  
PI Mao Y, Xie Y;  
XX  
DR WPI; 2001-626418/72.  
XX  
PT Human ATP-dependent serine hydrolase 9 and encoded polynucleotide, used  
PT in diagnosis and treatment of malignant tumors, hemopathy, human  
PT immunodeficiency virus infection, immunological diseases and  
PT inflammation.  
XX  
PS Example 2; Page 17; 33pp; Chinese.  
XX  
CC The invention relates to human ATP-dependent serine hydrolase 9 with  
CC cytosolic, viral, immunomodulatory, anti-inflammatory and haemostatic  
CC activity. The protein and encoding polynucleotide are used in diagnosis  
CC and treatment of malignant tumour, haemopathy, human immunodeficiency  
CC virus (HIV) infection, immunological diseases and various inflammations.  
CC The polynucleotide is useful in gene therapy. The present sequence is  
CC that of a PCR primer, useful to the invention

XX Sequence 24 BP; 5 A; 8 C; 5 G; 6 T; 0 U; 0 Other;  
SQ

Query Match 2.1%; Score 20.8; DB 1; Length 24;  
Best Local Similarity 91.7%; Pred. No. 1.2e+03;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 924 ATGGAATCTACTCTGTATCCGAG 947  
DB 1 ATGAGTCTCACTCTGTCACCGAG 24

RESULT 414  
ABAB2841/C  
ID ABA82841 standard; DNA; 24 BP.  
XX

AC ABA82841;

DT 07-FEB-2002 (first entry)

DE Human protective DNA sequence CNI-00746 fragment #6.

KW Human; protective sequence; cell death; cancer; autoimmune disease;  
KW neurological disorder; stroke; cytostatic; neuroprotective; gene therapy;  
KW ds.

OS Homo sapiens.

PN W0200176457-A2.

PD 18-OCT-2001.

PF 09-APR-2001; 2001WO-US011663.

PR 11-APR-2000; 2000US-00547735.

PA (COGE-) COGENT NEUROSCIENCE INC.

PI Thomas MB, Portbury SD, Putnam K, Katz LC, Lo DC, Barney S;

DR WPI; 2002-025874/03.

DR P-PSDB; ABB44743.

PT New protective sequences and their products, useful for diagnosing and  
PT treating diseases involving cell death, including neurological disorders  
PT e.g. stroke and for identifying modulators of expression of the  
PT protective sequences.

PS Claim 2; Fig 11; 283pp; English.

XX The present invention relates to protective sequence proteins (ABB44624-  
CC ABB44830) and their coding sequences (ABA82701-ABA82937). The sequences,  
CC when introduced into a cell either predisposed to undergo cell death or  
CC in the process of undergoing cell death, prevent, delay or rescue the  
CC cell from death, hence, these sequences are named "protective sequences".  
CC The sequences are useful for treating and/or ameliorating cancer,  
CC autoimmune diseases and neurological disorders e.g. stroke. Further  
CC examples of diseases which may be treated by the present invention are  
CC given in the specification

XX Sequence 24 BP; 7 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 2.1%; Score 20.8; DB 1; Length 24;  
Best Local Similarity 91.7%; Pred. No. 1.2e+03;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 177 TTAGTAGAGATGAGATTTCAT 200  
DB 24 TTAGTAGAGACGAGATTTCACCAT 1

RESULT 415  
ABL59102/C

ID ABL59102 standard; DNA; 24 BP.

AC ABL59102;

DT 27-SEP-2002 (first entry)

DE PCR primer used to amplify an 82 bp Alu probe.

KW Yeast artificial chromosome; YAC; pPD39;  
KW transformation-associated recombination; PCR; primer; ss.

OS Synthetic.

PN US6391642-B1.

PD 21-MAY-2002.

PF 14-APR-1998; 98US-00060023.

PR 09-JUL-1996; 96WO-US011478.

PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

PI Resnick MA, Larionov VL, Kouprina NY, Perkins EL,

DR WPI; 2002-498777/53.

PT Preparing yeast artificial chromosomes, useful e.g. for cloning specific  
PT human nucleic acid, comprises recombination in yeast cells between a  
PT nucleic acid and a yeast vector.

PS Example 2; Col 35; 50pp; English.

XX The specification describes a method for making a yeast artificial  
CC chromosome (YAC) that includes an origin of replication (ori). The method  
CC comprises incorporating into yeast cells: a population of mammalian  
CC nucleic acid; and a vector that comprises a yeast centromere, selection  
CC marker, yeast telomere and a sequence that recombines with a region of  
CC the nucleic acid, so that in vivo recombination to a YAC occurs. This  
CC method, designated transformation-associated recombination, eliminates  
CC the need for an in vitro ligation step, and makes possible selective  
CC cloning of cDNAs for which only the 3'-sequence is known. The method is  
CC used for making a YAC. The method is also used for selective cloning of  
CC mammalian, specifically human, nucleic acid from a population,  
CC particularly radiation hybrids that contain only a small fragment of a  
CC human chromosome. PCR primers ABL59102-03 were used to amplify an 82 bp  
CC Alu probe from the pPD39 plasmid containing an Alu consensus sequence.  
CC The probe was used to identify human YACs, generated using the method of  
CC the invention

XX Sequence 24 BP; 4 A; 6 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 2.1%; Score 20.8; DB 1; Length 24;  
Best Local Similarity 91.7%; Pred. No. 1.2e+03;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 675 TCACGCAACCTCTGCTCCCGG 698  
DB 24 TCACGCAAGCTCGGCTCCCGG 1

RESULT 416

ID ABL14186

AC ABL14186 standard; DNA; 24 BP.

DT 21-MAY-2002 (first entry)

DE Human splicing factor 9.24 cDNA RT-PCR primer #2.

KW Human; splicing factor 9.24; ss; cytostatic; gene therapy; cancer;  
KW tumour; foetus deforming; protein metabolic disturbance related disease;

KW RT-PCR; reverse transcription-PCR; primer.  
XX Homo sapiens.  
OS  
XX WO200212302-A1.  
PN  
XX 14-FEB-2002.  
PD  
XX 18-JUN-2001; 2001WO-CN000982.  
PF  
XX 19-JUN-2000; 2000CN-00116576.  
PR  
XX (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.  
PA  
XX Mao Y, Xie Y;  
PI  
XX WPI; 2002-172132/22.  
DR  
XX Human splicing factor 9.24 polypeptide and encoding polynucleotide, used  
PT in diagnosis and treatment of tumors and protein metabolic disturbance  
PR related disease.  
XX  
PS Example 2; Page 12; 38pp; Chinese.  
XX  
CC The invention relates to the human splicing factor 9.24 polypeptide and  
CC the DNA sequence encoding it. The DNA and protein sequences are used in  
CC diagnosis and treatment of tumors, foetus deforming and protein  
CC metabolic disturbance related diseases. This sequence represents a  
CC reverse transcription-PCR (RT-PCR) primer used in isolation of cDNA  
CC encoding the human splicing factor 9.24 polypeptide of the invention  
XX  
SQ Sequence 24 BP; 5 A; 5 C; 7 G; 7 T; 0 U; 0 Other;  
XX  
Query Match 2.1%; Score 20.8; DB 1; Length 24;  
Best Local Similarity 91.7%; Pred. No. 1.2e+03;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 633 AACTCTGTACCCAGCTGGAGTG 656  
DB 1 AACTTGTCACTAGCTGGAGTG 24  
XX  
RESULT 417  
ABK12860  
ID ABK12860 strand; DNA; 24 BP.  
XX  
XX ABK12860;  
AC  
XX 18-JUN-2002 (first entry)  
DT  
XX Human topoisomerase I 9.79 protein, RT-PCR primer1.  
DE  
XX Human; topoisomerase I 9.79; teratogenesis; tumour; primer; ss; RT-PCR;  
KW reverse transcriptase PCR.  
XX  
XX Homo sapiens.  
OS  
XX CN1328155-A.  
PN  
XX 26-DEC-2001.  
PD  
XX 14-JUN-2000; 2000CN-00116475.  
PF  
XX 14-JUN-2000; 2000CN-00116475.  
PR  
XX 14-JUN-2000; 2000CN-00116475.  
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
XX  
XX Mao Y, Xie Y;  
PI  
XX WPI; 2002-281738/33.  
DR  
XX Human topoisomerase I 9.79 polypeptide and the polynucleotide encoding  
PT it, for treating teratogenesis and tumors.

XX  
PS Example 2; Page 18 (Disclosure); 32pp; Chinese.  
XX  
XX The present invention relates to a new human topoisomerase I 9.79  
CC polypeptide, the polynucleotide encoding it and a DNA recombination  
CC process used to produce the polypeptide. The invention also discloses the  
CC agonist resisting the polypeptide. The polypeptide and its antagonist are  
CC useful for treating teratogenesis and tumors. The present nucleic acid  
CC sequence represents a reverse transcriptase (RT)-PCR primer that was used  
CC in the methods of the invention to isolate the coding sequence of the  
CC human topoisomerase I 9.79 protein of the invention  
XX  
SQ Sequence 24 BP; 3 A; 8 C; 9 G; 4 T; 0 U; 0 Other;  
XX  
Query Match 2.1%; Score 20.8; DB 1; Length 24;  
Best Local Similarity 91.7%; Pred. No. 1.2e+03;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 540 GCCTGACCTCCCAAGTGGG 563  
DB 1 GGCTGGGCTCCCAAGTGGG 24  
XX  
RESULT 418  
ABZ25248/C  
ID ABZ25248 strand; DNA; 24 BP.  
XX  
XX ABZ25248;  
AC  
XX 24-APR-2003 (first entry)  
DT  
XX Human peroxidase 9.90 PCR primer #2.  
DE  
XX Human; peroxidase 9.90; enzyme; cancer; HIV infection; cytostatic;  
KW anti-HIV; PCR; primer; ss.  
XX  
XX Homo sapiens.  
OS  
XX CN1360029-A.  
PN  
XX 24-JUL-2002.  
PD  
XX 20-DEC-2000; 2000CN-00135148.  
PF  
XX 20-DEC-2000; 2000CN-00135148.  
PR  
XX 20-DEC-2000; 2000CN-00135148.  
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
XX  
XX Mao Y, Xie Y;  
PI  
XX WPI; 2002-733654/80.  
DR  
XX Polypeptide-human peroxidase protein 9.90 and polynucleotide for coding  
PT it.  
KW  
XX  
XX Example 2; Page 16 (Disclosure); 31pp; Chinese.  
PS  
XX The present invention relates to human peroxidase 9.90 (see ABP59112).  
CC The peroxidase is useful for treating diseases such as cancer and HIV  
CC infection. The present sequence is a PCR primer, which was used in an  
CC example from the invention  
XX  
SQ Sequence 24 BP; 7 A; 5 C; 8 G; 4 T; 0 U; 0 Other;  
XX  
Query Match 2.1%; Score 20.8; DB 1; Length 24;  
Best Local Similarity 91.7%; Pred. No. 1.2e+03;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 1099 CACCATTTGTGAGGCTGCTC 1122  
DB 24 CACCATTTGTGAGGCTGCTC 1

## RESULT 419

ABA02134

ID ABA02134 standard; DNA; 24 BP.

XX ABA02134;

XX 08-FEB-2002 (first entry)

XX Human zinc ion transport protein 26 RT-PCR primer, SEQ ID NO:3.

XX Human; zinc ion transport protein 26; rat Znt-1 homologue;

XX zinc transporter; recombinant production; malignant tumour; cancer;

XX blood disease; HIV infection; human immunodeficiency virus;

XX immune disorder; inflammatory condition; embryonic development disorder;

XX developmental disorder; growth disorder; cytostatic; anti-HIV;

XX antiinflammatory; immunomodulator; reverse transcription-PCR;

XX RT-PCR primer; 88.

XX Homo sapiens.

XX MO200181539-A2.

XX 01-NOV-2001.

XX 23-APR-2001; 2001WO-CN000610.

XX 27-APR-2000; 2000CN-00115461.

XX (BIOW-) B10MINDOW GENE DEV INC SHANGHAI.

XX Mao Y, Xie Y;

XX WPI; 2002-026163/03.

XX Human zinc ion transport protein 26 and encoded polynucleotide, used in

XX diagnosis and treatment of malignant tumors, hemopathy, human

XX immunodeficiency virus infection, immunological diseases and

XX inflammation.

XX Example 3; Page 11; 31pp; Chinese.

XX The invention relates to human zinc ion transport protein 26 (AA052621),

XX nucleic acids encoding it (ABA02133), and a method for the recombinant

XX production of zinc ion transport protein 26. The protein has a molecular

XX weight of 26 kD, and has 35% identity and 54% homology over a 210 amino

XX acid stretch with the rat zinc transporter Znt-1 (GenBank accession

XX number U71713). The present invention additionally discloses an

XX antagonist of zinc ion transport protein 26 for therapeutic use, and an

XX antibody which specifically binds to zinc ion transport protein 26. Zinc

XX ion transport protein 26, and nucleotides which encode it may be used for

XX treating a variety of diseases, such as malignant tumours, blood

XX diseases, HIV (human immunodeficiency virus) infection, immune disorders,

XX inflammatory conditions, embryonic development disorders, and development

XX and growth disorders. The protein may also be used to screen for

XX modulators of its activity or for peptide fingerprinting identification.

XX The polynucleotide can be used as a primer for nucleic acid amplification

XX reactions or as a probe for hybridisation reactions, or in producing gene

XX chips or microarrays. Sequences ABA02134-ABA02135 represent reverse

XX transcription-PCR (RT-PCR) primers used in an exemplification of the

XX invention to isolate human zinc ion transport protein 26 cDNA

XX Sequence 24 BP; 4 A; 6 C; 6 G; 8 T; 0 U; 0 Other;

XX Query Match 2.1%; Score 20.8; DB 1; Length 24;

XX Best Local Similarity 91.7%; Pred. No. 1.2e+03;

XX Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1096 TTTCACCATATTTGTGAGGCTGCT 1119

Db 1 TTTCACCATATTTGCGCAGGCTGCT 24

RESULT 420

## AA016055/c

ID AA016055 standard; DNA; 24 BP.

XX AA016055;

XX 29-JAN-2002 (first entry)

XX Human microtubulin 11 RT-PCR primer #2.

XX Human; ss; microtubulin 11; cancer; haemopathy; PCR primer;

XX human immunodeficiency virus infection; immunological disease;

XX inflammation; embryonic development disorder; nervous system disorder;

XX growth disorder; cytostatic; virucidal; immunomodulatory; antiinflammatory;

XX haemostatic.

XX Homo sapiens.

XX MO200174128-A2.

XX 11-OCT-2001.

XX 26-FEB-2001; 2001WO-CN000226.

XX 02-MAR-2000; 2000CN-00111820.

XX (BIOW-) B10MINDOW GENE DEV INC SHANGHAI.

XX Mao Y, Xie Y;

XX WPI; 2002-025780/03.

XX Human microtubulin 11 and encoded polynucleotide, applicable in diagnosis

XX and treatment of e.g. developmental disorders, cancer, hemopathy, HIV

XX infection, immunological diseases and various inflammations.

XX Example 2; Page 11; 31pp; Chinese.

XX The invention relates to an isolated polypeptide of human microtubulin

XX CC 11, the nucleic acid encoding it, a fragment, analogue or derivative of

XX CC it, a transformed cell expressing the protein from an expression vector,

XX CC antibodies against the protein and antagonists of the protein. The

XX CC polypeptide and encoded polynucleotide are applicable in diagnosis and

XX CC treatment of cancer, haemopathy, human immunodeficiency virus infection,

XX CC immunological diseases, various inflammations, embryonic development

XX CC disorders, disorders of the nervous system and growth disorders. The

XX CC present sequence is an RT-PCR (reverse transcriptase PCR) primer used to

XX CC isolate a nucleic acid encoding human microtubulin 11

XX Sequence 24 BP; 5 A; 9 C; 5 G; 5 T; 0 U; 0 Other;

XX Query Match 2.1%; Score 20.8; DB 1; Length 24;

XX Best Local Similarity 91.7%; Pred. No. 1.2e+03;

XX Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 645 CAGCGTGGAGTGCAGTGGCGCAT 668

Db 24 CAGACTGGAGTGCAGTGGCGCAT 1

## RESULT 421

ID ABS57470/c

XX ABS57470 standard; DNA; 24 BP.

XX ABS57470;

XX 27-FEB-2003 (first entry)

XX Human plasminogen activator inhibitor 2-9.9 cDNA RT-PCR primer #1.

XX Human; plasminogen activator inhibitor 2-9.9; primer; ss; thrombosis;

XX haemorrhagic disease; cerebral infarction; myocardial infarction; tumour;

XX haemopathy; human immunodeficiency virus; HIV; inflammation; cancer;

XX RT-PCR; reverse transcriptase.

```
XX OS Homo sapiens.
XX CN1352101-A.
XX 05-JUN-2002.
XX PF 06-NOV-2000; 2000CN-00127230.
XX PR 06-NOV-2000; 2000CN-00127230.
XX PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX PI Mao Y, Xie Y;
XX WPI; 2002-675822/73.
XX DR
XX PF New human plasminogen activator inhibitor 2-9.9 polypeptide for treating
XX PT e.g. hemorrhagic disease, thrombosis, cerebral infarction, various
XX PT tumors, hemopathy, human immunodeficiency virus infection, and
XX PT inflammations.
XX PS Example 2; Page 17 (Disclosure); 33pp; Chinese.
XX CC The invention relates to the human plasminogen activator inhibitor 2-9.9
XX CC polypeptide, the polynucleotide encoding the polypeptide and a DNA
XX CC recombination process used to produce the polypeptide. The polypeptide
XX CC and polynucleotide are used for treating various diseases, such as
XX CC haemorrhagic disease, thrombosis, cerebral infarction, myocardial
XX CC infarction, various tumors, haemopathy, human immunodeficiency virus
XX CC (HIV) infection and inflammations. This sequence represents a reverse
XX CC transcriptase PCR (RT-PCR) primer used for isolation of cDNA encoding
XX CC human plasminogen activator inhibitor 2-9.9
XX SQ Sequence 24 BP; 2 A; 9 C; 9 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 2.1%; Score 20.8; DB 1; Length 24;
XX Best Local Similarity 91.7%; Pred. No. 1.2e+03;
XX Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 873 ACAGGCGTGAGCCACGAGCCCGG 896
DB 24 ACAGGCGTGAGCCACGAGCCCGG 1
RESULT 422
AB221093
ID AB221093 standard; DNA; 24 BP.
XX AC AB221093;
XX DT 25-MAR-2003 (first entry)
XX DE Starch precursor protein binding protein 13.42 PCR primer #2.
XX KM Starch precursor protein binding protein 13.42; Alzheimer's disease;
XX KM tumour; development disorder; inflammation; immunological disease;
XX KM haemopathy; HIV infection; cytostatic; anti-HIV; PCR; primer; ss.
XX OS Unidentified.
XX OS CN1352014-A.
XX PN 05-JUN-2002.
XX PD 06-NOV-2000; 2000CN-00127264.
XX PF 06-NOV-2000; 2000CN-00127264.
XX PR 06-NOV-2000; 2000CN-00127264.
XX PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX PI Mao Y, Xie Y;
XX
```

```
DR WPI; 2002-699445/76.
XX PF New starch precursor protein binding protein 13.42 polypeptide for
XX PT treating e.g. Alzheimer's disease, malignant tumors, inflammations,
XX PT immunological diseases, hemopathy and human immunodeficiency virus
XX PT infection.
XX PS Example 2; Page 17 (Disclosure); 34pp; Chinese.
XX CC The present invention relates to starch precursor protein binding protein
XX CC 13.42 (see ABB98887). The protein can be used for treating various
XX CC diseases, such as Alzheimer's disease, malignant tumors, development
XX CC disorders, inflammations, immunological diseases, haemopathy and HIV
XX CC infection. The present sequence is a PCR primer, which was used in an
XX CC example from the invention
XX SQ Sequence 24 BP; 3 A; 6 C; 7 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 2.1%; Score 20.8; DB 1; Length 24;
XX Best Local Similarity 91.7%; Pred. No. 1.2e+03;
XX Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 932 TCACCTGTTACCCAGGCTGAGT 955
DB 1 TCACCTGTTGTCAGGCTGAGT 24
RESULT 423
ACA90126
ID ACA90126 standard; DNA; 24 BP.
XX AC ACA90126;
XX DT 10-JUN-2003 (first entry)
XX DE Human kinesin gene(s) antisense oligonucleotide #9.
XX KM Human; ss; antisense; kinesin; CENP-B; Eg5; MCAK; colon cancer; stroke;
XX KM T cell cancer; B cell lymphoma; pancreatic cancer; breast cancer;
XX KM leukaemia; bladder cancer; stomach cancer; brain cancer; bone cancer;
XX KM oesophageal cancer; liver cancer; adrenocarcinoma; lung cancer;
XX KM testicular cancer; heart cancer; ovarian cancer; uterine cancer;
XX KM head/neck cancer; cervical cancer; gall bladder cancer; spleen cancer;
XX KM parathyroid cancer; penile cancer; prostate cancer; skin cancer;
XX KM thyroid cancer; thymoid cancer; muscle cancer; ganglial cancer; melanoma;
XX KM myeloma sarcoma; teratocarcinoma; digestive cancer; ischaemia; epilepsy;
XX KM autoimmune disorder; viral infection; neurological disorder; meningitis;
XX KM liver disease; pancreatic disease; myocardial infarction; cerebral palsy;
XX KM Alzheimer's disease; Huntington's disease; Parkinson's disease;
XX KM amyotrophic lateral sclerosis; motor neuron disorder; multiple sclerosis;
XX KM retinitis pigmentosa; demyelinating disease; prion disease;
XX KM Creutzfeldt-Jakob disease; muscular dystrophy; schizophrenia; amnesia;
XX KM diabetic neuropathy; Tourette's disease; cystic fibrosis; infection;
XX KM diabetic mellitus; Grave's disease; gastrointestinal disorder;
XX KM ulcerative colitis; AIDS; allergic reactions; inflammatory bowel disease;
XX KM myasthenia gravis; rheumatoid arthritis; osteoarthritis; scleroderma;
XX KM Sjgren's syndrome; systemic lupus erythematosus; toxic shock syndrome.
XX OS Homo sapiens.
XX OS WO2003030832-A2.
XX PN 17-APR-2003.
XX PD 11-OCT-2002; 2002WO-US032596.
XX PF 12-OCT-2001; 2001US-0328444P.
XX PR (CHIR ) CHIRON CORP.
XX PA Reinhard C, Walter A;
XX PI WPI; 2003-381676/36.
XX
```



XX Treatment of disease e.g. cancer, rheumatoid arthritis, Alzheimer's  
 PT disease and Parkinson's disease involves administration of antisense  
 PT oligonucleotide.  
 XX  
 XX Claim 5, Page 6; 57pp; English.  
 XX  
 CC The invention relates to treatment of disease involving administering an  
 CC antisense oligonucleotide. The oligonucleotide inhibits the expression of  
 CC human kinesin gene. The human kinesin gene is CENP-B, human Eg5 or MCAK.  
 CC Also included are the antisense oligonucleotides appearing as ACA90118-  
 CC ACA90135, combination therapy involving administration of at least one  
 CC chemotherapeutic or radionuclide and further involves administration of  
 CC at least one anti-sense oligonucleotide (the oligonucleotide is  
 CC administered either separately or in combination) and a carrier. The human  
 CC composition comprising the AS oligonucleotide and a carrier. The human  
 CC kinesin gene-targeting antisense oligonucleotides are useful for  
 CC treatment of disease having aberrant cell proliferation such as cancer  
 CC e.g. colon cancer, T and B cell lymphoma, pancreatic cancer, breast  
 CC cancer, leukaemia, bladder cancer, stomach cancer, brain cancer,  
 CC oesophageal cancer, liver cancer, adrenal carcinoma, lung cancer,  
 CC testicular cancer, heart cancer, ovarian cancer, uterine cancer, head and  
 CC neck cancer, bone cancer, cervical cancer, gall bladder cancer,  
 CC parathyroid cancer, penile cancer, prostate cancer, skin cancer, spleen  
 CC cancer, thymus cancer, thyroid cancer, muscle cancer, ganglial cancer,  
 CC melanoma, myeloma sarcoma and teratocarcinomas, digestive cancer,  
 CC lymphoma, autoimmune disorder, viral infection, neurological disease,  
 CC condition associated with ischaemia and liver or pancreatic disease,  
 CC myocardial infarction, stroke, epilepsy, ischaemic cerebrovascular  
 CC disease, cerebral neoplasm, Alzheimer's disease, Pick's disease,  
 CC Huntington's disease, dementia, Parkinson's disease, extrapyramidal  
 CC disorder, amyotrophic lateral sclerosis, motor neuron disorders,  
 CC progressive neural muscular atrophy, retinitis pigmentosa, hereditary  
 CC ataxia, suppurative intracranial thrombophlebitis, multiple sclerosis,  
 CC demyelinating disease, bacterial and viral meningitis, brain abscess,  
 CC subdural empyema, myelitis, paralysis, viral central nervous system  
 CC disease, prion disease including kuru, Creutzfeldt-Jakob disease,  
 CC Gerstmann-Sträussler-Scheinker syndrome, insomnia, neurofibromatosis,  
 CC mental retardation, cerebral palsy, autonomic nervous system disorder,  
 CC muscular dystrophy, peripheral nervous system disorders, dermatomyositis,  
 CC anxiety, schizophrenia, amnesia, diabetic neuropathy, tardive dyskinesia,  
 CC Tourette's disease, cystic fibrosis, hypercholesterolaemia, diabetic  
 CC mellitus, hyper- and hypoglycaemia, Grave's disease, neuralgia, Cushing's  
 CC disease, Addison's disease, gastrointestinal disorders e.g. ulcerative  
 CC colitis, duodenal ulcer, AIDS, allergic reactions, autoimmune haemolytic  
 CC anaemia, proliferative glomerulonephritis, inflammatory bowel disease,  
 CC myasthenia gravis, rheumatoid arthritis, osteoarthritis, scleroderma,  
 CC Sjogren's syndrome, systemic lupus erythematosus, toxic shock syndrome,  
 CC viral, bacterial, fungal, helminthic and protozoal infections. The  
 CC present sequence is a human kinesin gene-targeting antisense  
 CC oligonucleotide of the invention  
 XX  
 XX Sequence 24 BP; 6 A; 11 C; 4 G; 3 T; 0 U; 0 Other;  
 SQ  
 Query Match 2.1%; Score 20.8; DB 1; Length 24;  
 Best Local Similarity 91.7%; Pred. No. 1.2e+03;  
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 359 GCTCAGCAGTCCACCTGCTCAG 362  
 DB 1 GCTCAGCAGTCCACCTGCTCAG 24  
 ACAG0127  
 ID ACAG0127 standard; DNA; 24 BP.  
 XX  
 AC ACAG0127;  
 XX  
 DT 10-JUL-2003 (first entry)  
 XX  
 DE Human kinesin gene(s) antisense oligonucleotide #10.  
 XX

KW Human; ss; antisense; kinesin; CENP-B; Eg5; MCAK; colon cancer; stroke;  
 KW T cell cancer; B cell lymphoma; pancreatic cancer; breast cancer;  
 KW leukaemia; bladder cancer; stomach cancer; brain cancer; bone cancer;  
 KW oesophageal cancer; liver cancer; adrenal carcinoma; lung cancer;  
 KW testicular cancer; heart cancer; ovarian cancer; uterine cancer;  
 KW head/neck cancer; cervical cancer; gall bladder cancer; spleen cancer;  
 KW parathyroid cancer; penile cancer; prostate cancer; skin cancer;  
 KW thymus cancer; thyroid cancer; muscle cancer; ganglial cancer; melanoma;  
 KW myeloma sarcoma; teratocarcinoma; digestive cancer; ischaemia; epilepsy;  
 KW autoimmune disorder; viral infection; neurological disorder; meningitis;  
 KW liver disease; pancreatic disease; myocardial infarction; cerebral palsy;  
 KW Alzheimer's disease; Huntington's disease; Parkinson's disease;  
 KW amyotrophic lateral sclerosis; motor neuron disorder; multiple sclerosis;  
 KW retinitis pigmentosa; demyelinating disease; prion disease;  
 KW Creutzfeldt-Jakob disease; muscular dystrophy; schizophrenia; amnesia;  
 KW diabetic neuropathy; Tourette's disease; cystic fibrosis; infection;  
 KW diabetic mellitus; Grave's disease; gastrointestinal disorder;  
 KW ulcerative colitis; AIDS; allergic reactions; inflammatory bowel disease;  
 KW myasthenia gravis; rheumatoid arthritis; osteoarthritis; scleroderma;  
 KW Sjogren's syndrome; systemic lupus erythematosus; toxic shock syndrome.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO2003030832-A2.  
 XX  
 PD 17-APR-2003.  
 XX  
 PF 11-OCT-2002; 2002WO-US032596.  
 XX  
 PR 12-OCT-2001; 2001US-032844P.  
 XX  
 PA (CHIR ) CHIRON CORP.  
 XX  
 PI Reinhard C, Walter A;  
 XX  
 DR WPI; 2003-381676/36.  
 XX  
 PT Treatment of disease e.g. cancer, rheumatoid arthritis, Alzheimer's  
 PT disease and Parkinson's disease involves administration of antisense  
 PT oligonucleotide.  
 XX  
 PS Claim 5, Page 6; 57pp; English.  
 XX  
 CC The invention relates to treatment of disease involving administering an  
 CC antisense oligonucleotide. The oligonucleotide inhibits the expression of  
 CC human kinesin gene. The human kinesin gene is CENP-B, human Eg5 or MCAK.  
 CC Also included are the antisense oligonucleotides appearing as ACA90118-  
 CC ACA90135, combination therapy involving administration of at least one  
 CC chemotherapeutic or radionuclide and further involves administration of  
 CC at least one anti-sense oligonucleotide (the oligonucleotide is  
 CC administered either separately or in combination) and a carrier. The human  
 CC composition comprising the AS oligonucleotide and a carrier. The human  
 CC kinesin gene-targeting antisense oligonucleotides are useful for  
 CC treatment of disease having aberrant cell proliferation such as cancer  
 CC e.g. colon cancer, T and B cell lymphoma, pancreatic cancer, breast  
 CC cancer, leukaemia, bladder cancer, stomach cancer, brain cancer,  
 CC oesophageal cancer, liver cancer, adrenal carcinoma, lung cancer,  
 CC testicular cancer, heart cancer, ovarian cancer, uterine cancer, head and  
 CC neck cancer, bone cancer, cervical cancer, gall bladder cancer,  
 CC parathyroid cancer, penile cancer, prostate cancer, skin cancer, spleen  
 CC cancer, thymus cancer, thyroid cancer, muscle cancer, ganglial cancer,  
 CC melanoma, myeloma sarcoma and teratocarcinomas, digestive cancer,  
 CC lymphoma, autoimmune disorder, viral infection, neurological disease,  
 CC condition associated with ischaemia and liver or pancreatic disease,  
 CC myocardial infarction, stroke, epilepsy, ischaemic cerebrovascular  
 CC disease, cerebral neoplasm, Alzheimer's disease, Pick's disease,  
 CC Huntington's disease, dementia, Parkinson's disease, extrapyramidal  
 CC disorder, amyotrophic lateral sclerosis, motor neuron disorders,  
 CC progressive neural muscular atrophy, retinitis pigmentosa, hereditary  
 CC ataxia, suppurative intracranial thrombophlebitis, multiple sclerosis,  
 CC demyelinating disease, bacterial and viral meningitis, brain abscess,  
 CC subdural empyema, myelitis, paralysis, viral central nervous system  
 CC disease, prion disease including kuru, Creutzfeldt-Jakob disease,  
 CC Gerstmann-Sträussler-Scheinker syndrome, insomnia, neurofibromatosis,  
 CC mental retardation, cerebral palsy, autonomic nervous system disorder,  
 CC muscular dystrophy, peripheral nervous system disorders, dermatomyositis,  
 CC anxiety, schizophrenia, amnesia, diabetic neuropathy, tardive dyskinesia,  
 CC Tourette's disease, cystic fibrosis, hypercholesterolaemia, diabetic  
 CC mellitus, hyper- and hypoglycaemia, Grave's disease, neuralgia, Cushing's  
 CC disease, Addison's disease, gastrointestinal disorders e.g. ulcerative  
 CC colitis, duodenal ulcer, AIDS, allergic reactions, autoimmune haemolytic  
 CC anaemia, proliferative glomerulonephritis, inflammatory bowel disease,  
 CC myasthenia gravis, rheumatoid arthritis, osteoarthritis, scleroderma,  
 CC Sjogren's syndrome, systemic lupus erythematosus, toxic shock syndrome,  
 CC viral, bacterial, fungal, helminthic and protozoal infections. The  
 CC present sequence is a human kinesin gene-targeting antisense  
 CC oligonucleotide of the invention  
 XX

CC Gerstmann-Strausler-Scheinker syndrome, insomnia, neurofibromatosis,  
CC mental retardation, cerebellar palsy, autonomic nervous system disorder,  
CC muscular atrophy, peripheral nervous system disorders, dermatomyositis,  
CC anxiety, schizophrenia, anorexia, diabetic neuropathy, tardive dyskinesia,  
CC Tourette's disease, cystic fibrosis, hypercholesterolemia, diabetic  
CC mellitus, hyper- and hypoglycaemia, Grave's disease, neuralgia, Cushing's  
CC disease, Addison's disease, gastrointestinal disorders e.g. ulcerative  
CC colitis, duodenal ulcer, AIDS, allergic reactions, autoimmune haemolytic  
CC anaemia, proliferative glomerulonephritis, inflammatory bowel disease,  
CC myaesthesia gravis, rheumatoid arthritis, osteoarthritis, scleroderma,  
CC Sjogren's syndrome, systemic lupus erythematosus, toxic shock syndrome,  
CC viral, bacterial, fungal, helminthic and protozoal infections. The  
CC present sequence is a human kinesin gene-targeting antisense  
CC oligonucleotide of the invention  
XX  
SQ Sequence 24 BP; 6 A; 7 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 2.1%; Score 20.8; DB 1; Length 24;  
Best Local Similarity 91.7%; Pred. No. 1.2e+03;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 867 GGGATTACAGCGGTGAGCCACC 890  
Db 1 GGGATTACAGCGCATGAGCCACCC 24

## RESULT 425

ACC57313  
ID ACC57313 standard; DNA; 24 BP.

AC ACC57313;

DT 27-JUN-2003 (first entry)

DE Zinc finger protein 11.55 related PCR primer #SBQ ID 3.

KM Zinc finger protein, 11.55; human immunodeficiency virus; HIV; cancer;

XX PCR; primer; ss.

OS Unidentified.

PM CN1363594-A.

PD 14-AUG-2002.

PF 05-JAN-2001; 2001CN-00105078.

PR 05-JAN-2001; 2001CN-00105078.

PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.

PI Mao Y, Xie Y;

DR WPI; 2003-000323/01.

PT Polypeptide-zinc finger protein 11.55 and polynucleotide encoding it.

PS Example 2; Page 17 (disclosure); 33pp; Chinese.

CC The invention relates to a novel zinc finger protein designated 11.55.

CC Also disclosed are the polynucleotide encoding it, and a process for

CC preparing the polypeptide using DNA recombination techniques. The

CC application of the polypeptide is in treating diseases such as cancer and

CC human immunodeficiency virus (HIV) infection. The current sequence

CC represents a zinc finger protein 11.55 related PCR primer  
XX  
SQ Sequence 24 BP; 5 A; 6 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 2.1%; Score 20.8; DB 1; Length 24;  
Best Local Similarity 91.7%; Pred. No. 1.2e+03;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 198 CATGTTGTCAGGCTGCTCGAA 221

Db 1 CATGTTGTCAGGCTGCTCGAA 24

## RESULT 426

ID ADG83872  
ID ADG83872 standard; DNA; 24 BP.

AC ADG83872;

DT 11-MAR-2004 (first entry)

DE Human SLCA14 forward PCR primer SBQ ID NO.13.

KM differentiation; ulcerative colitis; Crohn's disease;

XX target genetic marker gene; human; PCR primer; ss.

OS Synthetic.

PM Homo sapiens.

PD WO2004001073-A1.

PF 31-DEC-2003.

PR 25-JUN-2003; 2003WO-SB001105.

PR 25-JUN-2002; 2002SE-00001954.

PR 25-JUN-2002; 2002SE-00001956.

PR 15-JUL-2002; 2002US-0395629P.

PR 15-JUL-2002; 2002US-0395631P.

PR 18-JUL-2002; 2002SE-00002251.

PR 18-JUL-2002; 2002SE-00002252.

PR 18-JUL-2002; 2002SE-00002256.

PR 04-SEP-2002; 2002US-0407682P.

PR 10-SEP-2002; 2002US-0407713P.

PR 10-SEP-2002; 2002US-0409213P.

PA (INDE-) INDEX PHARM AB.

PI Dieckmann A, Loeffberg R, Von Stein O, Von Stein P;

DR WPI; 2004-071745/07.

PT Differentiating between ulcerative colitis and Crohn's disease based on

PT the analysis of gene expression profiles in biopsy samples comprises

PT determining the expression levels of at least two of a number of marker

PT genes.  
XX  
PS Claim 7; SEQ ID NO 13; 30pp; English.

CC The present invention describes a method for differentiating between

CC ulcerative colitis and Crohn's disease based on the analysis of gene

CC expression profiles in biopsy samples obtained from inflamed and

CC optionally non-inflamed areas in the intestines of the patient. The

CC method comprises determining the expression levels of at least two of a

CC number of marker genes chosen from any of the 7 sequences SEQ ID NO.1 to

CC 7 (see ADG83886, ADG83887, ADG83888, ADG83889, ADG83890, ADG83891 and  
CC ADG83892). The method can be used for differentiating between ulcerative  
CC colitis and Crohn's disease based on the analysis of gene expression  
CC profiles in biopsy samples obtained from inflamed and optionally non-  
CC inflamed areas in the intestines of the patient. The present sequence  
CC represents a PCR primer for a target genetic marker gene sequence which  
CC is used in the exemplification of the present invention.  
XX  
SQ Sequence 24 BP; 5 A; 4 C; 9 G; 6 T; 0 U; 0 Other;

Query Match 2.1%; Score 20.8; DB 1; Length 24;  
Best Local Similarity 91.7%; Pred. No. 1.2e+03;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 862 GTGCTGGATTACAGCGGTGAGCC 885  
Db 1 GTGCTGAGATTACAGGTGTGAGCC 24

KM	Cytostatic; immunostimulant; gene therapy; vaccine; human;	XX
KM	zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;	XX
KM	chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;	XX
KM	developmental disorder; ss.	XX
XX		XX
XX	Homo sapiens.	XX
PN	EP1281758-A2.	XX
PD		XX
XX	05-FEB-2003.	XX
XX		XX
PF	30-JUL-2002; 2002EP-00016874.	XX
PR	02-AUG-2001; 2001US-00922181.	XX
PA	(AEOM-) AEOMICA INC.	XX
PI	Shannon M, Gu Y, Nguyen C;	XX
PI	wp1; 2003-423107/40.	XX
PT		XX
PT	New zinc finger-containing proteins and nucleic acids, useful in	XX
PT	manufacturing a medicament for treating or preventing a disorder	XX
PT	associated with decreased or increased expression or activity of MD23,	XX
PT	MD24, MD27 or MD212, e.g. cancer.	XX
PS		XX
PS	Example 8; SEQ ID NO 5725; 103pp; English.	XX
XX		XX
XX	The present invention relates to novel human zinc finger-containing	XX
CC	proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is	XX
CC	encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,	XX
CC	MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome	XX
CC	15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,	XX
CC	or in manufacturing a medicament for treating or preventing a disorder	XX
CC	associated with decreased or increased expression or activity of MD23,	XX
CC	MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic	XX
CC	acids and proteins are also useful for diagnosing or monitoring a disease	XX
CC	caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic	XX
CC	acids can also be used as probes to detect and characterize gross	XX
CC	alterations in MD23, MD24, MD27, or MD212 genetic loci. The probes are	XX
CC	useful in constructing microarrays for measuring gene expression. The	XX
CC	proteins are useful as therapeutic agents for gene therapy or as	XX
CC	vaccines. The present sequence was used to illustrate the invention.	XX
XX		XX
XX		XX
XX	Sequence 25 BP; 8 A; 1 C; 4 G; 12 T; 0 U; 0 Other;	XX
XX		XX
XX	Query Match	2.1%; Score 20.8; DB 1; Length 25;
XX	Best Local Similarity	91.7%; Pred. No. 1.2e+03;
XX	Matches	22; Conservative 0; Mismatches 2; Indels 0; Gaps 0
OY	766 ATTTTGTGATTTTACTAGAGA 789	
DB	1 AATATTTGTATTTTACTAGAGA 24	
RESULT 429		
ADB04618		
ID	ADB04618 standard; DNA; 25 BP.	
XX		
XX	ADB04618;	
AC		
XX		
XX	20-NOV-2003 (first entry)	
XX		
DE	Human MD27 scanning oligonucleotide SEQ ID 5604.	
KM	Cytostatic; immunostimulant; gene therapy; vaccine; human;	
KM	zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;	
KM	chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;	
KM	developmental disorder; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	EP1281758-A2.	

```
XX 05-FEB-2003.
PD
XX
XX 30-JUL-2002; 2002EP-00016874.
PF
XX 02-AUG-2001; 2001US-00922181.
PR
XX (AEOM-) AEOMICA INC.
PA
XX Shannon M, Gu Y, Nguyen C;
PI
XX WPI; 2003-423107/40.
DR
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
PT
XX
XX Example 8; SEQ ID NO 5604; 103pp; English.
PS
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
XX
XX Sequence 25 BP; 5 A; 6 C; 10 G; 4 T; 0 U; 0 Other;
SQ
XX
XX Query Match 2.1%; Score 20.8; DB 1; Length 25;
XX Best Local Similarity 91.7%; Pred. No. 1.2e+03;
XX Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 647 GGCTGGAGTGCAGTGGCGCATCT 670
DB 1 GGCTGGAGTGCAGTGGCGCCACAGCT 24
XX
XX RESULT 430
XX ADB04738
XX ID ADB04738 standard; DNA; 25 BP.
XX
XX ADB04738;
AC
XX 20-NOV-2003 (first entry)
DT
XX
XX Human MD27 scanning oligonucleotide SEQ ID 5724.
DE
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX
XX Homo sapiens.
OS
XX
XX EPI281758-A2.
PN
XX
XX 05-FEB-2003.
PD
XX 30-JUL-2002; 2002EP-00016874.
PF
XX 02-AUG-2001; 2001US-00922181.
PR
XX (AEOM-) AEOMICA INC.
PA
XX
```

```
XX Shannon M, Gu Y, Nguyen C;
PI
XX WPI; 2003-423107/40.
DR
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
PT
XX
XX Example 8; SEQ ID NO 5724; 103pp; English.
PS
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
XX
XX Sequence 25 BP; 8 A; 0 C; 4 G; 13 T; 0 U; 0 Other;
SQ
XX
XX Query Match 2.1%; Score 20.8; DB 1; Length 25;
XX Best Local Similarity 91.7%; Pred. No. 1.2e+03;
XX Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 766 ATTTTGTATTTTACTAGAGA 789
DB 2 AATATTTGTATTTTACTAGAGA 25
XX
XX RESULT 431
XX ADB04740
XX ID ADB04740 standard; DNA; 25 BP.
XX
XX ADB04740;
AC
XX 20-NOV-2003 (first entry)
DT
XX
XX Human MD27 scanning oligonucleotide SEQ ID 5726.
DE
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX
XX Homo sapiens.
OS
XX
XX EPI281758-A2.
PN
XX
XX 05-FEB-2003.
PD
XX 30-JUL-2002; 2002EP-00016874.
PF
XX 02-AUG-2001; 2001US-00922181.
PR
XX (AEOM-) AEOMICA INC.
PA
XX Shannon M, Gu Y, Nguyen C;
PI
XX WPI; 2003-423107/40.
DR
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
```

```
PT MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 5726; 103pp; English.
PS
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded in therapy,
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 25 BP; 7 A; 1 C; 5 G; 12 T; 0 U; 0 Other;
Query Match 2.1%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.2e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 768 TTTTGTATTTTGTAGAGATG 791
DB 2 TATTTGTATTTTGTAGAGACG 25
RESULT 432
ADB04617
ID ADB04617 standard; DNA; 25 BP.
XX
XX ADB04617;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human MD27 scanning oligonucleotide SEQ ID 5603.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MD23; MD24; MD27; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX
XX Homo sapiens.
XX
XX EP1281758-A2.
XX
XX 05-FEB-2003.
XX
XX 30-JUL-2002; 2002EP-00016874.
XX
XX 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M, Gu Y, Nguyen C;
XX
XX WPI, 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acid, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 5603; 103pp; English.
XX
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
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CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 25 BP; 4 A; 6 C; 11 G; 4 T; 0 U; 0 Other;
Query Match 2.1%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.2e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 647 GGCTGAGTGCAGTGGCGCAATCT 670
DB 2 GGCTGAGTGCAGTGGCCCAAGCT 25
RESULT 433
ADB04578
ID ADB04578 standard; DNA; 25 BP.
XX
XX ADB04578;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human MD27 scanning oligonucleotide SEQ ID 5564.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MD23; MD24; MD27; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX
XX Homo sapiens.
XX
XX EP1281758-A2.
XX
XX 05-FEB-2003.
XX
XX 30-JUL-2002; 2002EP-00016874.
XX
XX 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M, Gu Y, Nguyen C;
XX
XX WPI, 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 5564; 103pp; English.
XX
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
```

CC useful in constructing microarrays for measuring gene expression. The  
CC proteins are useful as therapeutic agents for gene therapy or as  
CC vaccines. The present sequence was used to illustrate the invention.  
XX  
SQ Sequence 25 BP; 4 A; 2 C; 4 G; 15 T; 0 U; 0 Other;

Query Match 2.1%; Score 20.8; DB 1; Length 25;  
Best Local Similarity 91.7%; Pred. No. 1.2e+03;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 607 TTTTAAATTTTGGACAGAGCTC 630  
DB 2 TTTTATTTTGGACAGAGCTC 25

## RESULT 434

ID ADB04746 standard; DNA; 25 BP.

AC ADB04746;

XX 20-NOV-2003 (first entry)

DE Human MD27 scanning oligonucleotide SEQ ID 5732.

XX Cytostatic; immunostimulant; gene therapy; vaccine; human;  
XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;  
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
KW developmental disorder; ss.

XX Homo sapiens.

OS EPI281758-A2.

PN 05-FEB-2003.

PF 30-JUL-2002; 2002EP-00016874.

PR 02-AUG-2001; 2001US-00922181.

XX (AEOM-) AEOMICA INC.

PI Shannon M, Gu Y, Nguyen C;

XX WPI; 2003-423107/40.

XX New zinc finger-containing proteins and nucleic acids, useful in  
PT manufacturing a medicament for treating or preventing a disorder  
PT associated with decreased or increased expression or activity of MD23,  
PT MD24, MD27 or MD212, e.g. cancer.

XX Example 8; SEQ ID NO 5732; 103bp; English.

XX The present invention relates to novel human zinc finger-containing  
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is  
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,  
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome  
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,  
CC or in manufacturing a medicament for treating or preventing a disorder  
CC associated with decreased or increased expression or activity of MD23,  
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic  
CC acids and proteins are also useful for diagnosing or monitoring a disease  
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic  
CC acids can also be used as probes to detect and characterize gross  
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are  
CC useful in constructing microarrays for measuring gene expression. The  
CC proteins are useful as therapeutic agents for gene therapy or as  
CC vaccines. The present sequence was used to illustrate the invention.

XX Sequence 25 BP; 5 A; 1 C; 9 G; 10 T; 0 U; 0 Other;

Query Match 2.1%; Score 20.8; DB 1; Length 25;  
Best Local Similarity 91.7%; Pred. No. 1.2e+03;

Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 773 TGTATTTTAGTAGAGGCGGT 796  
DB 1 TGTATTTTAGTAGAGCGGGCT 24

RESULT 435  
ID ADB04580 standard; DNA; 25 BP.

AC ADB04580;

XX 20-NOV-2003 (first entry)

DE Human MD27 scanning oligonucleotide SEQ ID 5566.

XX Cytostatic; immunostimulant; gene therapy; vaccine; human;  
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;  
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
KW developmental disorder; ss.

XX Homo sapiens.

PN EPI281758-A2.

XX 05-FEB-2003.

PF 30-JUL-2002; 2002EP-00016874.

PR 02-AUG-2001; 2001US-00922181.

XX (AEOM-) AEOMICA INC.

PI Shannon M, Gu Y, Nguyen C;

XX WPI; 2003-423107/40.

XX New zinc finger-containing proteins and nucleic acids, useful in  
PT manufacturing a medicament for treating or preventing a disorder  
PT associated with decreased or increased expression or activity of MD23,  
PT MD24, MD27 or MD212, e.g. cancer.

XX Example 8; SEQ ID NO 5566; 103bp; English.

XX The present invention relates to novel human zinc finger-containing  
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is  
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,  
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome  
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,  
CC or in manufacturing a medicament for treating or preventing a disorder  
CC associated with decreased or increased expression or activity of MD23,  
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic  
CC acids and proteins are also useful for diagnosing or monitoring a disease  
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic  
CC acids can also be used as probes to detect and characterize gross  
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are  
CC useful in constructing microarrays for measuring gene expression. The  
CC proteins are useful as therapeutic agents for gene therapy or as  
CC vaccines. The present sequence was used to illustrate the invention.

XX Sequence 25 BP; 4 A; 2 C; 5 G; 14 T; 0 U; 0 Other;

Query Match 2.1%; Score 20.8; DB 1; Length 25;  
Best Local Similarity 91.7%; Pred. No. 1.2e+03;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 608 TTTTAAATTTTGGACAGAGCTC 631  
DB 1 TTTTATTTTGGACAGAGCTC 24

## RESULT 436

AD011741  
ID AD011741 standard; DNA; 25 BP.  
XX  
AC AD011741;  
XX  
XX 15-JUL-2004 (first entry)  
XX  
DE Single multiplex PCR primer #1113.  
XX  
KW ss: primer; simultaneous amplification;  
KW single multiplex polymerase chain reaction; multifactorial disease;  
KW genetic alteration; pharmacogenetic reaction; genotyping; polymorphism;  
KW gene expression profiling.  
XX  
OS Synthetic.  
XX  
PN WO2004033649-A2.  
XX  
PD 22-APR-2004.  
XX  
PF 07-OCT-2003; 2003WO-US031874.  
XX  
PR 07-OCT-2002; 2002US-0417009P.  
XX  
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.  
XX  
PI Li H, Li J;  
XX  
DR WPI; 2004-340914/31.  
XX  
PT Designing primers for simultaneous amplification of target DNA fragments  
PT in a single multiplex polymerase chain reaction, for high throughput  
PT multiplex DNA sequence amplification, comprises aligning two primers.  
XX  
PS Disclosure; Page 38; 120pp; English.  
XX  
XX The invention relates to a method of designing primers for simultaneous  
CC amplification of target DNA fragments in a single multiplex polymerase  
CC chain reaction by aligning a first primer and a second primer. The method  
CC comprises: (a) aligning a first primer and a second primer; and (b)  
CC selecting the first primer where the first primer at its 3' end does not  
CC contain four or more bases that are perfectly matching to the 3' end  
CC sequence of the first primer or a second primer, the first primer at its  
CC 3' end does not contain seven or more bases that are perfectly matching  
CC except one mismatch to the 3' end sequence of the first primer or the  
CC second primer, the first primer at its 3' end does not contain six or  
CC more bases that are perfectly matching to a sequence anywhere of the  
CC first primer or the second primer, and the first primer at its 3' end  
CC does not contain eleven or more bases that are perfectly matching except  
CC one mismatch to a sequence anywhere of the first primer or the second  
CC primer. The method is useful for designing primers for simultaneous  
CC amplification of target DNA fragments in a single multiplex polymerase  
CC chain reaction. It is also useful in the identification of multiple genes  
CC related to multifactorial diseases, the genome-scale detection of genetic  
CC alterations, the studies in pharmacogenetic reactions, the genotyping  
CC genetic polymorphisms in a large population, the gene expression  
CC profiling in various samples and high throughput genotyping technologies.  
CC This sequence corresponds to an example of a primer of the invention.  
XX  
SQ Sequence 25 BP; 5 A; 4 C; 8 G; 8 T; 0 U; 0 Other;  
XX  
Query Match 2.1%; Score 20.8; DB 1; Length 25;  
Best Local Similarity 91.7%; Pred. No. 1.2e+03;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 181 TAGAGATGAGCTTCTCCATGTTG 204  
DB 1 TAGAGATGAGCTTCTCCATGTTG 24  
RESULT 437  
AAZ25152  
ID AAZ25152 standard; DNA; 22 BP.

XX  
AC AAZ25152;  
XX  
XX 13-DEC-1999 (first entry)  
XX  
DE Human short interspersed repetitive element PCR primer #10.  
XX  
KW Human; short interspersed repetitive element; SINE; PCR; primer;  
KW Oncohychnus; restriction primer; short interspersed repeated sequence;  
KW eukaryote; restricted polymerase chain reaction fingerprinting;  
KW identification; DNA specimen; discrimination; ss.  
XX  
OS Synthetic.  
XX  
PN Homo sapiens.  
XX  
PN JP2913035-B1.  
XX  
PD 28-JUN-1999.  
XX  
PF 10-JUL-1998; 98JP-00195692.  
XX  
PR 10-JUL-1998; 98JP-00195692.  
XX  
PA (NORQ) NORINSUISANSHO SUIANCHO YOSHOKU KENKYUSHOCHO.  
XX  
DR WPI; 1999-583348/50.  
XX  
PT Restriction primer for distinguishing individuals with short interspersed  
PT repeated sequence of eukaryotes by restricted polymerase chain reaction  
PT fingerprinting.  
XX  
PS Claim 6; Page 3; 17pp; Japanese.  
XX  
XX The present invention describes a restriction primer for eukaryotic short  
CC interspersed repeated sequences (SINE), which has one or more additional  
CC bases that are a mismatch to, or are unrelated to, the 3'-terminal end of  
CC the SINE. The annealing temperature of the primer to the DNA sequence is  
CC kept higher than the fusion temperature of the primer during polymerase  
CC chain reaction (PCR). The PCR fragments obtained are subjected to  
CC electrophoresis to obtain a fingerprint. By comparing the polymorphs from  
CC the electrophoresis band pattern, eukaryotic individuals are  
CC distinguished. The primer is used for amplifying a eukaryotic  
CC deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by  
CC polymerase chain reaction (PCR) fingerprinting. In particular it may be  
CC used individual identification of humans for medical and legal  
CC applications and ecological studies. DNA specimens in traces  
CC (approximately 10 ng in mass) can be used for individual discrimination  
CC of eukaryotes using the primer in a polymerase chain reaction (PCR).  
CC AAZ25143 to AAZ25191 represent specifically claimed examples of primers  
CC from the present invention  
XX  
SQ Sequence 22 BP; 6 A; 5 C; 7 G; 4 T; 0 U; 0 Other;  
XX  
Query Match 2.1%; Score 20.4; DB 1; Length 22;  
Best Local Similarity 95.5%; Pred. No. 1.1e+03;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 868 GGATACAGCGGTGACCA 889  
DB 1 GGATACAGCGGTGACCA 22  
RESULT 438  
AAZ25149  
ID AAZ25149 standard; DNA; 22 BP.  
XX  
XX AAZ25149;  
XX  
XX 13-DEC-1999 (first entry)  
XX  
DE Human short interspersed repetitive element PCR primer #7.  
XX  
KW Human; short interspersed repetitive element; SINE; PCR; primer;

KW OncoRhynchus; restriction primer; short interspersed repeated sequence;  
KW eukaryote; restricted polymerase chain reaction fingerprinting;  
KM identification; DNA specimen; discrimination; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX JP2913035-B1.  
XX  
XX 28-JUN-1999.  
XX  
XX 10-JUL-1998; 98JP-00195692.  
XX  
XX 10-JUL-1998; 98JP-00195692.  
XX  
XX (NORQ ) NORINSUISANSHO SUI SANCHO YOSHOKU KENKYUSHOCHO.  
XX  
XX WPI; 1999-583348/50.  
XX  
XX Restriction primer for distinguishing individuals with short interspersed  
PT repeated sequence of eukaryotes by restricted polymerase chain reaction  
PT fingerprinting.  
XX  
XX Claim 6; Page 3; 17pp; Japanese.  
XX  
XX The present invention describes a restriction primer for eukaryotic short  
CC interspersed repeated sequences (SINE), which has one or more additional  
CC bases that are a mismatch to, or are unrelated to, the 3'-terminal end of  
CC the SINE. The annealing temperature of the primer to the DNA sequence is  
CC kept higher than the fusion temperature of the primer during polymerase  
CC chain reaction (PCR). The PCR fragments obtained are subjected to  
CC electrophoresis to obtain a fingerprint. By comparing the polymorphs from  
CC the electrophoresis band pattern, eukaryotic individuals are  
CC distinguished. The primer is used for amplifying a eukaryotic  
CC deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by  
CC polymerase chain reaction (PCR) fingerprinting. In particular it may be  
CC used individual identification of humans for medical and legal  
CC applications and ecological studies. DNA specimens in traces  
CC (approximately 10 ng in mass) can be used for individual discrimination  
CC of eukaryotes using the primer in a polymerase chain reaction (PCR).  
CC AA225143 to AA225191 represent specifically claimed examples of primers  
CC from the present invention  
CC  
SQ Sequence 22 BP; 6 A; 5 C; 8 G; 3 T; 0 U; 0 Other;  
XX  
XX  
XX Query Match 2.1%; Score 20.4; DB 1; Length 22;  
XX Best Local Similarity 95.5%; Pred. No. 1.1e+03;  
XX Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 868 GGATTACAGCGCTGAGCCACCA 889  
DB 1 GGATTACAGCGCTGAGCCACCA 22  
XX  
XX  
XX RESULT 439  
XX AA225146  
XX AA225146 standard; DNA; 22 BP.  
XX  
XX AA225146;  
XX  
XX 13-DEC-1999 (first entry)  
XX  
XX Human short interspersed repetitive element PCR primer #4.  
XX  
XX Human, short interspersed repetitive element; SINE; PCR; primer;  
KW OncoRhynchus; restriction primer; short interspersed repeated sequence;  
KW eukaryote; restricted polymerase chain reaction fingerprinting;  
XX identification; DNA specimen; discrimination; ss.  
XX  
XX Synthetic.  
OS Homo sapiens.  
XX  
XX JP2913035-B1.

XX  
XX 28-JUN-1999.  
XX  
XX 10-JUL-1998; 98JP-00195692.  
XX  
XX 10-JUL-1998; 98JP-00195692.  
XX  
XX (NORQ ) NORINSUISANSHO SUI SANCHO YOSHOKU KENKYUSHOCHO.  
XX  
XX WPI; 1999-583348/50.  
XX  
XX Restriction primer for distinguishing individuals with short interspersed  
PT repeated sequence of eukaryotes by restricted polymerase chain reaction  
PT fingerprinting.  
XX  
XX Claim 6; Page 3; 17pp; Japanese.  
XX  
XX The present invention describes a restriction primer for eukaryotic short  
CC interspersed repeated sequences (SINE), which has one or more additional  
CC bases that are a mismatch to, or are unrelated to, the 3'-terminal end of  
CC the SINE. The annealing temperature of the primer to the DNA sequence is  
CC kept higher than the fusion temperature of the primer during polymerase  
CC chain reaction (PCR). The PCR fragments obtained are subjected to  
CC electrophoresis to obtain a fingerprint. By comparing the polymorphs from  
CC the electrophoresis band pattern, eukaryotic individuals are  
CC distinguished. The primer is used for amplifying a eukaryotic  
CC deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by  
CC polymerase chain reaction (PCR) fingerprinting. In particular it may be  
CC used individual identification of humans for medical and legal  
CC applications and ecological studies. DNA specimens in traces  
CC (approximately 10 ng in mass) can be used for individual discrimination  
CC of eukaryotes using the primer in a polymerase chain reaction (PCR).  
CC AA225143 to AA225191 represent specifically claimed examples of primers  
CC from the present invention  
CC  
SQ Sequence 22 BP; 7 A; 5 C; 7 G; 3 T; 0 U; 0 Other;  
XX  
XX  
XX Query Match 2.1%; Score 20.4; DB 1; Length 22;  
XX Best Local Similarity 95.5%; Pred. No. 1.1e+03;  
XX Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 868 GGATTACAGCGCTGAGCCACCA 889  
DB 1 GGATTACAGCGCTGAGCCACCA 22  
XX  
XX  
XX RESULT 440  
XX AAC69376/C  
XX AAC69376 standard; DNA; 22 BP.  
XX  
XX AAC69376;  
XX  
XX 29-JAN-2001 (first entry)  
XX  
XX Human ABC1 BAC contig polymorphic site, SEQ ID NO:275.  
XX  
XX Human ABC1 cholesterol transporter; chromosome 9q31;  
KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;  
KW Tangier disease; TD; familial HDL deficiency; FHL; polymorphism;  
KW cardiovascular disease; coronary artery disease; coronary stenosis;  
KW cerebrovascular disease; peripheral vascular disease;  
KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;  
KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;  
KW prognosis; prophylaxis; drug screening; transgenic animal; de.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO20005318-A2.  
XX  
XX 21-SEP-2000.  
XX  
XX 15-MAR-2000; 2000WO-IB000532.  
XX  
XX



PR 15-MAR-1999; 99US-0124702P.  
PR 08-JUN-1999; 99US-0138048P.  
PR 17-JUN-1999; 99US-0139600P.  
PR 01-SEP-1999; 99US-0151977P.  
XX (UYBR-) UNIV BRITISH COLUMBIA.  
PA (XENO-) XENON BIORESEARCH INC.  
XX Hayden MR, Wilson AR, Pimstone SN,  
XX WPI, 2000-587528/55.  
XX  
XX New ABC1 polypeptide is useful for treating diseases associated with ABC1  
PT biological activity, e.g. Alzheimer's disease, Huntington's disease and  
PT cancer.  
XX  
XX Example, Fig 11; 229pp; English.  
XX  
XX The invention relates to the human ABC1 cholesterol transporter protein  
XX (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is  
XX a member of the ATP-binding cassette (ABC transporter) superfamily of  
XX proteins, and plays a crucial role in cholesterol transport, particularly  
XX intracellular cholesterol trafficking in monocytes and fibroblasts, being  
XX involved in cholesterol efflux from the cell. The gene encoding ABC1 is  
XX located on chromosome 9q31, and mutations in this gene are associated  
XX with two genetic HDL (high density lipoprotein) deficiency disorders,  
XX Tangier disease (TD) and familial HDL deficiency (FHD). These diseases  
XX are distinguishable in that TD is an autosomal recessive disorder, while  
XX FHD is inherited as an autosomal dominant trait. Low levels of HDL ('good  
XX cholesterol') in the blood correlate with a high risk of cardiovascular  
XX disease, particularly coronary artery disease, but also cerebrovascular  
XX disease, coronary restenosis, and peripheral vascular disease.  
XX Conversely, a high level of HDL has protective effects against  
XX cardiovascular disease. The invention provides genetic constructs and  
XX transgenic cells and non-human animals comprising human ABC1 nucleic  
XX acids, and methods of gene therapy for the treatment or prevention of  
XX cardiovascular disease comprising the administration of an expression  
XX vector encoding ABC1 or an active fragment thereof. The invention also  
XX encompasses compounds which mimic ABC1 activity, compounds which  
XX stimulate ABC1 expression and methods of screening for such compounds. It  
XX further relates to methods for determining whether a patient has an  
XX increased risk for cardiovascular disease due to polymorphisms in the  
XX ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat or  
XX prevent cardiovascular disease, especially coronary artery disease,  
XX cerebrovascular disease, coronary restenosis or peripheral vascular  
XX disease. They may also be used in the treatment of diseases associated  
XX with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick  
XX disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.  
XX The invention specifically excludes proteins with the exact amino acid  
XX sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic  
XX acid with the exact sequence as GenBank Accession No: A7012376.1. The  
XX present sequence represents a polymorphic site of the human ABC1 gene  
XX  
XX Sequence 22 BP; 6 A; 2 C; 11 G; 3 T; 0 U; 0 Other:  
SQ  
XX  
XX Query Match 2.1%; Score 20.4; DB 1; Length 22;  
XX Best Local Similarity 95.5%; Pred. No. 1.1e+03;  
XX Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 533 TCCTCTGCTGCTGAGCTCCCA 554  
DB 22 TTCTCTGCTGCTGAGCTCCCA 1

RESULT 441  
AAF74132  
ID AAF74132 standard; DNA; 22 BP.  
XX  
XX AAF74132;  
XX  
XX 30-APR-2001 (first entry)  
XX  
XX Primer #66.  
DE

XX  
XX solute carrier family 6 neurotransmitter transporter; serotonin 4; SLC6A4;  
XX genotyping; allele specific oligonucleotide; ss.  
XX  
XX Homo sapiens.  
XX WO200109161-A1.  
XX  
XX  
XX 08-FEB-2001.  
XX  
XX 31-JUL-2000; 2000WO-US020638.  
XX  
XX  
XX 29-UTL-1999; 99US-0146290P.  
XX  
XX (GENA-) GENAISANCE PHARM INC.  
XX  
XX Denton RR, Duda A, Nandabalan K, Sanchis A, Stephens JC,  
XX WPI; 2001-123317/13.  
XX  
XX New isolated polynucleotide comprising a polymorphic variant for the  
PT solute carrier family 6 neurotransmitter transporter, serotonin member 4  
PT gene for identifying drugs for treating disorders related to expression  
PT of the protein.  
XX  
XX Example 1; Page 38; 152pp; English.  
XX  
XX The present invention relates to a polymorphic variant of a reference  
XX sequence for the solute carrier family 6 neurotransmitter transporter,  
XX serotonin member 4 (SLC6A4) gene or a fragment of it or a sequence  
XX complementary to the first sequence. The invention is used in producing a  
XX recombinant organism that can be used to express SLC6A4 for protein  
XX structure analysis and binding studies. A composition comprising a  
XX genotyping oligonucleotide is used to detect a polymorphism in the SLC6A4  
XX gene  
XX  
XX Sequence 22 BP; 6 A; 6 C; 6 G; 4 T; 0 U; 0 Other:  
SQ  
XX  
XX Query Match 2.1%; Score 20.4; DB 1; Length 22;  
XX Best Local Similarity 95.5%; Pred. No. 1.1e+03;  
XX Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 870 ATTACGAGCTGTAGCCACACG 891  
DB 1 ATTACGAGCTGTAGCCACACG 22

RESULT 442  
ADL66997  
ID ADL66997 standard; DNA; 22 BP.  
XX  
XX ADL66997;  
XX  
XX 03-JUN-2004 (first entry)  
XX  
XX Multiplex PCR primer #1.  
XX  
XX DNA polymerase; anti-DNAp antibody; reverse transcriptase;  
XX anti-RT antibody; single strand binding protein; SSB; ss; primer.  
XX  
XX Synthetic.  
XX WO2004022770-A2.  
XX  
XX 18-MAR-2004.  
XX  
XX 05-SEP-2003; 2003WO-US027705.  
XX  
XX 05-SEP-2002; 2002US-0408609P.  
XX  
XX 19-NOV-2002; 2002US-0427867P.  
XX  
XX (INVT-) INVITROGEN CORP.  
XX

PI Park K;  
XX  
XX WPI; 2004-248479/23.  
XX  
XX New compositions comprising one or more anti-reverse transcriptase  
PT antibodies, anti-DNA polymerases or single strand binding proteins,  
XX useful for synthesizing nucleic acids.  
XX  
XX Example 4; Page 89; 201pp; English.  
XX  
XX The invention relates to a new composition which comprises at least one  
CC anti-DNA polymerases (anti-DNAp) antibody and/or at least one anti-  
CC reverse transcriptase (anti-RT) antibody, and at least one single strand  
CC binding protein (SSB) or at least two different SSBs. The compositions  
CC are useful for nucleic acid synthesis reactions or are generated during  
CC nucleic acid synthesis reactions. The methods are useful for synthesizing  
CC one or more nucleic acid molecules. The compositions and methods are also  
CC be used in amplifying nucleic acid molecules, in reverse transcription of  
CC nucleic acid molecules and in coupled or uncoupled reverse  
CC transcription/amplification. The present sequence is used in the  
CC exemplification of the present invention.  
XX  
XX Sequence 22 BP; 4 A; 3 C; 10 G; 5 T; 0 U; 0 Other;  
SQ  
Query Match 2.1%; Score 20.4; DB 1; Length 22;  
Best Local Similarity 95.5%; Pred. No. 1.1e+03;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
QY 647 GGCTGAGTGCAGTGGCGCAAT 668  
DB 1 GGCTGAGTGCAGTGGCGCAAT 22  
XX  
RESULT 443  
ID ADO30457 standard; DNA; 22 BP.  
XX  
XX ADO30457;  
AC  
XX  
XX 29-JUL-2004 (first entry)  
DT  
XX  
DE Human novel GPCR PGR4 RT-PCR primer, SEQ ID NO:1560.  
XX  
XX G protein-coupled receptor; GPCR; drug screening; diagnosis;  
KW transgenic mouse; neurological disorder; cardiovascular disorder;  
KW colon disorder; intestinal disorder; immune disorder; bone disorder;  
KW muscular disorder; blood disorder; liver disorder; cancer;  
KW joint disorder; metabolic disorder; nutritive disorder; breast disorder;  
KW kidney disorder; lung disorder; prostate disorder; testis disorder;  
KW ovary disorder; uterus disorder; pancreas disorder; spleen disorder;  
KW skin disorder; stomach disorder; antiparkinsonian; anti-anemic;  
KW chymus disorder; thyroid disorder; antidiarrheal; antiarrhythmic;  
KW cytostatic; antiinflammatory; vasotropic; antidiabetic;  
KW CNS; central nervous system; respiratory; antidiarrheal; antidiabetic;  
KW virucide; hepatotropic; antibacterial; antianemic; anorectic;  
KW dermatological; anticancer; antithyroid; antiallergic; anorectic;  
KW immunosuppressive; nephrotoxic; gene therapy; GPCR modulator; human;  
KW PGR4; reverse transcription-PCR; RT-PCR; primer; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO2004040000-A2.  
PN  
XX  
XX 13-MAY-2004.  
PD  
XX  
XX 09-SEP-2003; 2003WO-US028226.  
PF  
XX  
XX 09-SEP-2002; 2002US-0409303P.  
PR  
XX 09-APR-2003; 2003US-0461329P.  
XX  
XX (PRIM-) PRIMAL INC.  
PA  
XX Galanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;  
PI

PI Madisen L, McIlwain KL, Pavlova MN, Vassiliadis D, Zeng H;  
XX  
XX WPI; 2004-390329/36.  
XX  
XX Novel mammalian G protein coupled receptors, useful for identifying  
PT compounds that modulate diagnosing and treating disease condition  
PT associated with GPCR dysfunction e.g. autoimmune disease, angina  
XX pectoris, Parkinson's disease.  
XX  
XX Disclosure; SEQ ID NO 1560; 542pp; English.  
XX  
XX The invention relates to human and mouse G protein-coupled receptors  
CC (GPCRs) and nucleic acids encoding them. The invention also relates to  
CC sequences at least 90% identical to the GPCR proteins and nucleic acids  
CC of the invention; methods of treating, preventing or diagnosing diseases  
CC associated with GPCRs of the invention; methods of screening for  
CC compounds useful in the treatment of GPCR-related diseases; a transgenic  
CC mouse comprising a GPCR gene or the invention; a mouse comprising a  
CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived  
CC from the transgenic mice; kits comprising several mice, each of which has  
CC a mutation in a different GPCR gene of the invention; and kits comprising  
CC probes which hybridise to GPCR polynucleotides of the invention. The  
CC invention further discloses variants of the GPCR polypeptides and vectors  
CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may  
CC be used in the diagnosis, treatment or prevention of a wide variety of  
CC diseases including neurological disorders (e.g., Alzheimer's disease,  
CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);  
CC disorders of the adrenal gland; disorders of the colon or intestine  
CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel  
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or  
CC myocardial infarction); muscular disorders; blood disorders (e.g.,  
CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or  
CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid  
CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,  
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related  
CC diseases); and disorders of the kidney, liver, lung, breast, ovary,  
CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and  
CC thyroid (e.g., cancers). The present sequence represents a PCR primer  
CC used in the isolation of cDNA encoding the novel human GPCR PGR4. Note:  
CC The full sequence data for this patent did not form part of the printed  
CC specification; those sequences not shown were obtained in electronic  
CC format directly from WIPO at [ftp.wipo.int/pub/published\\_pat\\_sequences](http://ftp.wipo.int/pub/published_pat_sequences).  
XX  
XX Sequence 22 BP; 3 A; 4 C; 8 G; 7 T; 0 U; 0 Other;  
SQ  
Query Match 2.1%; Score 20.4; DB 1; Length 22;  
Best Local Similarity 95.5%; Pred. No. 1.1e+03;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
QY 201 GTTGCTCAGGCTGCTCGAAC 222  
DB 1 GTTGCTCAGGCTGCTCGAAC 22  
XX  
RESULT 444  
ID AAF69748 standard; DNA; 23 BP.  
XX  
XX AAF69748;  
AC  
XX  
XX 18-APR-2001 (first entry)  
DT  
XX  
XX Human IL4alpha gene PCR primer #84.  
DE  
XX  
XX Polymorphism; human; interleukin 4 receptor-alpha; IL4R-alpha;  
KW allergic disease; PCR primer; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200104270-A1.  
PN  
XX  
XX 18-JAN-2001.  
PD  
XX  
XX

PF 13-JUL-2000; 2000WO-US019094.  
XX  
XX 13-JUL-1999; 99US-0143435P.  
XX  
XX (GENA-) GENAISSANCE PHARM INC.  
PA  
XX Chew A, Denton RR, Duda A, Nandabalan K, Stephens JC;  
PI Windemuth AK;  
XX  
XX MPI; 2001-103078/11.  
DR  
XX  
XX New isolated polynucleotide useful for the identification of therapeutics  
PT in allergic diseases is new.  
XX  
XX Example 1; Page 64; 188pp; English.  
XX  
XX The present invention relates to polymorphisms of the human interleukin 4  
CC receptor-alpha gene (IL4R-alpha; see AAF57718 for the reference  
CC sequence). Polynucleotides comprising polymorphic gene variants are  
CC useful for therapeutic purposes. For example, where a patient may benefit  
CC from expression of a particular IL4Ralpha protein isoform, an expression  
CC vector encoding the isoform may be administered to the patient. It may  
CC desirable to decrease or block expression of a particular IL4Ralpha  
CC isogene, which may be done by turning off by transforming a targeted  
CC organ, tissue or cell population with an expression vector that expresses  
CC high levels of untranslatable mRNA for the isogene. Specific therapeutics  
CC identified by these methods may be useful for allergic diseases. The  
CC present sequence is a PCR primer for human IL4R-alpha  
XX  
XX Sequence 23 BP; 5 A; 8 C; 3 G; 7 T; 0 U; 0 Other;  
SQ  
Query Match 2.1%; Score 20.4; DB 1; Length 23;  
Best Local Similarity 95.5%; Pred. No. 1.2e+03;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 578 CCACATACCTGCTTAATTTT 599  
DB 1 CCACACACCTGCTTAATTTT 22  
RESULT 445  
AAH49787  
ID AAH49787 standard; DNA; 24 BP.  
XX  
XX AAH49787;  
AC  
XX  
XX 25-SEP-2001 (first entry)  
DT  
XX  
XX Human uncoiling enzyme 9 coding sequence PCR primer #2.  
DE  
XX  
XX Human; uncoiling enzyme 9; cancer; haemopathy; HIV infection;  
KM immunological disease; inflammation; gene therapy; PCR primer; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200149860-A1.  
PN  
XX  
XX 12-JUL-2001.  
PD  
XX  
XX 18-DEC-2000; 2000WO-CN000616.  
PF  
XX  
XX 24-DEC-1999; 99CN-00125756.  
PR  
XX  
XX (BIOW-) BIOWINDOW GENE DEV LTD SHANGHAI.  
PA  
XX  
XX Mao Y, Xie Y;  
PI  
XX  
XX MPI; 2001-432884/46.  
DR  
XX  
XX Uncoiling enzyme 9 and encoded polynucleotide, applicable in diagnosis  
PT and treatment of endoparasitosis, hemopathy, HIV infection, immunological  
PT diseases and various inflammation.  
XX

PS Example 3; Page 11; 32pp; Chinese.  
XX  
XX The present invention provides the protein and coding sequences of human  
CC uncoiling enzyme 9. The sequences can be used in the treatment of cancer,  
CC haemopathy, HIV infection, immunological diseases and inflammation. The  
CC present sequence is a PCR primer for the coding sequence of the invention  
XX  
XX Sequence 24 BP; 5 A; 4 C; 7 G; 8 T; 0 U; 0 Other;  
SQ  
Query Match 2.1%; Score 20.4; DB 1; Length 24;  
Best Local Similarity 95.5%; Pred. No. 1.2e+03;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 182 AGAGATGAGTTTCTCCATGTT 203  
DB 1 AGAGATGAGTTTCTCCATGTT 22  
RESULT 446  
ABS56869  
ID ABS56869 standard; DNA; 24 BP.  
XX  
XX ABS56869;  
AC  
XX  
XX 30-JUN-2003 (first entry)  
DT  
XX  
XX Human receptor related tyrosine kinase 10.01 cDNA RT-PCR primer #2.  
DE  
XX  
XX Human; receptor related tyrosine kinase 10.01; primer; ss; peptic ulcer;  
KM embryonic development deformity; tumour; diabetes; menstrual disorder;  
KM cancer; anaemia; epilepsy; RT-PCR; reverse transcriptase.  
XX  
XX Homo sapiens.  
OS  
XX  
XX CN1345961-A.  
PN  
XX  
XX 24-APR-2002.  
PD  
XX  
XX 29-SEP-2000; 2000CN-00125572.  
PF  
XX  
XX 29-SEP-2000; 2000CN-00125572.  
PR  
XX  
XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.  
PA  
XX  
XX Mao Y, Xie Y;  
PI  
XX  
XX MPI; 2002-539360/58.  
DR  
XX  
XX New polypeptide-human receptor related tyrosine kinase 10.01 for treating  
PT embryonic development deformity, tumor, diabetes, menstrual disorder,  
PT peptic ulcer, anemia and epilepsy.  
XX  
XX Example 2; Page 18 (Disclosure); 34pp; Chinese.  
PS  
XX  
XX The invention relates to the human receptor related tyrosine kinase  
CC 10.01, a polynucleotide encoding the polypeptide and a method for  
CC producing the polypeptide by DNA recombination technology. The  
CC polypeptide is used for curing several diseases such as embryonic  
CC development deformity, tumours, diabetes, menstrual disorder, peptic  
CC ulcer, anaemia and epilepsy. This sequence represents a reverse  
CC transcriptase PCR (RT-PCR) primer used in isolation of cDNA encoding  
CC human receptor related tyrosine kinase 10.01  
XX  
XX Sequence 24 BP; 4 A; 7 C; 6 G; 7 T; 0 U; 0 Other;  
SQ  
Query Match 2.1%; Score 20.4; DB 1; Length 24;  
Best Local Similarity 95.5%; Pred. No. 1.2e+03;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 925 TGGATCTCACTCTGTACCA 946  
DB 3 TGGATCTCACTCTGTACCA 24

```
RESULT 448
AAH40563/C
ID AAH40563 standard; DNA; 25 BP.
XX
XX
XX AAH40563;
AC
XX
XX
XX 14-AUG-2001 (first entry)
DT
XX
XX SNP specific SNPE primer SEQ ID 3359.
DE
XX
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
XX SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
XX Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
XX inflammation; forensic investigation; paternity analysis; primer; ss.
XX
XX Homo sapiens.
XX
XX OS
XX PN WO200129262-A2.
XX
XX PD 26-APR-2001.
XX
XX PF 13-OCT-2000; 2000WO-US028436.
XX
XX PR 15-OCT-1999; 99US-0160096P.
XX
XX (ORCH-) ORCHID BIOSCIENCES INC.
XX
XX PA Picoult-Newburg L, Pohl M;
XX
XX PI
XX
XX DR MPI; 2001-290930/30.
XX
XX PT New genotyping oligonucleotide, useful for detecting the presence,
XX PT absence or identity of single polynucleotide polymorphism in a nucleic
XX PT acid sample.
XX
XX PS Claim 1; Page 67; 83pp; English.
XX
XX CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
XX CC primer extension (SNPE) primers, and the sequences of regions flanking
XX CC sites of single nucleotide polymorphisms SNPs. The present invention
XX CC includes kits for determining the presence or absence of a SNP, using the
XX CC oligonucleotides of the invention. The PCR primers are used to amplify a
XX CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
XX CC The oligonucleotides are useful for genotyping a nucleic acid sample by
XX CC performing a single-nucleotide primer extension reaction. The
XX CC oligonucleotides are useful for determining the presence, absence or
XX CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
XX CC assess by association analysis the genotype of an individual or group of
XX CC individuals, having a pathological phenotypic trait suspected of being
XX CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
XX CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
XX CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
XX CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
XX CC traits also include symptoms of or susceptibility to multifactorial
XX CC disease of which a component is or may be genetic such as autoimmune
XX CC diseases, including, rheumatoid arthritis, multiple sclerosis,
XX CC inflammation, cancer, nervous system diseases and infection by pathogenic
XX CC microorganism. The method is also useful in forensic investigations and
XX CC paternity analysis. The present sequence represents a single nucleotide
XX CC primer extension (SNPE) primer specific for a human SNP containing DNA
XX CC sequence
XX
XX SQ Sequence 25 BP; 7 A; 4 C; 11 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 2.1%; Score 20.4; DB 1; Length 25;
XX Best Local Similarity 95.5%; Pred. No. 1.2e+03;
XX Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
DB 22 TCCTGCCTCAGCCTCCCAAGTA 1
RESULT 448
AAH38991/C
ID AAH38991 standard; DNA; 25 BP.
XX
XX
XX AAH38991;
AC
XX
XX
XX 14-AUG-2001 (first entry)
DT
XX
XX SNP specific SNPE primer SEQ ID 1787.
DE
XX
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
XX SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
XX Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
XX inflammation; forensic investigation; paternity analysis; primer; ss.
XX
XX OS
XX PN WO200129262-A2.
XX
XX PD 26-APR-2001.
XX
XX PF 13-OCT-2000; 2000WO-US028436.
XX
XX PR 15-OCT-1999; 99US-0160096P.
XX
XX (ORCH-) ORCHID BIOSCIENCES INC.
XX
XX PA Picoult-Newburg L, Pohl M;
XX
XX PI
XX
XX DR MPI; 2001-290930/30.
XX
XX PT New genotyping oligonucleotide, useful for detecting the presence,
XX PT absence or identity of single polynucleotide polymorphism in a nucleic
XX PT acid sample.
XX
XX PS Claim 1; Page 59; 83pp; English.
XX
XX CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
XX CC primer extension (SNPE) primers, and the sequences of regions flanking
XX CC sites of single nucleotide polymorphisms SNPs. The present invention
XX CC includes kits for determining the presence or absence of a SNP, using the
XX CC oligonucleotides of the invention. The PCR primers are used to amplify a
XX CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
XX CC The oligonucleotides are useful for genotyping a nucleic acid sample by
XX CC performing a single-nucleotide primer extension reaction. The
XX CC oligonucleotides are useful for determining the presence, absence or
XX CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
XX CC assess by association analysis the genotype of an individual or group of
XX CC individuals, having a pathological phenotypic trait suspected of being
XX CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
XX CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
XX CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
XX CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
XX CC traits also include symptoms of or susceptibility to multifactorial
XX CC disease of which a component is or may be genetic such as autoimmune
XX CC diseases, including, rheumatoid arthritis, multiple sclerosis,
XX CC inflammation, cancer, nervous system diseases and infection by pathogenic
XX CC microorganism. The method is also useful in forensic investigations and
XX CC paternity analysis. The present sequence represents a single nucleotide
XX CC primer extension (SNPE) primer specific for a human SNP containing DNA
XX CC sequence
XX
XX SQ Sequence 25 BP; 5 A; 5 C; 11 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 2.0%; Score 20.2; DB 1; Length 25;
XX Best Local Similarity 88.0%; Pred. No. 1.3e+03;
XX Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

Oy 843 CCTGCTCGGCTCCCAAGTCTG 867  
Db 25 CCGGCTTGACTCCCAAGTCTG 1

## RESULT 449

AAH40899  
ID AAH40899 standard; DNA; 25 BP.

AC AAH40899;

DT 14-AUG-2001 (first entry)

DE SNP specific SNPE primer SEQ ID 3695.

Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;  
Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolemia;  
polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
inflammation; forensic investigation; paternity analysis; primer; ss.

OS Homo sapiens.

PN WO200129262-A2.

PD 26-APR-2001.

PF 13-OCT-2000; 2000WO-US028436.

PR 15-OCT-1999; 99US-0160096P.

PA (ORCH-) ORCHID BIOSCIENCES INC.

PI Picoult-Newburg L, Pohl M;

DR WPI; 2001-290930/30.

PT New genotyping oligonucleotide, useful for detecting the presence,  
PT absence or identity of single polynucleotide polymorphism in a nucleic  
PT acid sample.

PS Claim 1; Page 68; 83pp; English.

Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
primer extension (SNPE) primers, and the sequences of regions flanking  
sites of single nucleotide polymorphisms SNPs. The present invention  
includes kits for determining the presence or absence of a SNP, using the  
oligonucleotides of the invention. The PCR primers are used to amplify a  
SNP flanking sequence, the SNPE primer is used as a genotyping primer.  
The oligonucleotides are useful for genotyping a nucleic acid sample by  
performing a single-nucleotide primer extension reaction. The  
oligonucleotides are useful for determining the presence, absence or  
identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
assess by association analysis the genotype of an individual or group of  
individuals, having a pathological phenotypic trait suspected of being  
caused by one or more SNPs. Phenotypic traits include diseases e.g.  
agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular  
dystrophy, familial hypercholesterolemia, polycystic kidney disease,  
osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
traits also include symptoms of or susceptibility to multifactorial  
disease of which a component is or may be genetic such as autoimmune  
diseases, including, rheumatoid arthritis, multiple sclerosis,  
inflammation, cancer, nervous system diseases and infection by pathogenic  
microorganism. The method is also useful in forensic investigations and  
paternity analysis. The present sequence represents a single nucleotide  
primer extension (SNPE) primer specific for a human SNP containing DNA  
sequence

Sequence 25 BP; 3 A; 9 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 2.0%; Score 20.2; DB 1; Length 25;  
Best Local Similarity 88.0%; Pred. NO. 1.3e+03;

Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Oy 990 CCTCCCGGCTCAGCGATTCTCT 1014  
Db 1 CCTCCCGGCTTAGCGATTCTCT 25

## RESULT 450

AAH37979/C  
ID AAH37979 standard; DNA; 25 BP.

AC AAH37979;

DT 14-AUG-2001 (first entry)

DE SNP specific SNPE primer SEQ ID 775.

Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;  
Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolemia;  
polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
inflammation; forensic investigation; paternity analysis; primer; ss.

OS Homo sapiens.

PN WO200129262-A2.

PD 26-APR-2001.

PF 13-OCT-2000; 2000WO-US028436.

PR 15-OCT-1999; 99US-0160096P.

PA (ORCH-) ORCHID BIOSCIENCES INC.

PI Picoult-Newburg L, Pohl M;

DR WPI; 2001-290930/30.

PT New genotyping oligonucleotide, useful for detecting the presence,  
PT absence or identity of single polynucleotide polymorphism in a nucleic  
PT acid sample.

PS Claim 1; Page 53; 83pp; English.

Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
primer extension (SNPE) primers, and the sequences of regions flanking  
sites of single nucleotide polymorphisms SNPs. The present invention  
includes kits for determining the presence or absence of a SNP, using the  
oligonucleotides of the invention. The PCR primers are used to amplify a  
SNP flanking sequence, the SNPE primer is used as a genotyping primer.  
The oligonucleotides are useful for genotyping a nucleic acid sample by  
performing a single-nucleotide primer extension reaction. The  
oligonucleotides are useful for determining the presence, absence or  
identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
assess by association analysis the genotype of an individual or group of  
individuals, having a pathological phenotypic trait suspected of being  
caused by one or more SNPs. Phenotypic traits include diseases e.g.  
agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular  
dystrophy, familial hypercholesterolemia, polycystic kidney disease,  
osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
traits also include symptoms of or susceptibility to multifactorial  
disease of which a component is or may be genetic such as autoimmune  
diseases, including, rheumatoid arthritis, multiple sclerosis,  
inflammation, cancer, nervous system diseases and infection by pathogenic  
microorganism. The method is also useful in forensic investigations and  
paternity analysis. The present sequence represents a single nucleotide  
primer extension (SNPE) primer specific for a human SNP containing DNA  
sequence

Sequence 25 BP; 3 A; 6 C; 9 G; 7 T; 0 U; 0 Other;

Query Match 2.0%; Score 20.2; DB 1; Length 25;  
 Best Local Similarity 88.0%; Pred. No. 1.3e+03;  
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 869 GATTACAGCGGTGACGCCACACGCC 893  
 25 GATTACAGAGTGCACACACGCC 1

## RESULT 451

AAH37611/c  
 ID AAH37611 standard; DNA; 25 BP.  
 AC AAH37611;  
 XX  
 XX  
 DT 14-AUG-2001 (first entry)  
 DE SNP specific SNPE primer SEQ ID 407.  
 XX  
 XX

Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
 SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;  
 Leisch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;  
 poly cystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
 acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
 inflammation; forensic investigation; paternity analysis; primer; ss.

Homo sapiens.

WO200129262-A2.

26-APR-2001.

13-OCT-2000; 2000MO-US028436.

15-OCT-1999; 99US-0160096P.

(ORCH-) ORCHID BIOSCIENCES INC.

Picoult-Newburg L, Pohl M;

WPI; 2001-290930/30.

New genotyping oligonucleotide, useful for detecting the presence,  
 PT absence or identity of single polynucleotide polymorphism in a nucleic  
 PT acid sample.

Claim 1; Page 52; 83pp; English.

Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
 CC primer extension (SNPE) primers, and the sequences of regions flanking  
 CC sites of single nucleotide polymorphisms SNPs. The present invention  
 CC includes kits for determining the presence or absence of a SNP, using the  
 CC oligonucleotides of the invention. The PCR primers are used to amplify a  
 CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.  
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by  
 CC performing a single-nucleotide primer extension reaction. The  
 CC oligonucleotides are useful for determining the presence, absence or  
 CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
 CC assess by association analysis the genotype of an individual or group of  
 CC individuals, having a pathological phenotypic trait suspected of being  
 CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
 CC agammaglobulinemia, diabetes insipidus, Leisch-Nyhan syndrome, muscular  
 CC dystrophy, familial hypercholesterolaemia, poly cystic kidney disease,  
 CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
 CC traits also include symptoms of or susceptibility to multifactorial  
 CC disease of which a component is or may be genetic such as autoimmune  
 CC diseases, including, rheumatoid arthritis, multiple sclerosis,  
 CC inflammation, cancer, nervous system diseases and infection by pathogenic  
 CC microorganism. The method is also useful in forensic investigations and  
 CC paternity analysis. The present sequence represents a single nucleotide  
 CC primer extension (SNPE) primer specific for a human SNP containing DNA  
 XX sequence

SQ Sequence 25 BP; 16 A; 6 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 20.2; DB 1; Length 25;  
 Best Local Similarity 88.0%; Pred. No. 1.3e+03;  
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 165 TTGTATTTTTTTTTTTAGAGATCG 189  
 25 TTTTATTTTTTTTTTTAGAGATCG 1

## RESULT 452

AAH39587  
 ID AAH39587 standard; DNA; 25 BP.  
 AC AAH39587;  
 XX  
 XX  
 DT 14-AUG-2001 (first entry)  
 DE SNP specific SNPE primer SEQ ID 2383.  
 XX  
 XX

Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
 SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;  
 Leisch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;  
 poly cystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
 acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
 inflammation; forensic investigation; paternity analysis; primer; ss.

Homo sapiens.

WO200129262-A2.

26-APR-2001.

13-OCT-2000; 2000MO-US028436.

15-OCT-1999; 99US-0160096P.

(ORCH-) ORCHID BIOSCIENCES INC.

Picoult-Newburg L, Pohl M;

WPI; 2001-290930/30.

New genotyping oligonucleotide, useful for detecting the presence,  
 PT absence or identity of single polynucleotide polymorphism in a nucleic  
 PT acid sample.

Claim 1; Page 62; 83pp; English.

Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
 CC primer extension (SNPE) primers, and the sequences of regions flanking  
 CC sites of single nucleotide polymorphisms SNPs. The present invention  
 CC includes kits for determining the presence or absence of a SNP, using the  
 CC oligonucleotides of the invention. The PCR primers are used to amplify a  
 CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.  
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by  
 CC performing a single-nucleotide primer extension reaction. The  
 CC oligonucleotides are useful for determining the presence, absence or  
 CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
 CC assess by association analysis the genotype of an individual or group of  
 CC individuals, having a pathological phenotypic trait suspected of being  
 CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
 CC agammaglobulinemia, diabetes insipidus, Leisch-Nyhan syndrome, muscular  
 CC dystrophy, familial hypercholesterolaemia, poly cystic kidney disease,  
 CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
 CC traits also include symptoms of or susceptibility to multifactorial  
 CC disease of which a component is or may be genetic such as autoimmune  
 CC diseases, including, rheumatoid arthritis, multiple sclerosis,  
 CC inflammation, cancer, nervous system diseases and infection by pathogenic  
 CC microorganism. The method is also useful in forensic investigations and  
 CC paternity analysis. The present sequence represents a single nucleotide  
 CC primer extension (SNPE) primer specific for a human SNP containing DNA  
 CC sequence

CC sequence  
 XX SQ Sequence 25 BP; 4 A; 10 C; 4 G; 7 T; 0 U; 0 Other;  
 Query Match 2.0%; Score 20.2; DB 1; Length 25;  
 Best Local Similarity 88.0%; Pred. No. 1.3e+03;  
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 689 GCCTCCCGGGTCAAGTATCTCC 713  
 Db 1 GCCTCCCGGGTCAAGTATCTCC 25  
 RESULT 453  
 AAH39123  
 ID AAH39123 standard; DNA; 25 BP.  
 AC AAH39123;  
 XX  
 DT 14-AUG-2001 (first entry)  
 XX  
 DE SNP specific SNPE primer SEQ ID 1919.  
 XX  
 XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
 XX SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;  
 XX Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;  
 XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
 XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
 XX inflammation; forensic investigation; paternity analysis; primer; ss.  
 OS Homo sapiens.  
 XX  
 PN WO200129262-A2.  
 XX  
 PD 26-APR-2001.  
 XX  
 PF 13-OCT-2000; 2000WO-US028436.  
 XX  
 PR 15-OCT-1999; 99US-0160096P.  
 XX  
 PA (ORCH-) ORCHID BIOSCIENCES INC.  
 XX  
 PI Picoult-Newburg L, Pohl M;  
 DR WPI; 2001-290930/30.  
 XX  
 PT New genotyping oligonucleotide, useful for detecting the presence,  
 PT absence or identity of single polynucleotide polymorphism in a nucleic  
 PT acid sample.  
 XX  
 PS Claim 1; Page 59; 83pp; English.  
 XX  
 CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
 CC primer extension (SNPE) primers, and the sequences of regions flanking  
 CC sites of single nucleotide polymorphisms SNPs. The present invention  
 CC includes kits for determining the presence or absence of a SNP, using the  
 CC oligonucleotides of the invention. The PCR primers are used to amplify a  
 CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.  
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by  
 CC performing a single-nucleotide primer extension reaction. The  
 CC oligonucleotides are useful for determining the presence, absence or  
 CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
 CC assess by association analysis the genotype of an individual or group of  
 CC individuals, having a pathological phenotypic trait suspected of being  
 CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
 CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular  
 CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,  
 CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
 CC traits also include symptoms of or susceptibility to multifactorial  
 CC diseases of which a component is or may be genetic such as autoimmune  
 CC diseases, including, rheumatoid arthritis, multiple sclerosis,  
 CC inflammation, cancer, nervous system diseases and infection by pathogenic  
 CC microorganism. The method is also useful in forensic investigations and

CC paternity analysis. The present sequence represents a single nucleotide  
 CC primer extension (SNPE) primer specific for a human SNP containing DNA  
 CC sequence  
 XX SQ Sequence 25 BP; 4 A; 8 C; 5 G; 8 T; 0 U; 0 Other;  
 Query Match 2.0%; Score 20.2; DB 1; Length 25;  
 Best Local Similarity 88.0%; Pred. No. 1.3e+03;  
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 693 CCCGGTCAAGTATCTCTGCC 717  
 Db 1 CCTGGTTCAATGATCTCTGCC 25  
 RESULT 454  
 AAH40067/c  
 ID AAH40067 standard; DNA; 25 BP.  
 AC AAH40067;  
 XX  
 DT 14-AUG-2001 (first entry)  
 XX  
 DE SNP specific SNPE primer SEQ ID 2863.  
 XX  
 XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
 XX SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;  
 XX Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;  
 XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
 XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
 XX inflammation; forensic investigation; paternity analysis; primer; ss.  
 OS Homo sapiens.  
 XX  
 PN WO200129262-A2.  
 XX  
 PD 26-APR-2001.  
 XX  
 PF 13-OCT-2000; 2000WO-US028436.  
 XX  
 PR 15-OCT-1999; 99US-0160096P.  
 XX  
 PA (ORCH-) ORCHID BIOSCIENCES INC.  
 XX  
 PI Picoult-Newburg L, Pohl M;  
 DR WPI; 2001-290930/30.  
 XX  
 PT New genotyping oligonucleotide, useful for detecting the presence,  
 PT absence or identity of single polynucleotide polymorphism in a nucleic  
 PT acid sample.  
 XX  
 PS Claim 1; Page 64; 83pp; English.  
 XX  
 CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
 CC primer extension (SNPE) primers, and the sequences of regions flanking  
 CC sites of single nucleotide polymorphisms SNPs. The present invention  
 CC includes kits for determining the presence or absence of a SNP, using the  
 CC oligonucleotides of the invention. The PCR primers are used to amplify a  
 CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.  
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by  
 CC performing a single-nucleotide primer extension reaction. The  
 CC oligonucleotides are useful for determining the presence, absence or  
 CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
 CC assess by association analysis the genotype of an individual or group of  
 CC individuals, having a pathological phenotypic trait suspected of being  
 CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
 CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular  
 CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,  
 CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
 CC traits also include symptoms of or susceptibility to multifactorial  
 CC diseases of which a component is or may be genetic such as autoimmune  
 CC diseases, including, rheumatoid arthritis, multiple sclerosis,







SQL Sequence 25 BP; 3 A; 9 C; 5 G; 8 T; 0 U; 0 Other;  
Query Match 2.0%; Score 20.2; DB 1; Length 25;  
Best Local Similarity 88.0%; Pred. No. 1.3e+03;  
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
DB 1 TCCTGCTCAGTCTCCGAGTAGCT 25  
536 TCCTGCTCAGCTCCGAGTAGCT 560  
RESULT 457  
ADB04614  
ID ADB04614 standard; DNA; 25 BP.  
AC ADB04614;  
XX 20-NOV-2003 (first entry)  
XX Human MD27 scanning oligonucleotide SEQ ID 5600.  
XX  
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;  
XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;  
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
XX developmental disorder; ss.  
XX Homo sapiens.  
XX  
XX EP1281758-A2.  
XX  
XX 05-FEB-2003.  
XX  
XX 30-JUL-2002; 2002EP-00016874.  
XX  
XX 02-AUG-2001; 2001US-00922181.  
XX  
XX (AEOM-) AEOMICA INC.  
XX  
XX Shannon M, Gu Y, Nguyen C;  
XX  
XX WPI; 2003-423107/40.  
XX  
XX New zinc finger-containing proteins and nucleic acids, useful in  
XX manufacturing a medicament for treating or preventing a disorder  
XX associated with decreased or increased expression or activity of MD23,  
XX MD24, MD27 or MD212, e.g. cancer.  
XX  
XX Example 8; SEQ ID NO 5600; 103bp; English.  
XX  
XX The present invention relates to novel human zinc finger-containing  
XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is  
XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,  
XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome  
XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,  
XX or in manufacturing a medicament for treating or preventing a disorder  
XX associated with decreased or increased expression or activity of MD23,  
XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic  
XX acids and proteins are also useful for diagnosing or monitoring a disease  
XX caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic  
XX acids can also be used as probes to detect and characterize gross  
XX alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are  
XX useful in constructing microarrays for measuring gene expression. The  
XX proteins are useful as therapeutic agents for gene therapy or as  
XX vaccines. The present sequence was used to illustrate the invention.  
SQL Sequence 25 BP; 4 A; 7 C; 10 G; 4 T; 0 U; 0 Other;  
Query Match 2.0%; Score 20.2; DB 1; Length 25;  
Best Local Similarity 88.0%; Pred. No. 1.3e+03;  
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
DB 1 CCAGGCTGAGTGCAGTGGCGCAA 667  
643 CCAGGCTGAGTGCAGTGGCGCAA 667  
II |||||

DB 1 CCTGGGCTGAGTGCAGTGGCCCA 25  
RESULT 458  
ADB04577  
ID ADB04577 standard; DNA; 25 BP.  
AC ADB04577;  
XX 20-NOV-2003 (first entry)  
XX  
XX Human MD27 scanning oligonucleotide SEQ ID 5563.  
XX  
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;  
XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;  
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
XX developmental disorder; ss.  
XX Homo sapiens.  
XX  
XX EP1281758-A2.  
XX  
XX 05-FEB-2003.  
XX  
XX 30-JUL-2002; 2002EP-00016874.  
XX  
XX 02-AUG-2001; 2001US-00922181.  
XX  
XX (AEOM-) AEOMICA INC.  
XX  
XX Shannon M, Gu Y, Nguyen C;  
XX  
XX WPI; 2003-423107/40.  
XX  
XX New zinc finger-containing proteins and nucleic acids, useful in  
XX manufacturing a medicament for treating or preventing a disorder  
XX associated with decreased or increased expression or activity of MD23,  
XX MD24, MD27 or MD212, e.g. cancer.  
XX  
XX Example 8; SEQ ID NO 5563; 103bp; English.  
XX  
XX The present invention relates to novel human zinc finger-containing  
XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is  
XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,  
XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome  
XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,  
XX or in manufacturing a medicament for treating or preventing a disorder  
XX associated with decreased or increased expression or activity of MD23,  
XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic  
XX acids and proteins are also useful for diagnosing or monitoring a disease  
XX caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic  
XX acids can also be used as probes to detect and characterize gross  
XX alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are  
XX useful in constructing microarrays for measuring gene expression. The  
XX proteins are useful as therapeutic agents for gene therapy or as  
XX vaccines. The present sequence was used to illustrate the invention.  
SQL Sequence 25 BP; 4 A; 1 C; 4 G; 16 T; 0 U; 0 Other;  
Query Match 2.0%; Score 20.2; DB 1; Length 25;  
Best Local Similarity 88.0%; Pred. No. 1.3e+03;  
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
DB 1 TATTTTATTTTGTGACAGAGT 629  
605 TATTTTATTTTGTGACAGAGT 629  
TTTTTTTTTTTTTTTGACAGAGT 25  
RESULT 459  
ADB04684  
ID ADB04684 standard; DNA; 25 BP.  
AC ADB04684;  
AC

XX		DT	20-NOV-2003	(first entry)	
XX		DE	Human MDZ7 scanning oligonucleotide SEQ ID 5670.		
XX		KW	Cytostatic; immunosuppressant; gene therapy; vaccine; human;		
XX		KM	zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;		
XX		KX	chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;		
XX		OS	developmental disorder; ss.		
XX		PB	Homo sapiens.		
XX		PN	EPI281758-A2.		
XX		PD	05-FEB-2003.		
XX		PF	30-JUL-2002; 2002EP-00016874.		
XX		PR	02-AUG-2001; 2001US-00922181.		
XX		PA	(AEOM-) AEOMICIA INC.		
XX		PI	Shannon M, Gu Y, Nguyen C;		
XX		DR	WP1, 2003-423107/40.		
XX		PT	New zinc finger-containing proteins and nucleic acids, useful in		
XX		PT	manufacturing a medicament for treating or preventing a disorder		
XX		PT	associated with decreased or increased expression or activity of MDZ3,		
XX		MDZ4, MDZ7 or MDZ12, e.g. cancer.			
XX		PS	Example 8; SEQ ID NO 5670; 103bp; English.		
CC		CC	The present invention relates to novel human zinc finger-containing		
CC		CC	proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is		
CC		CC	encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,		
CC		CC	MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome		
CC		CC	15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,		
CC		CC	or in manufacturing a medicament for treating or preventing a disorder		
CC		CC	associated with decreased or increased expression or activity of MDZ3,		
CC		CC	MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic		
CC		CC	acids and proteins are also useful for diagnosing or monitoring a disease		
CC		CC	caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic		
CC		CC	acids can also be used as probes to detect and characterize gross		
CC		CC	alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are		
CC		CC	useful in constructing microarrays for measuring gene expression. The		
CC		CC	proteins are useful as therapeutic agents for gene therapy or as		
CC		CC	vaccines. The present sequence was used to illustrate the invention.		
SQ		Sequence	25 BP; 3 A; 8 G; 7 T; 0 U; 0 Other;		
OY		Query Match	2.0%; Score 20.2; DB 1; Length 25;		
Dn		Best Local Similarity	88.0%; Pred No. 1.3e+03;		
		Matches	22; Conservative 0; Mismatches 3; Indels 0; Gaps 0		
		538 CTGCTCAGACCTCGCAAGTAGCTGG	562		
		1 CTGCTTCAGTCTCCGCAGTAGCTGG	25		
RESULT 460		ID	AADB04683 standard; DNA; 25 BP.		
AD B04683		AC	AADB04683;		
XX XX		DT	20-NOV-2003 (First entry)		
XX XX		DE	Human MDZ7 scanning oligonucleotide SEQ ID 5669.		
XX XX		KW	Cytostatic; immunosuppressant; gene therapy; vaccine; human;		
XX XX		KM	zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;		
XX XX		KX	chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;		

```

KW developmental disorder; ss.
XX
XX Homo sapiens.
OS
XX EPI281758-A2.
PN
XX 05-FEB-2003.
PD
XX
XX 30-JUL-2002; 2002EP-00016874.
PF
XX
XX 02-AUG-2001; 2001US-00922181.
PR
XX
XX (AEOM-) AEOMICA INC.
PA
XX
XX Shannon M, Gu Y, Nguyen C;
PI
XX
XX WPI; 2003-423107/40.
DR
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
PS
XX
XX Example 8; SEQ ID NO 5669; 103pp; English.
XX
XX The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
CC
XX
SQ Sequence 25 BP; 3 A; 9 C; 6 G; 7 T; 0 U; 0 Other;

Query Match          2.0%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.3e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      537 CCTGCCTCAGCCTCCCAAGTGCCTG 561
      |||||
DB      1 CCTGCCTCAGTCTCCCGAGTAGCTG 25

RESULT 461
ADB04576
ID      ADB04576 standard; DNA; 25 BP.
XX
XX ADB04576;
AC
XX
XX 20-NOV-2003 (first entry)
DT
XX
XX Human MD27 scanning oligonucleotide SEQ ID 5562.
DE
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
XX Homo sapiens.
OS
XX
XX EPI281758-A2.
PN
XX
XX 05-FEB-2003.
PD
XX
XX

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PF 30-JUL-2002; 2002EP-00016874.
XX
XX 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M, Gu Y, Nguyen C;
XX
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 5562; 103pp; English.
XX
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
XX
XX Sequence 25 BP; 4 A; 1 C; 4 G; 16 T; 0 U; 0 Other;
XX
XX
XX Query Match          2.0%; Score 20.2; DB 1; Length 25;
XX Best Local Similarity 88.0%; Pred. No. 1.3e+03;
XX Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 604 TTTATTTTATTTTGGACAGAG 628
XX      |||||
XX      1 TTTTATTTTGGACAGAG 25
XX
XX Db
XX
XX RESULT 462
XX ADB04681
XX ID ADB04681 standard; DNA; 25 BP.
XX
XX AC ADB04681;
XX
XX DT 20-NOV-2003 (first entry)
XX
XX DE Human MD27 scanning oligonucleotide SEQ ID 5667.
XX
XX KM Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX
XX OS Homo sapiens.
XX
XX PN EPI281758-A2.
XX
XX PD 05-FEB-2003.
XX
XX PF 30-JUL-2002; 2002EP-00016874.
XX
XX PR 02-AUG-2001; 2001US-00922181.
XX
XX PA (AEOM-) AEOMICA INC.
XX
XX PI Shannon M, Gu Y, Nguyen C;
XX
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```
DR WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 5667; 103pp; English.
XX
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
XX
XX Sequence 25 BP; 3 A; 10 C; 5 G; 7 T; 0 U; 0 Other;
XX
XX
XX Query Match          2.0%; Score 20.2; DB 1; Length 25;
XX Best Local Similarity 88.0%; Pred. No. 1.3e+03;
XX Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 535 CTCCTGCTTCAGCTCCCAAGTAGC 559
XX      |||||
XX      1 CTCCTGCTTCAGCTCCCAAGTAGC 25
XX
XX Db
XX
XX RESULT 463
XX ADP70378/c
XX ID ADP70378 standard; DNA; 25 BP.
XX
XX AC ADP70378;
XX
XX DT 12-AUG-2004 (first entry)
XX
XX DE Probe used to analyse human testin-related gene (TRG) expression.
XX
XX KM human leukocyte antigen; HLA-B52; HLA-B62; cytotoxic T-cell; CTL;
XX TRG2-41; TRG1-20; cytototoxic; epithelial cancer; lung; stomach; colon;
XX prostate; melanoma; vaccine; human; testin-related gene; ss; probe.
XX
XX OS Homo sapiens.
XX
XX PN JP2004141154-A.
XX
XX PD 20-MAY-2004.
XX
XX PF 29-SEP-2003; 2003JP-00338402.
XX
XX PR 30-SEP-2002; 2002JP-00286676.
XX
XX PA (ITOY/) ITO Y.
XX
XX PN WPI; 2004-382710/36.
XX
XX DR Novel tumor antigens TRG1-20 and TRG2-41 capable of recognizing and
XX inducing human leukocyte antigen B52 or B62 constraint property of
XX cytotoxic T lymphocyte, useful for treating cancer e.g., colon cancer,
XX prostate cancer, melanoma.
XX
XX PS Claim 21; SEQ ID NO 9; 34pp; Japanese.
XX
XX CC The invention relates to a novel peptide comprising a TRG1-20 sequence
XX capable of recognizing and inducing the human leukocyte antigen (HLA)-B52
```

or HLA-B62 constraint property of a cytotoxic T-cell (CTL) or a peptide comprising a TRG2-41 sequence capable of recognising and inducing the HLA-B62 of a CTL. The peptide of the invention demonstrates cytotoxic activity and may be useful for inducing a cytotoxic T-cell in order to treat cancer, preferably epithelial cancer, more preferably lung cancer, stomach cancer, colon cancer, prostatic cancer and/or melanoma. The treatment may comprise the use of a vaccine. The current sequence is that of the probe of the invention which was used to analyse human testin-related gene (TRG) expression.

Sequence 25 BP; 7 A; 9 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 20.2; DB 1; Length 25;

Best Local Similarity 88.0%; Pred. No. 1.3e+03; Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

181 TAGAGATGAGTTTCTCCATGTTGG 205  
DB 25 TAGAGACGGGTTTCCCATGTTGG 1

RESULT 464

AAT73704 AAT73704 standard; DNA, 20 BP.

AAT73704;

27-FEB-1998 (first entry)

PCR primer used to prepare probes for diagnosing Alzheimer's disease.

PCR primer BK33; Alzheimer's disease; probe; diagnosis; fluorescence;

yeast artificial chromosome library; YAC; chromosome 14; present; ss.

Synthetic.

FR2742758-A1.

27-JUN-1997.

28-OCT-1994; 94FR-00012941.

28-OCT-1994; 94FR-00012941.

(ASFR-) ASSOC FR CONTRA MYOPATHIES ASSOC LOI.

Weissenbach J, Heilig R;

WPI; 1997-353201/33.

Probes for diagnosing Alzheimer's disease - hybridising with chromosome 14 segments cloned in yeast artificial chromosome library.

Example 1; Page 8; 21pp; French.

PCR primers AAT73703-4 were used to prepare probes (containing Alu repeats) for detecting a mutation in the locus of chromosome 14 associated with a presenile form of Alzheimer's disease. Each of the probes hybridises with one of the two human chromosomal DNA segments cloned in the CEPH yeast artificial chromosome (YAC) library under the accession numbers YAC 934A3 identifiable by genetic marker D14S251 and YAC 854F5 (identifiable by genetic marker D14S76). The probes are useful for diagnosis of the form of Alzheimer's disease associated with chromosome 14 by a method comprising making a preparation of metaphase chromosomes from the patient's lymphoblastoid cells on a microscope slide, contacting the preparation under DNA hybridisation conditions with the pair of probes or with one of the probes and another probe that hybridises with YAC 905C2 from the same library, and detecting the hybridised probes and their relative positions on a significant number of pairs of chromosomes

Sequence 20 BP; 4 A; 4 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

865 CTGGATTACAGGGCTGAGC 884  
DB 1 CTGGATTACAGGGCTGAGC 20

RESULT 465

AAT73703/C AAT73703 standard; DNA, 20 BP.

AAT73703;

27-FEB-1998 (first entry)

PCR primer SRI used to prepare probes for diagnosing Alzheimer's.

PCR primer SRI; Alzheimer's disease; probe; diagnosis; fluorescence;

yeast artificial chromosome library; YAC; chromosome 14; present; ss.

Synthetic.

FR2742758-A1.

27-JUN-1997.

28-OCT-1994; 94FR-00012941.

28-OCT-1994; 94FR-00012941.

(ASFR-) ASSOC FR CONTRA MYOPATHIES ASSOC LOI.

Weissenbach J, Heilig R;

WPI; 1997-353201/33.

Probes for diagnosing Alzheimer's disease - hybridising with chromosome 14 segments cloned in yeast artificial chromosome library.

Example 1; Page 8; 21pp; French.

PCR primers AAT73703-4 were used to prepare probes (containing Alu repeats) for detecting a mutation in the locus of chromosome 14 associated with a presenile form of Alzheimer's disease. Each of the probes hybridises with one of the two human chromosomal DNA segments cloned in the CEPH yeast artificial chromosome (YAC) library under the accession numbers YAC 934A3 identifiable by genetic marker D14S251 and YAC 854F5 (identifiable by genetic marker D14S76). The probes are useful for diagnosis of the form of Alzheimer's disease associated with chromosome 14 by a method comprising making a preparation of metaphase chromosomes from the patient's lymphoblastoid cells on a microscope slide, contacting the preparation under DNA hybridisation conditions with the pair of probes or with one of the probes and another probe that hybridises with YAC 905C2 from the same library, and detecting the hybridised probes and their relative positions on a significant number of pairs of chromosomes

Sequence 20 BP; 3 A; 9 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+03; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

643 CCCAGGCTGAGTGACGTGG 662  
DB 20 CCCAGGCTGAGTGACGTGG 1

RESULT 466

AAV85582 AAV85582 standard; DNA, 20 BP.

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XX AAV85582;
XX 10-FEB-1999 (first entry)
XX LRP5 PCR primer Gpi 1F.
XX LRP5; LDL-receptor related protein; LRP-3; IDDM; diagnosis; endocytosis;
XX insulin dependent diabetes mellitus; autoimmune disease;
XX glomerulonephritis; inflammation; viral infection; osteoporosis;
XX hypercholesterolemia; Alzheimer's disease; low density lipoprotein;
XX PCR primer; ss.
XX Synthetic.
XX Homo sapiens.
XX WO9846743-A1.
XX 22-OCT-1998.
XX 15-APR-1998; 98WO-GB001102.
XX 15-APR-1997; 97US-0043553P.
XX 05-JUN-1997; 97US-0048740P.
XX (WELI ) WELLCOME TRUST LTD.
XX (MERI ) MERCK & CO INC.
XX Todd JA, Hess JM, Caskey CT, Cox RD, Gerhold D, Hammond H;
XX Hey P, Kawaguchi Y, Merriman TR, Metzker ML, Nakagawa Y;
XX Phillips MS, Twells RCJ;
XX WPI; 1998-594573/50.
XX New isolated LDL-receptor related protein - used to develop products for
XX treating, e.g. elevated triglyceride levels, diabetes, autoimmune
XX disorders, inflammation or Alzheimer's disease.
XX Claim 12; Page 98; 200pp; English.
XX The present invention describes LRP5 (low density lipoprotein (LDL)
XX receptor related protein, previously designated LRP-3). AAV8552 to
XX CAAV8586 represent PCR primer used for obtaining LRP5 cDNA. Nucleic acid
XX molecules (NAs) encoding LRP5 can be used for determining if an
XX individual is susceptible to insulin dependent diabetes mellitus (IDDM).
XX The NAs or proteins can be used for reducing triglyceride levels in the
XX serum of an individual. Therapies that affect LRP5 may also be useful in
XX the treatment of autoimmune diseases such as glomerulonephritis, diseases
XX and disorders involving disruption of endocytosis and/or antigen
XX presentation, cytokine clearance and/or inflammation, viral infection,
XX pathogenic bacterial toxin contamination, elevation of free fatty acids
XX or hypercholesterolemia, type 2 diabetes, osteoporosis, Alzheimer's
XX disease and cardiovascular disease. Products from the present invention
XX can also be used for detection, diagnosis and drug screening
XX
XX Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 2.0%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.1e+03;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1112 AGGCTGATCTCAACTCTG 1131
XX |||||
XX 1 AGGCTGATCTCAACTCTG 20
XX
XX RESULT 467
XX AAV69963
XX ID AAV69963 standard; DNA; 20 BP.
XX
XX AAV69963;
XX
XX 04-FEB-1999 (first entry)

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```

XX Human c-fos protein antisense oligonucleotide #25.
XX Human; c-fos; c-jun; activating protein 1; Ap-1; diagnosis; metastasis;
XX antisense oligonucleotide; phosphorothioate; regulation;
XX malignant tumour; cell cycle expression; hyperproliferative disease; ss.
XX
XX Synthetic.
XX Homo sapiens.
XX Key Location/Qualifiers
XX modified_base 1..20
XX /note= "phosphorothioate linkages"
XX
XX WO9846272-A1.
XX 22-OCT-1998.
XX 14-APR-1998; 98WO-US007386.
XX 14-APR-1997; 97US-00837201.
XX (ISIS-) ISIS PHARM INC.
XX Dean NM, McKay R, Miraglia L, Baker B;
XX WPI; 1998-609906/51.
XX Antisense oligonucleotides regulating Activating Protein 1 subunits -
XX hybridise with c-fos and c-jun mRNA, used for regulating metastasis, cell
XX cycle expression and hyperproliferative disease.
XX Claim 5; Page 76; 120pp; English.
XX AAV69949 to AAV69977 represent antisense oligonucleotides which are
XX specifically hybridisable with a region of a nucleic acid encoding human
XX c-Fos protein. The antisense compound regulates the expression of the c-
XX Fos protein. The present invention also describes antisense
XX oligonucleotides which regulate the c-Jun protein. The antisense
XX oligonucleotides are used for the diagnosis and treatment of diseases or
XX disorders associated with Activating Protein 1 expression, of which c-Fos
XX and c-Jun are subunits. The antisense oligonucleotides are used in
XX compositions as c-Fos and/or c-Jun together with a carrier and a
XX chemotherapeutic agent. They are used to regulate the expression of c-Fos
XX or c-Jun in cells or tissues, preferably by inhibiting metastasis. They
XX also regulate cell cycle expression and can be used to treat an animal
XX with, or being prone to, a hyperproliferative disease
XX
XX Sequence 20 BP; 3 A; 10 C; 4 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 2.0%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.1e+03;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 843 CCGCTCGGCTCCCAAG 862
XX |||||
XX 1 CCGCTCGGCTCCCAAG 20
XX
XX RESULT 468
XX AA237736/C
XX ID AA237736 standard; DNA; 20 BP.
XX
XX AA237736;
XX
XX 07-JAN-2000 (first entry)
XX Human mdm2 phosphorothioate oligodeoxynucleotide #266.
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
XX antisense; modulation; oligonucleotide; expression; inhibition;
XX hyperproliferation; blood cancer; brain cancer; breast cancer;

```

KW lung cancer; soft tissue cancer; psoriasis; fibrosis; atherosclerosis;  
KM restenosis; ss.  
XX  
XX Synthetic.  
OS Homo sapiens.  
OS  
XX WO9949065-A1.  
XX  
XX 30-SEP-1999.  
XX  
XX 26-MAR-1999; 99WO-US006702.  
XX  
XX 26-MAR-1998; 98US-00048810.  
XX  
XX (ISIS-) ISIS PHARM INC.  
XX  
XX Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowse LM;  
XX WPI; 1999-610754/52.  
XX  
XX New antisense compounds used to treat eg. hyperproliferative conditions.  
XX  
XX Example 9; Page 55; 157pp; English.  
XX  
XX AA237473-237738 represent human mdm2 phosphorothioate oligonucleotides.  
XX  
XX AA237471, AA237472, AA237739, AA237740 and AA237741 are used in the  
XX exemplification of the present invention. The present invention describes  
XX novel nucleotide antisense compounds, targeted to the 5' untranslated,  
XX translation termination codon, or 3' untranslated region of a nucleic  
XX acid encoding human mdm2, that modulates expression of human mdm2. The  
XX oligonucleotides mediate their effect by antisense inhibition of  
XX hyperproliferative gene expression. The antisense compound is used to  
XX treat an animal having a disease or condition associated with mdm2,  
XX especially a hyperproliferative condition, more particularly cancer,  
XX especially of the blood, brain, breast, lung or soft tissue, or  
XX psoriasis, fibrosis, atherosclerosis or restenosis  
XX  
XX Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;  
SQ  
Query Match 2.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 851 GGCTCCCAAGTCTGGGA 870  
DB 20 GGCTCCCAAGTCTGGGA 1  
RESULT 469  
AA237712/C  
ID AA237712 standard; DNA; 20 BP.  
XX  
XX AA237712;  
XX  
XX 07-JAN-2000 (first entry)  
XX  
XX Human mdm2 phosphorothioate oligodeoxynucleotide #242.  
XX  
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
XX antisense; modulation; oligonucleotide; expression; inhibition;  
XX hyperproliferation; blood cancer; brain cancer; breast cancer;  
XX lung cancer; soft tissue cancer; psoriasis; fibrosis; atherosclerosis;  
XX restenosis; ss.  
XX  
XX Synthetic.  
OS Homo sapiens.  
OS  
XX WO9949065-A1.  
XX  
XX 30-SEP-1999.  
XX  
XX 26-MAR-1999; 99WO-US006702.  
XX  
XX

PR 26-MAR-1998; 98US-00048810.  
XX  
XX (ISIS-) ISIS PHARM INC.  
XX  
XX Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowse LM;  
XX WPI; 1999-610754/52.  
XX  
XX New antisense compounds used to treat eg. hyperproliferative conditions.  
XX  
XX Example 9; Page 54; 157pp; English.  
XX  
XX AA237473-237738 represent human mdm2 phosphorothioate oligonucleotides.  
XX  
XX AA237471, AA237472, AA237739, AA237740 and AA237741 are used in the  
XX exemplification of the present invention. The present invention describes  
XX novel nucleotide antisense compounds, targeted to the 5' untranslated,  
XX translation termination codon, or 3' untranslated region of a nucleic  
XX acid encoding human mdm2, that modulates expression of human mdm2. The  
XX oligonucleotides mediate their effect by antisense inhibition of  
XX hyperproliferative gene expression. The antisense compound is used to  
XX treat an animal having a disease or condition associated with mdm2,  
XX especially a hyperproliferative condition, more particularly cancer,  
XX especially of the blood, brain, breast, lung or soft tissue, or  
XX psoriasis, fibrosis, atherosclerosis or restenosis  
XX  
XX Sequence 20 BP; 5 A; 7 C; 5 G; 3 T; 0 U; 0 Other;  
SQ  
Query Match 2.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 937 CTGTTACCCAGCTGAGTG 956  
DB 20 CTGTTACCCAGCTGAGTG 1  
RESULT 470  
AA237737/C  
ID AA237737 standard; DNA; 20 BP.  
XX  
XX AA237737;  
XX  
XX 07-JAN-2000 (first entry)  
XX  
XX Human mdm2 phosphorothioate oligodeoxynucleotide #267.  
XX  
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
XX antisense; modulation; oligonucleotide; expression; inhibition;  
XX hyperproliferation; blood cancer; brain cancer; breast cancer;  
XX lung cancer; soft tissue cancer; psoriasis; fibrosis; atherosclerosis;  
XX restenosis; ss.  
XX  
XX Synthetic.  
OS Homo sapiens.  
OS  
XX WO9949065-A1.  
XX  
XX 30-SEP-1999.  
XX  
XX 26-MAR-1999; 99WO-US006702.  
XX  
XX 26-MAR-1998; 98US-00048810.  
XX  
XX (ISIS-) ISIS PHARM INC.  
XX  
XX Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowse LM;  
XX WPI; 1999-610754/52.  
XX  
XX New antisense compounds used to treat eg. hyperproliferative conditions.  
XX  
XX Example 9; Page 55; 157pp; English.  
XX  
XX

CC AA237473-237738 represent human mdm2 phosphorothioate oligonucleotides.  
 CC AA237471, AA237472, AA237739, AA237740 and AA237741 are used in the  
 CC exemplification of the present invention. The present invention describes  
 CC novel nucleotide antisense compounds, targeted to the 5' untranslated,  
 CC translation termination codon, or 3' untranslated region of a nucleic  
 CC acid encoding human mdm2, that modulates expression of human mdm2. The  
 CC oligonucleotides mediate their effect by antisense inhibition of  
 CC hyperproliferative gene expression. The antisense compound is used to  
 CC treat an animal having a disease or condition associated with mdm2,  
 CC particularly a hyperproliferative condition, more particularly cancer,  
 CC especially of the blood, brain, breast, lung or soft tissue, or  
 CC psoriasis, fibrosis, atherosclerosis or restenosis  
 CC  
 SQ Sequence 20 BP; 4 A; 7 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 388 CAAAGTGTGGATTACAG 407  
 DB 20 CAAAGTGTGGATTACAG 1

RESULT 471  
 ID AAA96410 standard; DNA; 20 BP.

AC AAA96410;  
 XX  
 DT 08-FEB-2001 (first entry)

DE Primer used to amplify a sara43/44 polymorphic microsatellite repeat.

XX Autoimmune disease; polymorphic microsatellite repeat; PMR; CD28 gene;  
 XX ICOS gene; CTLA4 gene; costimulatory receptor gene locus; GGR1; lupus;  
 XX insulin-dependent diabetes mellitus; IDDM; Addison's disease; leprosy;  
 XX Graves disease; autoimmune hypochyroidism; myasthenia gravis; thymoma;  
 XX chryoiditis; postpartum thyroiditis; rheumatoid arthritis;  
 XX Hashimoto's disease; coeliac disease; PCR primer; ss.

OS Homo sapiens.  
 XX  
 XX WO200056856-A2.  
 XX  
 XX 28-SEP-2000.

XX 24-MAR-2000; 2000MO-US007938.

XX 25-MAR-1999; 99US-0126215P.

XX (GBMY ) GENETICS INST INC.

XX Ling V, Wu P, Gray GS;

XX WPI; 2000-628257/60.

XX Determining predisposition of humans to develop autoimmune disease  
 PT involves detecting polymorphic microsatellite repeat sequence within  
 PT human costimulatory receptor gene locus.  
 XX  
 XX

XX Claim 16; Page 154; 160pp; English.

XX PCR primers AAA96409-10 were used to amplify polymorphic microsatellite  
 CC repeat (PMR) sequences from the human costimulatory receptor gene locus  
 CC (hCGR). The primers are used in the method of the invention. The  
 CC specification describes a method for determining the predisposition of a  
 CC human subject to develop autoimmune disease. The method comprises  
 CC detecting a PMR sequence in the CD28, ICOS gene or CTLA4 gene of the  
 CC human costimulatory receptor gene locus (hCGR). PMR sequences vary in  
 CC length among individuals and can be amplified to generate products that  
 CC differ in size. These products can then be detected by rapid and  
 CC convenient high resolution processes. The method is useful for

CC determining the predisposition of insulin-dependent diabetes mellitus  
 CC (IDDM), Addison's disease, Graves disease, autoimmune hypochyroidism,  
 CC myasthenia gravis, thymoma, lupus, thyroiditis, postpartum thyroiditis,  
 CC rheumatoid arthritis, Hashimoto's disease, coeliac disease and leprosy.  
 CC PMR sequences within hCGR are useful as markers in a variety of assays  
 CC and in the field of forensic medicine, disease diagnosis and human genome  
 CC mapping  
 CC  
 SQ Sequence 20 BP; 3 A; 9 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 643 CCCAGGCTGGAGTGCAGTGG 662  
 DB 20 CCCAGGCTGGAGTGCAGTGG 1

RESULT 472  
 ID AA235378  
 XX AA235378 standard; DNA; 20 BP.

AC AA235378;

XX 27-MAR-2000 (first entry)

DE Interspersed repeated sequence PCR primer ALU5.

XX Human; absorptive hypercalciuria; osteoporosis; nephrolithiasis;  
 XX osteopathic; anticalcitic; chromosome 1q23.3-q24; therapy; diagnosis;  
 XX PCR primer; ss.

XX Homo sapiens.

XX WO967426-A1.

XX 29-DEC-1999.

XX 23-JUN-1999; 99WO-US014347.

XX 23-JUN-1998; 98US-0090348P.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX Reed-Glומר BY, Pak CVC;

XX WPI; 2000-116959/10.

XX Novel genomic region useful in screening for absorptive hypercalciuria or  
 PT osteoporosis with hypercalciuria.  
 XX  
 XX

XX Example 3; Page 125; 153pp; English.

XX The present sequence is that of interspersed repeated sequence PCR (IRS-  
 CC PCR) primer ALU5 used to identify human-specific sequences in yeast  
 CC artificial chromosomes (YAC) derived from the human chromosome 1q23.3-q24  
 CC region. The chromosomal region contains the locus associated with  
 CC absorptive hypercalciuria (AH). IRS-PCR fingerprints were generated, and  
 CC genes contained within YACs were identified by exon trapping. CDNA  
 CC corresponding to the AH gene was isolated (see AA235376). Identification  
 CC of the AH genomic region allows genetic screening for increased risk of  
 CC developing AH or osteoporosis with hypercalciuria  
 CC  
 SQ Sequence 20 BP; 5 A; 5 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 868 GGATTACAGGCGTACGACAC 887  
 DB 1 GGATTACAGGCGTACGACAC 20

KW	hyperproliferative disorder; developmental disorder; antisense;
KM	phosphorothioate backbone, ss.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
FH	Key
FT	modified_base
FT	1..20
FT	/tag= a
FT	/mod_base= OTHER
FT	/note= "Phosphorothioate backbone"
FT	1..5
FT	/tag= b
FT	/mod_base= OTHER
FT	/note= "Methoxyethyl residues"
FT	2
FT	/tag= d
FT	/mod_base= mSc
FT	3
FT	/tag= e
FT	/mod_base= mSc
FT	4
FT	/tag= f
FT	/mod_base= mSc
FT	11
FT	/tag= g
FT	/mod_base= mSc
FT	16..20
FT	/tag= c
FT	/mod_base= OTHER
FT	/note= "Methoxyethyl residues"
FT	20
FT	/tag= h
FT	/mod_base= mSc
XX	
PN	WO200152865-A1.
XX	
PD	26-JUL-2001.
XX	
PF	16-JAN-2001; 2001WO-US001411.
XX	
PR	21-JAN-2000; 2000US-00489856.
XX	
PA	(ISIS-) ISIS PHARM INC.
XX	
PI	Monia BP, McKay R, Butler MM, Wyatt JR;
XX	
DR	WPt; 2001-442247/47.
XX	
PT	Antisense compound 8 to 30 nucleobases in length comprising a compound
PT	that is targeted to a nucleic acid molecule encoding glycogen synthase
PT	kinase 3 alpha, useful for the treatment of e.g. diabetes and
PT	hyperproliferative disorders.
XX	
PS	Example 15; Page 83; 115pp; English.
XX	
CC	The invention relates to an antisense compound 8 to 30 nucleobases in
CC	length targeted to a nucleic acid encoding glycogen synthase kinase 3
CC	alpha. The antisense compound specifically hybridises with and inhibits
CC	the expression of glycogen synthase kinase 3 alpha. The antisense
CC	compound is useful for the treatment of a disease associated with
CC	glycogen synthase kinase 3 alpha such as diabetes, a neurological
CC	disorder, a haematopoietic disorder, a hyperproliferative disorder or a
CC	developmental disorder. The antisense compounds may also be used
CC	prophylactically to prevent or delay infection, inflammation or tumour
CC	formation. The present sequence is a phosphorothioate antisense
CC	oligonucleotide targeted to human glycogen synthase kinase 3 alpha
CC	genomic DNA
XX	
SQ	Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
Query Match	2.0%; Score 20; DB 1; Length 20;
Best Local Similarity	100.0%; Pred No. 1.le+03;



Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 385 TCCCAAAGTCTGGATTAC 404  
 |||||  
 DB 1 TCCCAAAGTCTGGATTAC 20

RESULT 475  
 AAK95176/c  
 ID AAK95176 standard; DNA; 20 BP.

AC AAK95176;

DT 06-NOV-2001 (first entry)

DE Human cDNA clone-specific primer, SEQ ID NO: 4421.

KW Human; full length cDNA; cDNA synthesis; oligo-capping; PCR primer; ss.

OS Homo sapiens.

PN EP130094-A2.

PD 05-SEP-2001.

PF 07-JUL-2000; 2000EP-00114089.

PR 08-JUL-1999; 99JP-00194486.

PR 11-JAN-2000; 2000JP-00118774.

PR 02-MAY-2000; 2000JP-00183765.

(HELI-) HELIX RES INST.

PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
 Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

WPI; 2001-524255/58.

PT 830 Primers useful for synthesizing full length cDNA clones and their use  
 in genetic manipulation.

PS Example 18; Page 132; 1380pp + Sequence Listing; English.

CC The invention relates to primers for synthesizing full length cDNA  
 clones. 830 cDNA molecules encoding a human protein have been isolated  
 and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have  
 been determined. Primers for synthesizing the full length cDNA are useful  
 for clarifying the function of the protein encoded by the cDNA. The full  
 length clones were obtained by construction of full length enriched cDNA  
 libraries that were synthesized by the oligo-capping method. The primers  
 enable the production of the full length cDNA easily without any special  
 methods. The present sequence is a primer used to amplify a human cDNA  
 clone provided in the invention

CC Sequence 20 BP; 4 A; 7 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 388 CAAAGTCTGGATTACAGG 407  
 |||||  
 DB 20 CAAAGTCTGGATTACAGG 1

RESULT 476  
 AAF80866/c

ID AAF80866 standard; DNA; 20 BP.

AC AAF80866;

DT 02-MAY-2001 (first entry)

DE Human mdm2 phosphorothioate oligonucleotide #240.

KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

OS Homo sapiens.

PN US6184212-B1.

PD 06-FEB-2001.

PF 26-MAR-1999; 99US-00280805.

PR 26-MAR-1998; 98US-00048810.

(ISIS-) ISIS PHARM INC.

PI Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowseart LM;

WPI; 2001-190948/19.

PT Novel antisense compound 8-30 nucleobases in length targeted to a nucleic  
 acid molecule encoding human mdm-2 useful for modulating the expression  
 of human mdm-2 and reducing hyperproliferation of human cells.

PS Example 9; Col 31; 77pp; English.

CC The present invention relates to an antisense compound 8-30 nucleobases  
 in length targeted to nucleobases 1-308 of the 5' untranslated region,  
 CC 1776-1806 of the translation termination codon region or 1818-2370 of the  
 CC 3' untranslated region of a nucleic acid molecule encoding human mdm-2.  
 CC The invention is useful for reducing hyperproliferation of human cells,  
 CC modulating the expression of mdm2 in human cells or tissues or in vitro.  
 CC The hyperproliferative disorder includes cancer or psoriasis

CC Sequence 20 BP; 5 A; 7 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 937 CTGTACCCAGGCTGGAGTG 956  
 |||||  
 DB 20 CTGTACCCAGGCTGGAGTG 1

RESULT 477

ID AAF80891/c

AC AAF80891;

DT 02-MAY-2001 (first entry)

DE Human mdm2 phosphorothioate oligonucleotide #265.

KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

OS Homo sapiens.

PN US6184212-B1.

PD 06-FEB-2001.

PF 26-MAR-1999; 99US-00280805.

PR 26-MAR-1998; 98US-00048810.

(ISIS-) ISIS PHARM INC.

PI Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowseart LM;

WPI; 2001-190948/19.

PT Novel antisense compound 8-30 nucleobases in length targeted to a nucleic  
acid molecule encoding human mdm-2 useful for modulating the expression  
of human mdm-2 and reducing hyperproliferation of human cells.  
XX  
PS Example 9; Col 33; 77bp; English.  
XX  
CC The present invention relates to an antisense compound 8-30 nucleobases  
in length targeted to nucleobases 1-308 of the 5' untranslated region,  
CC 1776-1806 of the translation termination codon region or 1818-2370 of the  
CC 3' untranslated region of a nucleic acid molecule encoding human mdm-2.  
CC The invention is useful for reducing hyperproliferation of human cells,  
CC modulating the expression of mdm2 in human cells or tissues or in vitro.  
CC The hyperproliferative disorder includes cancer or psoriasis  
CC  
XX Sequence 20 BP; 4 A; 7 C; 3 G; 6 T; 0 U; 0 Other;  
SQ  
Query Match 2.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 20 CAAAGTCTGGGATTACAG 1  
OY 388 CAAAGTCTGGGATTACAG 407  
DB 20 CAAAGTCTGGGATTACAG 1  
RESULT 478  
AAF0890/C  
ID AAF0890 standard; DNA; 20 BP.  
AC AAF0890;  
DT 02-MAY-2001 (first entry)  
XX  
XX Human mdm2 phosphorothioate oligonucleotide #264.  
XX  
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.  
XX  
XX Homo sapiens.  
XX  
XX US6184212-B1.  
XX  
XX 06-FEB-2001.  
XX  
XX 26-MAR-1999; 99US-00280805.  
XX  
XX 26-MAR-1998; 98US-00048810.  
XX  
XX (ISIS-) ISIS PHARM INC.  
XX  
XX Miragila LJ, Nero P, Graham MJ, Monia BP, Cowseart LM;  
PI MPI; 2001-190948/19.  
XX  
XX Novel antisense compound 8-30 nucleobases in length targeted to a nucleic  
acid molecule encoding human mdm-2 useful for modulating the expression  
of human mdm-2 and reducing hyperproliferation of human cells.  
XX  
PS Example 9; Col 33; 77bp; English.  
XX  
CC The present invention relates to an antisense compound 8-30 nucleobases  
in length targeted to nucleobases 1-308 of the 5' untranslated region,  
CC 1776-1806 of the translation termination codon region or 1818-2370 of the  
CC 3' untranslated region of a nucleic acid molecule encoding human mdm-2.  
CC The invention is useful for reducing hyperproliferation of human cells,  
CC modulating the expression of mdm2 in human cells or tissues or in vitro.  
CC The hyperproliferative disorder includes cancer or psoriasis  
CC  
XX Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;  
SQ  
Query Match 2.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 851 GGCTCCCAAGTCTGGGA 870  
DB 20 GGCTCCCAAGTCTGGGA 1  
RESULT 479  
AAH38246  
ID AAH38246 standard; DNA; 20 BP.  
XX  
XX AAH38246;  
AC  
DT 14-AUG-2001 (first entry)  
XX  
XX SNP specific lower PCR primer SEQ ID 1042.  
DE  
DE  
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
XX SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;  
XX Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;  
XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
XX inflammation; forensic investigation; paternity analysis; PCR primer; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200129262-A2.  
XX  
XX 26-APR-2001.  
XX  
XX 13-OCT-2000; 2000WO-US028436.  
XX  
XX 15-OCT-1999; 99US-0160096P.  
XX  
XX (ORCH-) ORCHID BIOSCIENCES INC.  
XX  
XX Picoule-Newburg L, Pohl M;  
PI MPI; 2001-290930/30.  
XX  
XX New genotyping oligonucleotide, useful for detecting the presence,  
PT absence or identity of single polynucleotide polymorphism in a nucleic  
PT acid sample.  
XX  
XX Claim 1; Page 55; 83pp; English.  
XX  
XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
CC primer extension (SNPE) primers, and the sequences of regions flanking  
CC sites of single nucleotide polymorphisms SNPs. The present invention  
CC includes kits for determining the presence or absence of a SNP, using the  
CC oligonucleotides of the invention. The PCR primers are used to amplify a  
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.  
CC The oligonucleotides are useful for genotyping a nucleic acid sample by  
CC performing a single-nucleotide primer extension reaction. The  
CC oligonucleotides are useful for determining the presence, absence or  
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
CC assess by association analysis the phenotype of an individual or group of  
CC individuals, having a pathological phenotypic trait suspected of being  
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular  
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,  
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
CC traits also include symptoms of or susceptibility to multifactorial  
CC disease of which a component is or may be genetic such as autoimmune  
CC diseases, including, rheumatoid arthritis, multiple sclerosis,  
CC inflammation, cancer, nervous system diseases and infection by pathogenic  
CC microorganism. The method is also useful in forensic investigations and  
CC paternity analysis. The present sequence represents a PCR primer specific  
CC for a human SNP containing DNA sequence  
XX  
SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;  
Query Match 2.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY		385	TCCCAAGTGGGATTAC	404
Dd		1	TCCCAGAATGTCTGCATTC	20
RESULT	480			
AAS29506/C				
ID	AAS29506	standard; DNA;	20 BP.	
XX	AAS29506;			
DT	21-NOV--2001	(first entry)		
DE	Human mdm2 antisense oligonucleotide 31791.			
KW	Human; mdm2; hyperproliferative disorder; cancer; psoriasis; athroscleorosis; tumour; cytostatic; anti prostatic; anti arteriosclerotic; vasotropic; antisense; phosphothioate; ss.			
OS	Homo sapiens.			
FH	Key	Location/Qualifiers		
FT	modified_base	1..20		
FT	/tag= a	/mod_base= OTHER		
FT	/note= "OTHER= All phosphorthioate linkages,			
FT	additionally bases 1-6 and bases 15-20 are 2'-O-			
FN	methoxyethyl bases, and bases 7-14 are deoxynucleotides"			
US	US2001016575-A1.			
PD	23-AUG--2001.			
PR	02-JAN--2001;	2001US-00752983.		
PR	26-MAR--1998;	98US-00048810.		
PR	26-MAR--1999;	99US-00280805.		
PA	(MIRA/) MIRAGLIA L J.			
PA	(NERO/) NERO P.			
PA	(GRAH/) GRAHAM M J.			
PA	(MONI/) MONIA B P.			
PA	(CONS/) COMSERT L M.			
PI	Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowseert LM;			
DR	WPI; 2001-535565/59.			
PT	An antisenese compound, useful for treating e.g. cancer, comprises nucleobases targeted a region (e.g. translation termination codon region) of a nucleic acid encoding human mdm2.			
PS	Example 9; Page 18; 81bp; English.			
XX	The present invention relates to antisenese compounds, 8-30 nucleobases in length targeted to the 5' untranslated region, translation termination start codon region, 3' untranslated region, coding region or translation start site of a nucleic acid encoding human mdm2, where the antisenese compound modulates the expression of human mdm2. The antisenese oligonucleotides of the invention are useful for encoding human mdm2 and for inhibiting the expression of human mdm2. They may be used for treating an animal having a disease or condition associated with amplification of mdm2 gene or overexpression of mdm2 e.g. a hypertrophic disorder such as cancer (blood, brain, breast, lung, or a soft tissue cancer) and psoriasis, fibrosis, atherosclerosis or restenosis, tumours, colorectal carcinoma and chronic myelogenous leukemia. The antisenese compound may be administered with a chemotherapeutic agent to overcome drug resistance. CC The antisenese compound reduces hyperproliferation of human cells. The method, which involves the use of the antisenese compound, is also useful for detecting the role of mdm2 expression in various cell functions and physiological processes and useful in both clinical research and diagnostic tools. AAS29242-AAS29507 represent the human mdm2 antisenese			

CC	Oligonucleotides of the present invention		
XX	Sequence 20 BP; 4 A; 7 C; 3 G; 6 T; 0 U; 0 Other;		
XX	Query Match	2.0%; Score 20; DB 1; Length 20;	
XX	Best Local Similarity	100.0%; Pred. No. 1.1e+03;	
XX	Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	388 CAAAGTCTGGGATTACAG 407		
DB	20 CAAAGTCTGGGATTACAG 1		
RESULT 481			
AAAS29505/C			
ID	AAAS29505 standard; DNA; 20 BP.		
AC	AAAS29505;		
XX			
DT	21-NOV-2001 (first entry)		
DE			
XX	Human mdm2 antisense oligonucleotide 31630.		
XX			
KM	Human; mdm2; hyperproliferative disorder; cancer; psoriasis;		
KM	atherosclerosis; tumour; cytostatic; anti psoriatic;		
KM	anti arteriosclerotic; vasotropic; antisense; phosphorothioate; ss.		
OS			
XX	Homo sapiens.		
Key	Location/Qualifiers		
EH	modified_base 1..20		
FT	/*tag= a		
FT	/mod_base= OTHER		
FT	/note= "OTHER= All phosphorothioate linkages,		
FT	additionally bases 1-6 and bases 15-20 are 2'-O-		
FT	methoxyethyl bases, and bases 7-14 are deoxynucleotides"		
PN			
XX	US2001016575-A1.		
PD			
XX	23-AUG-2001.		
PF	02-JAN-2001; 2001US-00752983.		
XX			
PR	26-MAR-1998; 98US-00048810.		
PR	26-MAR-1999; 99US-00280805.		
XX			
PA	(MIRA/) MIRAGLIA L J.		
PA	(NERO/) NERO P.		
PA	(GRAH/) GRAHAM M J.		
PA	(MONI/) MONIA B P.		
PA	(COMS/) COMSERT L M.		
XX			
PI	Miraglia LJ, Nero P, Graham MJ, Monia BP, Comsert LM;		
DR	WPI; 2001-535565/59.		
XX			
XX	An antisense compound, useful for treating e.g. cancer, comprises		
PT	nucleosides targeted a region (e.g. translation termination codon region)		
PT	of a nucleic acid encoding human mdm2.		
XX			
PS	Example 9; Page 18; 81pp; English.		
XX			
CC	The present invention relates to antisense compounds, 8-30 nucleobases in		
CC	length targeted to the 5' untranslated region, translation termination		
CC	codon region, 3' untranslated region, coding region or translation start		
CC	site of a nucleic acid encoding human mdm2, where the antisense compound		
CC	modulates the expression of human mdm2. The antisense oligonucleotides of		
CC	the invention are useful for encoding human mdm2 and for inhibiting the		
CC	expression of human mdm2. They may be used for treating an animal having		
CC	a disease or condition associated with amplification of mdm2 gene or		
CC	overexpression of mdm2 e.g. a hyperproliferative disorder such as cancer		
CC	(blood, brain, breast, lung, or a soft tissue cancer) and psoriasis,		
CC	fibrosis, atherosclerosis or restenosis, tumours, colorectal carcinoma		

	CC	and chronic myelogenous leukemia.	The antisense compound may be administered with a chemotherapeutic agent to overcome drug resistance.
	CC	The antisense compound reduces hyperproliferation of human cells.	The method, which involves the use of the antisense compound, is also useful for detecting the role of mdm2 expression in various cell functions and physiological processes and useful in both clinical research and diagnostic tools.
	CC	AAS29481-AAS29507 represent the human mdm2 antisense oligonucleotides of the present invention	
	XX	Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;	
	SO	Query Match	2.0%; Score 20; DB 1; Length 20;
		Best Local Similarity	100.0%; Pred.No. 1.1e+03;
		Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
Oy		851 GGCTTCCCAAGTGCTGGGA 870       	
Db		20 GGCTTCACCAAGTGCTGGGA 1	
RESULT 482	ID	AAS29481/c	AAS29481 standard; DNA; 20 BP.
XX	AC	AAS29481;	
XX	DT	21-NOV-2001 (first entry)	
DE	XX	Human mdm2 antisense oligonucleotide 31781.	
KW	XX	Human; mdm2; hyperproliferative disorder; cancer; psoriasis; atherosclerosis; tumour; cytosstatic; anti psoriatic; anti arteriosclerotic; vasotropic; anticancer; phosphorothioate; ss.	
XX	OS	Homo sapiens.	
XX	Key	Location/Qualifiers	
FT	FH	modified_base	1..20
FT	FT	/tag= a	
FT	FT	/mod_base= OTHER	
FT	FT	/note= "OTHER= All phosphorothioate linkages, additionally bases 1-6 and bases 15-20 are 2'-O-methoxyethyl bases, and bases 7-14 are deoxynucleotides"	
XX	FN	US2001016575-A1.	
PD	XX	23-AUG-2001.	
PF	XX	02-JAN-2001; 2001US-00752983.	
PR	XX	26-MAR-1998; 98US-00048810.	
PR	XX	26-MAR-1999; 99US-00280805.	
PA	(MIRA//) MIRAGLIA L J.		
PA	(NERO//) NERO P.		
PA	(GRAH//) GRAHAM M J.		
PA	(MONI//) MONIA B P.		
PA	(COMS//) COMBERT L M.		
PI	Miraglia LJ, Nero P, Graham MJ, Monia BP, Combert LM;		
DR	WIJ; 2001-535565/59.		
PT	An antisense compound, useful for treating e.g. cancer, comprises nucleobases targeted a region (e.g. translation termination codon region) of a nucleic acid encoding human mdm2.		
PT	Example 9; Page 18; 81pp; English.		
PS	The present invention relates to antisense compounds, 8-30 nucleobases in length targeted to the 5' untranslated region, translation start codon region, 3' untranslated region, coding region or translation start site of a nucleic acid encoding human mdm2, where the antisense compound		

CC	modulates the expression of human mdm2. The antisense oligonucleotides of
CC	the invention are useful for encoding human mdm2 and for inhibiting the
CC	expression of human mdm2. They may be used with amplification of mdm2 gene or
CC	overexpression of mdm2 e.g. a hyperproliferative disorder such as cancer
CC	(blood, brain, breast, lung, or a soft tissue cancer) and psoriasis,
CC	fibrosis, atherosclerosis or restenosis, tumours, colorectal carcinoma
CC	and chronic myelogenous leukemia. The antisense compound may be
CC	administered with a chemotherapeutic agent to overcome drug resistance.
CC	The antisense compound reduces hyperproliferation of human cells. The
CC	method, which involves the use of the antisense compound, is also useful
CC	for detecting the role of mdm2 expression in various cell functions and
CC	physiological processes and useful in both clinical research and
CC	diagnostic tools. AA529242-AA529507 represent the human mdm2 antisense
CC	oligonucleotides of the present invention
CC	
XX	
XX	Sequence 20 BP; 5 A; 7 C; 5 G; 3 T; 0 U; 0 Other;
XX	
QY	Query Match 2.0%; Score 20; DB 1; Length 20;
Db	Best Local Similarity 100.0%; Pred. No. 1.1e+03;
	Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0
	937 CTGTTACCCAGGCTGAGTG 956
	20 CTGTTACCCAGGCTGAGTG 1
RESULT 483	
AAK98932	
ID	AAK98932 strand; DNA; 20 BP.
XX	
XX	AAK98932:
AC	
XX	
XX	24-MAY-2002 (first entry)
DE	
XX	Human Beta-globin 5' MAR antisense primer BMRI.
XX	
KW	Expression vector: beta-globin nuclear matrix attachment region; MAR;
KW	SV40 virus; gactrin; tumour growth factor beta soluble receptor II;
KW	TGF-beta SRII; TGF-beta-overexpressed disease; human; PCR; primer; ss.
XX	
OS	Homo sapiens.
XX	
XX	WO200214525-A2.
PD	
XX	21-FEB-2002.
XX	
PF	27-JUL-2001, 2001WO-KR001285.
XX	
XX	29-JUL-2000, 2000KR-00043996.
XX	
PA	(MOGA-) MOGAM BIOTECHNOLOGY RES. INST.
PA	(PANG-) PAN-GEN BIOTECH LAB INC.
XX	
XX	
XX	Kim J, Kim J, Oh S, Yoon J, Baek K, Chung S, Park D, Yoon Y;
XX	WPI; 2002-269202/31.
DR	
XX	
PT	New expression vectors for use in animal cells (e.g. pMS, pSG and pMSG
PT	vectors), useful for producing recombinant proteins in various animal
PT	cells and recombinant protein having a unique structure and function.
XX	
PS	
XX	Example 1; Page 77; 85pp; English.
CC	The invention relates to new expression vectors for animal cells
CC	comprising a beta-globin nuclear matrix attachment region (MAR) sequence
CC	or its complementary sequence at 5'-terminal end of a promoter and/or a
CC	SV40 virus poly-A signal and transcription termination site of gactrin
CC	gene. The expression vectors are useful for producing recombinant
CC	proteins in various animal cells and recombinant protein having a unique
CC	structure and function. The vectors, which have increased expression
CC	efficiency and levels for foreign genes, are useful for expressing
CC	foreign proteins used in an animal cell system, e.g. tumour growth factor

CC beta soluble receptor II (TGF-beta SRII), which can be used for treatment  
CC of TGF-beta-overexpressed disease. This polynucleotide sequence  
CC represents a PCR primer of human Beta-globin 5' MAR of the invention  
XX  
SQ Sequence 20 BP; 3 A; 6 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 722 CCTCTGACTAGCTGGACT 741  
DB 1 CCTCTGACTAGCTGGACT 20

RESULT 484  
ABS59253/c  
ID ABS59253 standard; DNA; 20 BP.

XX ABS59253;

DT 05-NOV-2002 (first entry)

XX Human CAS gene antisense oligonucleotide, ISIS 128206.

XX Human; ss; antisense; cellular apoptosis susceptibility gene;  
XX antiinflammatory; antitumour; cytostatic; CAS; CSE1; CSP;  
XX chromosome 20q13; mitosis; apoptosis; proliferation; cancer;  
XX Importin-alpha; nuclear localisation; cell cycle;  
XX hyperproliferative disorder; degenerative disorder; Alzheimer's disease;  
XX Parkinson's disease; amyotrophic lateral sclerosis; ALS;  
XX retinitis pigmentosa; blood cell disorder; gene therapy; infection;  
XX inflammation; tumour.

XX Homo sapiens.  
OS Synthetic.

XX Location/Qualifiers  
FH Key 1..20  
FT modified\_base

FT /tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER = phosphorothioate backbone, all cytidine  
FT residues are 5-methylcytidines"

FT modified\_base

FT /tag= b  
FT /mod\_base= OTHER  
FT /note= "OTHER = 2'-O-methoxyethyl nucleotides"

FT modified\_base

FT /tag= c  
FT /mod\_base= OTHER  
FT /note= "OTHER = 2'-O-methoxyethyl nucleotides"

XX WO200246367-A2.

XX 13-JUN-2002.

XX 29-OCT-2001; 2001WO-US051048.

XX 01-NOV-2000; 2000US-00705299.

XX (ISIS-) ISIS PHARM INC.

XX Cowsett LM, Freier SM;

XX WPI; 2002-608254/65.

XX New antisense compound that hybridizes and inhibits nucleic acid encoding  
PT cellular apoptosis susceptibility gene, useful for treating a  
PT hyperproliferative disorder such as cancer.

XX Claim 3; Page 91; 135pp; English.

XX The invention discloses antisense compounds, of 8 - 50 nucleobases in

CC length, targeted to a nucleic acid molecule encoding a human cellular  
CC apoptosis susceptibility gene (CAS or CSE1 or CSP), located on chromosome  
CC 20q13. CAS has been implicated in the regulation of mitosis, apoptosis  
CC and cellular proliferation and is highly expressed in some cancer cells.  
CC CAS has also been shown to mediate export of importin-alpha from the  
CC nucleus. Importin-alpha is a nuclear import receptor for nuclear  
CC localisation signal-containing proteins and deregulation of importin  
CC transport is involved in cell cycle defects. The antisense compounds  
CC specifically hybridise with, and inhibit expression of, the gene or  
CC specifically hybridise with an 8 nucleobase portion of its active site.  
CC The antisense compounds are useful for inhibiting the expression of a  
CC cellular apoptosis susceptibility gene in cells or tissues and for  
CC treating an animal having a disease or condition associated with a  
CC cellular apoptosis susceptibility gene, where the disease or condition is  
CC a hyperproliferative disorder such as cancer, preferably breast or colon  
CC cancer, degenerative disorders such as Alzheimer's disease, Parkinson's  
CC disease, amyotrophic lateral sclerosis (ALS), retinitis pigmentosa and  
CC blood cell disorders. The compounds are also useful for diagnostics,  
CC therapeutics, prophylaxis, as research reagents and kits, for  
CC distinguishing functions of various members of a biological pathway, in  
CC antisense gene therapy and prophylactically (e.g. to prevent or delay  
CC infection, inflammation or tumour formation). The antisense  
CC oligonucleotides in ABS59252-ABS59322 are targeted to the human CAS gene

Sequence 20 BP; 3 A; 6 C; 6 G; 5 T; 0 U; 0 Other;  
Query Match 2.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 381 AGCCTCCCAAGTCTGGGA 400  
DB 20 AGCCTCCCAAGTCTGGGA 1

RESULT 485  
ABS67840/c

ID ABS67840 standard; DNA; 20 BP.

XX ABS67840;

DT 29-NOV-2002 (first entry)

XX Human casein kinase 2-alpha prime antisense oligonucleotide #1.

XX Human; casein kinase 2-alpha prime; diabetes mellitus;  
XX hyperproliferative disorder; breast cancer; prostate cancer;  
XX liver cancer; infection; inflammation; tumour formation; cytostatic;  
XX antidiabetic; antiinflammatory; antimicrobial; phosphorothioate;  
XX antisense therapy; ss.

XX Homo sapiens.

XX WO200262951-A2.

XX 15-AUG-2002.

XX 01-FEB-2002; 2002WO-US002772.

XX 08-FEB-2001; 2001US-00780173.

XX (ISIS-) ISIS PHARM INC.

XX McKay R, Freier SM, Wyatt JR;

XX WPI; 2002-627539/67.

XX New antisense oligonucleotides targeted to nucleic acid encoding casein  
PT kinase 2-alpha prime, useful for diagnosing and/or treating a disease or  
PT condition associated with expression of casein kinase 2-alpha prime.

XX Claim 3; Page 94; 129pp; English.

XX

CC The present invention relates to antisense oligonucleotides and methods  
CC for modulating the expression of human or mouse casein kinase 2- $\alpha$   
CC prime. The antisense oligonucleotides are useful for inhibiting the  
CC expression of casein kinase 2- $\alpha$  prime, and for treating diseases or  
CC conditions associated with aberrant expression of casein kinase 2- $\alpha$   
CC prime. Such diseases include diabetes mellitus, and hyperproliferative  
CC disorders (particularly cancers e.g. breast cancer, prostate cancer, or  
CC liver cancer). The antisense compounds are also useful for diagnostics,  
CC therapeutics, prophylaxis, e.g. to prevent or delay infection,  
CC inflammation or tumour formation, as research reagents and kits, and in  
CC distinguishing between functions of various members of a biological  
CC pathway. ABS67840-ABS67917 represent human or mouse casein kinase 2- $\alpha$   
CC prime antisense oligonucleotides which comprise a phosphorothioate  
CC backbone  
XX  
SQ Sequence 20 BP; 3 A; 10 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 645 CAGGCTGAGTGCAGTGGCG 664  
DB 20 CAGGCTGAGTGCAGTGGCG 1

RESULT 486  
AAL40355  
ID AAL40355 standard; DNA; 20 BP.  
XX  
AC AAL40355;  
XX  
DT 19-SEP-2002 (first entry)  
XX  
DE Human caspase 6 antisense inhibition related oligo SEQ ID No 74.  
XX  
OS Muscular; cytosolic; neurotropic; neuroprotective; ophthalmological;  
XX antileptemic; osteopathic; caspase 6; Rieger's syndrome; bone metabolism;  
XX ataxia telangiectasia; hyperproliferative disorder; cholesterol disorder;  
XX haematopoietic disorder; cancer; neurological; Alzheimer's disease;  
XX apoptotic; human; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200229066-A1.  
XX  
PD 11-APR-2002.  
XX  
PF 03-OCT-2001; 2001WO-US030871.  
XX  
PR 04-OCT-2000; 2000US-00679299.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Brown-Driver VL, Zhang H, Watt AT;  
XX  
DR WPI; 2002-471315/50.  
XX  
PT An antisense oligonucleotide of 8 to 50 nucleotides in length that  
XX inhibits caspase 6, is useful for treating Rieger's syndrome.  
XX  
PS Example 15; Page 89; 141p; English.  
XX  
CC The invention relates to an antisense oligonucleotide compound of 8 to 50  
CC nucleotides in length that is targeted to a nucleic acid molecule  
CC encoding caspase 6, where the oligonucleotide specifically hybridises  
CC with and inhibits the expression of caspase 6. The oligonucleotide of the  
CC invention specifically hybridises to and inhibits expression of caspase 6  
CC in cells or tissues. The oligonucleotides can be administered  
CC therapeutically or prophylactically to treat an animal having a disease  
CC or condition associated with caspase 6, such as Rieger's syndrome or  
CC ataxia telangiectasia, hyperproliferative disorder, a haematopoietic  
CC disorder, a bone metabolism or cholesterol disorder, various types of

CC cancer, neurological conditions such as Alzheimer's disease and other de-  
CC regulated apoptotic pathological conditions. This polynucleotide sequence  
CC represents a human caspase 6 oligonucleotide relating to the invention.  
CC NOTE: This phosphorothioate oligonucleotide sequence has 2'-MOE wings and  
CC a deoxy gap  
XX  
SQ Sequence 20 BP; 3 A; 4 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 TTGGTCAGGCTGCTCGAA 221  
DB 1 TTGGTCAGGCTGCTCGAA 20

RESULT 487  
AAL40351  
ID AAL40351 standard; DNA; 20 BP.  
XX  
AC AAL40351;  
XX  
DT 19-SEP-2002 (first entry)  
XX  
DE Human caspase 6 antisense inhibition related oligo SEQ ID No 70.  
XX  
OS Muscular; cytosolic; neurotropic; neuroprotective; ophthalmological;  
XX antileptemic; osteopathic; caspase 6; Rieger's syndrome; bone metabolism;  
XX ataxia telangiectasia; hyperproliferative disorder; cholesterol disorder;  
XX haematopoietic disorder; cancer; neurological; Alzheimer's disease;  
XX apoptotic; human; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200229066-A1.  
XX  
PD 11-APR-2002.  
XX  
PF 03-OCT-2001; 2001WO-US030871.  
XX  
PR 04-OCT-2000; 2000US-00679299.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Brown-Driver VL, Zhang H, Watt AT;  
XX  
DR WPI; 2002-471315/50.  
XX  
PT An antisense oligonucleotide of 8 to 50 nucleotides in length that  
XX inhibits caspase 6, is useful for treating Rieger's syndrome.  
XX  
PS Claim 3; Page 89; 141p; English.  
XX  
CC The invention relates to an antisense oligonucleotide compound of 8 to 50  
CC nucleotides in length that is targeted to a nucleic acid molecule  
CC encoding caspase 6, where the oligonucleotide specifically hybridises  
CC with and inhibits the expression of caspase 6. The oligonucleotide of the  
CC invention specifically hybridises to and inhibits expression of caspase 6  
CC in cells or tissues. The oligonucleotides can be administered  
CC therapeutically or prophylactically to treat an animal having a disease  
CC or condition associated with caspase 6, such as Rieger's syndrome or  
CC ataxia telangiectasia, hyperproliferative disorder, a haematopoietic  
CC disorder, a bone metabolism or cholesterol disorder, various types of  
CC cancer, neurological conditions such as Alzheimer's disease and other de-  
CC regulated apoptotic pathological conditions. This polynucleotide sequence  
CC represents a human caspase 6 oligonucleotide relating to the invention.  
CC NOTE: This phosphorothioate oligonucleotide sequence has 2'-MOE wings and  
CC a deoxy gap  
XX  
SQ Sequence 20 BP; 6 A; 4 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 387 CCAAGTCTGGGATTACG 406  
DB 1 CCAAGTCTGGGATTACG 20

## RESULT 488

ABL40354  
ID ABL40354 standard; DNA; 20 BP.

AC AAL40354;

DT 19-SEP-2002 (first entry)

DE Human caspase 6 antisense inhibition related oligo SEQ ID No 73.

KW Muscular; cytosolic; neurotrophic; neuroprotective; ophthalmological;  
KW anti-leukemic; osteopathic; caspase 6; Rieger's syndrome; bone metabolism;  
KW ataxia telangiectasia; hyperproliferative disorder; cholesterol disorder;  
KW haematopoietic disorder; cancer; neurological; Alzheimer's disease;  
KW apoptotic; human; ds.

OS Homo sapiens.

PN WO200229066-A1.

PD 11-APR-2002.

PF 03-OCT-2001; 2001WO-US030871.

PR 04-OCT-2000; 2000US-00679299.

XX (ISIS-) ISIS PHARM INC.

PI Brown-Driver VL, Zhang H, Watt AF,

DR WPI; 2002-471315/50.

PT An antisense oligonucleotide of 8 to 50 nucleotides in length that  
inhibits caspase 6, is useful for treating Rieger's syndrome.

PS Claim 3; Page 89; 141pp; English.

XX The invention relates to an antisense oligonucleotide compound of 8 to 50  
CC nucleotides in length that is targeted to a nucleic acid molecule  
CC encoding caspase 6, where the oligonucleotide specifically hybridises  
CC with and inhibits the expression of caspase 6. The oligonucleotide of the  
CC invention specifically hybridises to and inhibits expression of caspase 6  
CC in cells or tissues. The oligonucleotides can be administered  
CC therapeutically or prophylactically to treat an animal having a disease  
CC or condition associated with caspase 6, such as Rieger's syndrome or  
CC ataxia telangiectasia, hyperproliferative disorder, a haematopoietic  
CC disorder, a bone metabolism or cholesterol disorder, various types of  
CC cancer, neurological conditions such as Alzheimer's disease and other de-  
CC regulated apoptotic pathological conditions. This polynucleotide sequence  
CC represents a human caspase 6 oligonucleotide relating to the invention.  
CC NOTE: This phosphorothioate oligonucleotide sequence has 2'-MOE wings and  
CC a deoxy gap  
XX

SO Sequence 20 BP; 3 A; 9 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 CTGGTCTGGAAGTCCGACC 230  
DB 1 CTGGTCTGGAAGTCCGACC 20

RESULT 489

ABL44512/C  
ID ABL44512 standard; DNA; 20 BP.

AC ABL44512;

DT 11-APR-2002 (first entry)

DE Human chromosome 1p36-35 PCR primer SEQ ID NO:1556.

KW Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;  
KW PCR primer; ss.

OS Homo sapiens.

PN JP2001321190-A.

PD 20-NOV-2001.

PF 12-MAR-2001; 2001JP-00068285.

PR 10-MAR-2000; 2000JP-00066716.

XX (RIKA) RIKAGAKU KENKYUSHO.

PA (GENO-) GENOTEX YG.

DR WPI; 2002-144136/19.

PT Arraying genome clones.

PS Claim 4; Page 35; 528pp; Japanese.

XX The present invention describes a method of arraying genome clones. The  
CC method comprises: (a) clones of the genomic libraries contained in  
CC multiwell plates numbered for discrimination are mixed in each of the  
CC multiwell plates; (b) a primer designed based on the chromosome marker  
CC sequence is added to the mixture to carry out an amplification reaction;  
CC (c) a signal corresponding to the marker is detected from the resultant  
CC amplified product to specify the discrimination Nos. of the multiwell  
CC plates containing the clones having said marker sequence; (d) the order  
CC of the markers is changed so that the same discrimination Nos. succeed to  
CC the maximum in the specified discrimination Nos. to array the multiwell  
CC plates; (e) the clones in the multiwell plates of the specified  
CC discrimination Nos. are mixed respectively in each wells of longitudinal  
CC and lateral directions; (f) the mixed clones are cultured and the  
CC resultant cultures are amplified by using the above primer; (g) signals  
CC are detected from the amplified products; (h) the clones in the multiwell  
CC plates are specified from the detected result; and (i) the clones are  
CC reconstituted as the positions on the chromosome and arrayed. The  
CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent  
CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634  
CC represent PCR primers for human chromosome 21q22.1, which are  
CC specifically claimed for use in the present invention  
XX

SO Sequence 20 BP; 4 A; 4 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 542 CTCAGCTCCCAAGTAGCTG 561  
DB 20 CTCAGCTCCCAAGTAGCTG 1

## RESULT 490

ABL44004  
ID ABL44004 standard; DNA; 20 BP.

AC ABL44004;

DT 11-APR-2002 (first entry)

DE Human chromosome 1p36-35 PCR primer SEQ ID NO:1048.

XX Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;  
KW PCR primer; ss.  
XX  
XX Homo sapiens.  
OS  
XX JP2001321190-A.  
XX  
XX 20-NOV-2001.  
PD  
XX  
XX 12-MAR-2001; 2001JP-00068285.  
PF  
XX  
XX 10-MAR-2000; 2000JP-00066716.  
PR  
XX  
XX (RIKA) RIKAGAKU KENKYUSHO.  
PA  
XX (GENO-) GENOTEX YG.  
PA  
XX WPI; 2002-144136/19.  
DR  
XX  
XX Arraying genome clones.  
PT  
XX  
XX Claim 4; Page 25; 528pp; Japanese.  
PS  
XX  
XX The present invention describes a method of arraying genome clones. The  
CC method comprises: (a) clones of the genomic libraries contained in  
CC multiwell plates numbered for discrimination are mixed in each of the  
CC multiwell plates; (b) a primer designed based on the chromosome marker  
CC sequence is added to the mixture to carry out an amplification reaction;  
CC (c) a signal corresponding to the marker is detected from the resultant  
CC amplified product to specify the discrimination Nos. of the multiwell  
CC plates containing the clones having said marker sequence; (d) the order  
CC of the markers is changed so that the same discrimination Nos. succeed to  
CC the maximum in the specified discrimination Nos. to array the multiwell  
CC plates; (e) the clones in the multiwell plates of the specified  
CC discrimination Nos. are mixed respectively in each well of longitudinal  
CC and lateral directions; (f) the mixed clones are cultured and the  
CC resultant cultures are amplified by using the above primer; (g) signals  
CC are detected from the amplified products; (h) the clones in the multiwell  
CC plates are specified from the detected result; and (i) the clones are  
CC reconstituted as the positions on the chromosome and arrayed. The  
CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent  
CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634  
CC represent PCR primers for human chromosome 21q22.1, which are  
CC specifically claimed for use in the present invention  
CC  
XX  
SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;  
Query Match 2.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 384 CTCGCCAAGTCTGGGATTG 403  
DB 1 CTCGCCAAGTCTGGGATTG 20  
RESULT 491  
ABA92187  
ID ABA92187 standard; DNA; 20 BP.  
XX  
XX ABA92187;  
AC  
XX  
XX 06-JUN-2002 (first entry)  
DT  
XX  
XX Polymorphism 506B13CA1 reverse PCR primer.  
DE  
XX  
XX NALPN; nycetalopin; human; congenital stationary night blindness; CSNB;  
KW glycosylphosphatidylinositol; GPI; proteoglycan; retina; polymorphism;  
KW marker; PCR; primer; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX CA2306241-A1.  
PN

XX  
PD 12-NOV-2001.  
XX  
XX 12-MAY-2000; 2000CA-02306241.  
PF  
XX  
XX 12-MAY-2000; 2000CA-02306241.  
PR  
XX  
XX (BECH/) BECH-HANSEN N T.  
PA  
XX  
XX Bech-Hansen NT;  
PI  
XX  
XX WPI; 2002-242157/30.  
DR  
XX  
XX Novel purified mammalian retinal, kidney glycosylphosphatidylinositol-  
PT anchored small leucine-rich proteoglycan and polynucleotides encoding  
PT them used to diagnose complete X-linked congenital stationary night  
PT blindness.  
PT  
XX  
XX Example 1; Page 28; 44pp; English.  
PS  
XX  
XX The present sequence is that of a reverse primer used, with the forward  
CC primer given in ABA92186, in PCR analysis of polymorphism 506B13CA1  
CC (DXS10042). This was 1 of 3 novel markers identified in a genotype  
CC analysis of X-linked congenital stationary night blindness (CSNB)  
CC families. The new, and some previously known, markers allowed an analysis  
CC of selected recombinant X chromosomes to determine the CSNB1 minimal  
CC region. To identify candidate genes for the CSNB1 locus, a robust  
CC physical map of the CSNB1 minimal region in Xp11.4 was developed. This  
CC identified the NALPN gene encoding nycetalopin (see AM51108). An extended  
CC NALPN cDNA sequence (see ABA92185) was established by sequencing of PCR  
CC and RAGE products obtained from retinal RNA. 11 different mutations were  
CC identified in NALPN, none of which were observed in normal individuals.  
CC These included missense mutations, insertions and deletions of the coding  
CC region that are predicted to disrupt specific functions of nycetalopin.  
CC and may be informative as to the structure-function relationship of the  
CC protein. Such information may be useful for targeting therapy for retinal  
CC disease. Identification of the NALPN gene will also provide a tool for  
CC the diagnosis of complete X-linked CSNB in individuals suspected of  
CC having this disorder  
XX  
SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;  
Query Match 2.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 385 TCCCAAGTCTGGGATTAC 404  
DB 1 TCCCAAGTCTGGGATTAC 20  
RESULT 492  
ABA92208  
ID ABA92208 standard; DNA; 20 BP.  
XX  
XX ABA92208;  
AC  
XX  
XX 06-JUN-2002 (first entry)  
DT  
XX  
XX Reverse PCR primer for polymorphism 506B13CA1.  
DE  
XX  
XX NYX; nycetalopin; human; congenital stationary night blindness; CSNB;  
KW glycosylphosphatidylinositol; GPI; retina; SLP; SLP;  
KW small leucine-rich proteoglycan; therapy; diagnosis; PCR; primer; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX CA2345915-A1.  
PN  
XX  
XX 12-NOV-2001.  
PD  
XX  
XX 14-MAY-2001; 2001CA-02345915.  
PF  
XX



PR 12-MAY-2000; 2000CA-02306241.  
 XX (BECH/) BECH-HANSEN N T.  
 PA  
 XX  
 PI Bech-Hansen NT;  
 XX  
 DR WPI; 2002-242185/30.  
 XX  
 PT Novel purified mammalian glycosyl-inositol phospholipid-anchored small  
 PT leucine-rich proteoglycan, and genes encoding proteoglycan which are  
 PT useful for diagnosing complete X-linked congenital stationary night  
 PT blindness.  
 PS  
 XX Example 1; Page 26; 65pp; English.  
 XX  
 CC The present sequence is that of a reverse primer used, with the forward  
 CC primer given in ABA92207, in PCR analysis of polymorphism 506B13CA1  
 CC (DXS10042). This was 1 of 3 novel markers identified in a genotype  
 CC analysis of X-linked congenital stationary night blindness (CSNB)  
 CC families. The new, and some previously known, markers allowed an analysis  
 CC of selected recombinant X chromosomes to determine the CSNB1 minimal  
 CC region. To identify candidate genes for the CSNB1 locus, a robust  
 CC physical map of the CSNB1 minimal region in Xp11.4 was developed. This  
 CC identified the NYX gene encoding nyctalopin (see AAMS1131). An extended  
 CC NYX cDNA sequence (see ABA92206) was established by sequencing of PCR and  
 CC RACE products obtained from retinal RNA. 14 different mutations were  
 CC identified in NYX genes from different CSNB families, none of which were  
 CC observed in normal individuals. These included missense, insertion, stop  
 CC and deletion mutations that are predicted to disrupt specific functions  
 CC of nyctalopin. The invention provides a method and kit for diagnosing  
 CC complete X-linked CSNB, which involves screening for alterations in the  
 CC gene nucleotide sequence. It also provides a method of screening drug  
 CC candidates that affect nyctalopin expression or production  
 CC  
 SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;  
 Query Match 2.0%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 385 TCCCAAGTCTGGATTAC 404  
 DB 1 TCCCAAGTCTGGATTAC 20  
 RESULT 493  
 ID AAS96659 standard; DNA; 20 BP.  
 AC AAS96659;  
 XX  
 DT 09-APR-2002 (first entry)  
 XX  
 DE Telomerase reverse transcriptase, antisense oligonucleotide #69.  
 XX  
 KM Telomerase reverse transcriptase; TERT; cytosolic; apoptosis;  
 KM cell growth inhibitor; antisense oligonucleotide; antisense technology;  
 KM ss.  
 KW  
 XX Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200188198-A1.  
 PD  
 XX 22-NOV-2001.  
 XX  
 PF 15-MAY-2001; 2001WO-US015774.  
 PR 16-MAY-2000; 2000US-00572423.  
 PR 07-DEC-2000; 2000US-00733294.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX

PI Monia BP, Gaarde WA, Freier SM, Mancewicz E;  
 XX  
 DR WPI; 2002-075321/10.  
 XX  
 PT New compound targeted to nucleic acid molecule encoding telomerase  
 PT transcriptase (TERT), which specifically hybridizes with and inhibits  
 PT expression of TERT, useful for modulating apoptosis and inhibiting cell  
 PT growth.  
 XX  
 PS Example 19; Page 91; 154pp; English.  
 XX  
 CC The invention describes a compound, 8-50 nucleobases in length targeted  
 CC to a nucleic acid molecule encoding human TERT (telomerase reverse  
 CC transcriptase), where the compound specifically hybridizes with and  
 CC inhibits the expression of TERT. A series of oligonucleotides were  
 CC designed to target different regions of the human TERT RNA. These were 20  
 CC nucleotides in length and composed of a central gap region consisting of  
 CC ten 2'-deoxynucleotides, flanked on both sides (5' and 3' directions) by  
 CC five-nucleotide wings. The wings were composed of 2'-methoxyethyl (2'-  
 CC MOE) nucleotides. The compounds were analysed for their effect on human  
 CC TERT mRNA levels by reverse transcriptase (RT)-polymerase chain reaction  
 CC (PCR). The compound is useful for inhibiting the expression of TERT in  
 CC cells or tissues, for treating a human having disease or condition  
 CC associated with TERT, for modulating apoptosis, for inhibiting cell  
 CC growth (preferably, cancer cell growth), in antisense therapy and for  
 CC diagnostics and therapeutics. This sequence is an antisense  
 CC oligonucleotide used to modulate the activity of nucleic acid molecules  
 CC encoding TERT, described in the method of the invention  
 CC  
 SQ Sequence 20 BP; 4 A; 3 C; 8 G; 5 T; 0 U; 0 Other;  
 Query Match 2.0%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 863 TGCTGGATTACAGGCGTCA 882  
 DB 1 TGCTGGATTACAGGCGTCA 20  
 RESULT 494  
 ID ABR91100/c  
 AC ABR91100 standard; DNA; 20 BP.  
 XX  
 AC ABR91100;  
 XX  
 DT 05-DEC-2002 (first entry)  
 XX  
 DE PCR primer Alu3, for human DNA derived from chromosome 21.  
 XX  
 KM Human; fluorescent labelling technique; fluorescent intercalating dye;  
 KM nucleic acid detection; electrophoresis; diagnostic assay;  
 KM cell labelling; PCR; primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6428667-B1.  
 PD  
 XX 06-AUG-2002.  
 XX  
 PF 10-OCT-2000; 2000US-00686147.  
 PR 14-MAR-1990; 90US-00493307.  
 PR 06-FEB-1992; 92US-00831823.  
 PR 02-DEC-1993; 93US-00161231.  
 PR 07-NOV-1997; 97US-00966398.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 PA  
 XX Glazer AN, Mathies RA, Peck K;  
 XX  
 DR WPI; 2002-722081/78.  
 XX

PT Detection of separated molecules involves use of a group comprising a  
PT double stranded DNA probe and fluorescent molecule.  
PS Disclosure; Col 8; 7pp; English.  
XX  
XX  
XX The present invention relates to novel fluorescent labelling techniques  
CC and fluorescent labels. The method and compositions of the invention are  
CC useful for detecting molecules using fluorescent labels where fluorescent  
CC intercalating dyes have strong non-covalently binding affinities for the  
CC dsDNA. The method is useful for detecting molecules e.g. nucleic acids,  
CC in electrophoresis methods. The method can also be applied to diagnostic  
CC assays and cell labelling. The fluorescent label is sensitive, stable and  
CC resistant to self-quenching. The present sequence represents a PCR primer  
CC used to amplify human DNA derived from chromosome 21  
SQ Sequence 20 BP; 4 A; 7 C; 3 G; 6 T; 0 U; 0 Other;  
Query Match 2.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 388 CAAAGTGTGGGATTACAGG 407  
DB 20 CAAAGTGTGGGATTACAGG 1  
RESULT 495  
ACC40946  
ID ACC40946 strand; DNA; 20 BP.  
XX  
XX ACC40946;  
AC  
XX  
XX 23-MAY-2003 (first entry)  
DT  
XX  
XX Human superoxide dismutase 1 antisense inhibitor # ISIS 150500.  
DE  
XX Human; superoxide dismutase 1; antisense; neuroprotective; cyostatic;  
XX antiinflammatory; amyotrophic lateral sclerosis; apoptosis;  
KW hyperproliferative disorder; therapy; infection; inflammation; tumour;  
KM ss.  
XX  
XX Homo sapiens.  
OS  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FH 1..20  
FT modified\_base  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "Phosphorothioate linkages. All cytosines are 5-  
FT methylcytosine"  
FT 1..5  
FT modified\_base  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"  
FT 16..20  
FT modified\_base  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"  
XX  
XX WO2003000707-A2.  
XX  
XX 03-JAN-2003.  
PD  
XX 19-JUN-2002; 2002WO-US019664.  
XX  
XX 21-JUN-2001; 2001US-00888360.  
PR  
XX (ISIS-) ISIS PHARM INC.  
XX  
XX Bennett FC, Doble K;  
PI  
XX WPI; 2003-184032/18.  
XX  
XX

PT Novel antisense compounds targeted to nucleic acids encoding human  
PT superoxide dismutase 1, for modulating expression of the dismutase and  
PT treating diseases or conditions, e.g. amyotrophic lateral sclerosis.  
PS Example 15; Page 77; 107pp; English.  
XX  
XX  
XX The invention relates to a compound of 8-50 nucleobases in length,  
CC targeted to a nucleic acid molecule encoding human superoxide dismutase  
CC 1. The compound specifically hybridises with and inhibits the expression  
CC of human superoxide dismutase 1 by hybridising with at least an 8-  
CC nucleobase portion of the nucleic acid molecule encoding the active site  
CC of the enzyme. The activity of compounds of the invention may be  
CC described as neuroprotective, cyostatic and antiinflammatory. The  
CC mechanism of action of compounds of the invention is antisense inhibition  
CC of human superoxide dismutase 1 expression by chimeric phosphorothioate  
CC oligonucleotides having 2'-methoxyethyl (2'-MOE) wings and a decoy gap.  
CC Compounds of the invention are useful for inhibiting the expression of  
CC human superoxide dismutase 1 in human cells or tissues, and for treating  
CC a disease or condition associated with this enzyme (antisense therapy),  
CC especially amyotrophic lateral sclerosis, a disease or condition arising  
CC from aberrant apoptosis and a hyperproliferative disorder. It may also be  
CC used in diagnostics, therapeutics and as a research reagent, e.g.  
CC prophylactically to prevent or delay infection, inflammation or tumour  
CC formation. Sequences given in records ACC40880-ACC40957 represent human  
CC superoxide dismutase 1 antisense inhibitor oligonucleotides  
SQ Sequence 20 BP; 5 A; 4 C; 8 G; 3 T; 0 U; 0 Other;  
Query Match 2.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 729 AGTAGCTGGAGCTACAGGCG 748  
DB 1 AGTAGCTGGAGCTACAGGCG 20  
RESULT 496  
ABZ79385  
ID ABZ79385 standard; DNA; 20 BP.  
XX  
XX ABZ79385;  
AC  
XX  
XX 01-MAY-2003 (first entry)  
DT  
XX  
XX Acetyl-Coenzyme A-carboxylase-alpha gene PCR primer, SEQ ID 72.  
DE  
XX Human; enzyme; acetyl-Coenzyme A-carboxylase-alpha; ACC-alpha; cancer;  
KW breast; ovary; PCR; primer; ss.  
XX  
XX Homo sapiens.  
OS  
OS WO2002100896-A2.  
XX  
XX 19-DEC-2002.  
PD  
XX 12-JUN-2002; 2002WO-FR002015.  
XX  
XX 13-JUN-2001; 2001FR-00007740.  
PR 05-MAR-2002; 2002FR-00002788.  
XX  
XX (CNRS ) CNRS CENT NAT RECH SCI.  
XX (UCLY-) UNIV LYON 1 BERNARD CLAUDE.  
XX  
XX Dalla Venezia NL, Magnard CM, Lenoir GM, Similkova-Brard O;  
XX WPI; 2003-175165/17.  
XX  
XX In vitro diagnosis of cancer, particularly breast and ovarian cancer, or  
XX susceptibility, comprises detecting alterations in the acetyl coenzyme A-  
XX carboxylase alpha gene or protein expression.  
XX  
XX Example 1; Page 11; 56pp; French.  
PS

```
XX The present invention relates to human acetyl-Coenzyme A-carboxylase-
CC alpha (ACC-alpha; see AB279442), which can be used for in vitro diagnosis
CC of cancer (or of an increased risk of developing it), by detecting ACC-
CC alpha gene mutations or polymorphisms, or altered ACC-alpha protein
CC expression, relative to a control population. The method is particularly
CC used to diagnose cancer, especially of breast or ovary, or for assessing
CC the risk of developing such cancers. The present sequence is a PCR
CC primer, which was used in an example from the invention
XX
SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
XX
Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 385 TCCCAAGTCTGGGATTAC 404
DB 1 TCCCAAGTCTGGGATTAC 20
XX
RESULT 497
ID AAL60008/C
XX AAL60008 standard; DNA; 20 BP.
XX
AC AAL60008;
XX
DT 27-AUG-2003 (first entry)
XX
DE Human GH-1 gene amplifying PCR primer, CRV156.lpl.
XX
KW Human; growth hormone 1; GH-1; single nucleotide polymorphism; SNP;
KW gene therapy; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO2003042226-A2.
XX
PD 22-MAY-2003.
XX
PF 07-NOV-2002; 2002WO-US035719.
XX
PR 09-NOV-2001; 2001US-0347448P.
XX
PA (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI Wood LS, Wagner S, Parodi LA;
XX
DR WPI; 2003-449555/42.
XX
PT New growth hormone 1 (GH-1) diagnostic polynucleotide, useful as markers
PT for the analysis of a disease, or of susceptibility to drug treatment for
PT GH-1 dysfunction or other diseases.
XX
PS Example 2; Page 30; 74pp; English.
XX
CC The invention relates to growth hormone 1 (GH-1) gene including single
CC nucleotide polymorphisms (SNP). The GH-1 diagnostic polynucleotide is
CC useful as markers for the analysis of a disease, of susceptibility to
CC drug treatment for GH-1 dysfunction or other diseases, or may be included
CC in any complete or partial genetic map of the human genome. GH-1 mutant
CC polypeptides are useful as antagonists of GH-1 hormone action.
CC Polynucleotides encoding these polypeptides are useful in gene therapy.
CC The present sequence is a PCR primer used for amplifying human GH-1 gene
XX
SQ Sequence 20 BP; 4 A; 6 C; 4 G; 6 T; 0 U; 0 Other;
XX
Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 387 CCAAGTCTGGGATTACAG 406
DB 1 CCAAGTCTGGGATTACAG 406
```

```
DB 20 CCAAGTCTGGGATTACAG 1
XX
RESULT 498
ID ADD21702/C
XX ADD21702 standard; DNA; 20 BP.
XX
AC ADD21702;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #265.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
KW atherosclerosis; restenosis; apoptosis modulation; p21; ss;
KW 2'-methoxyethoxy-residue; phosphorothioate backbone.
XX
OS Homo sapiens.
XX
PN WO2003048315-A2.
XX
PD 12-JUN-2003.
XX
PF 02-DEC-2002; 2002WO-US038281.
XX
PR 04-DEC-2001; 2001US-00005344.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Miraglia LJ, Nero PS, Graham MJ, Monia BP, Koller E, Chiang MY;
PI Manoharan M;
XX
DR WPI; 2003-577263/54.
XX
PT Novel antisense compound targeted to 5' untranslated region, coding
PT region, or intron:exon junction of nucleic acid molecule encoding mdm2,
PT useful for treating e.g. cancer, psoriasis or restenosis by inhibiting
PT mdm2 expression.
XX
PS Example 9; SEQ ID NO 267; 289pp; English.
XX
CC The invention comprises antisense oligonucleotides which are targeted to
CC the human mdm2 gene. The antisense oligonucleotides of the invention are
CC useful for reducing hyperproliferation of human cells. The antisense
CC oligonucleotides are also useful for treating: hyperproliferative
CC disorders (e.g. cancer), psoriasis, fibrosis, atherosclerosis, or
CC restenosis. The antisense oligonucleotides are also useful for modulating
CC apoptosis, and for increasing expression of p21. The present DNA sequence
CC represents a human mdm2 gene antisense oligonucleotide of the invention.
CC The present sequence contains 2'-methoxyethoxy-residues and has a
CC phosphorothioate backbone.
XX
SQ Sequence 20 BP; 4 A; 7 C; 3 G; 6 T; 0 U; 0 Other;
XX
Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 388 CCAAGTCTGGGATTACAG 407
DB 20 CCAAGTCTGGGATTACAG 1
XX
RESULT 499
ID ADD21701/C
XX ADD21701 standard; DNA; 20 BP.
XX
AC ADD21701;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #264.
```

XX antisense oligonucleotide; human; mdm2; hyperproliferation;  
KM hyperproliferative disorder; cancer; psoriasis; fibrosis;  
KM atherosclerosis; restenosis; apoptosis modulation; p21; ss;  
KM 2'-methoxyethoxy-residue; phosphorothioate backbone.  
XX  
OS Homo sapiens.  
XX  
XX WO2003048315-A2.  
XX  
XX 12-JUN-2003.  
XX  
XX 02-DEC-2002; 2002WO-US038281.  
XX  
XX 04-DEC-2001; 2001US-00005344.  
XX  
XX (ISIS-) ISIS PHARM INC.  
XX  
XX Miraglia LJ, Nero PS, Graham MJ, Monia BP, Koller E, Chiang MY,  
PI Manoharan M;  
XX  
XX WPI; 2003-577263/54.  
XX  
XX Novel antisense compound targeted to 5' untranslated region, coding  
PT region, or intron:exon junction of nucleic acid molecule encoding mdm2,  
PT useful for treating e.g. cancer, psoriasis or restenosis by inhibiting  
PT mdm2 expression.  
XX  
XX Example 9; SEQ ID NO 266; 289pp; English.  
XX  
XX The invention comprises antisense oligonucleotides which are targeted to  
CC the human mdm2 gene. The antisense oligonucleotides of the invention are  
CC useful for reducing hyperproliferation of human cells. The antisense  
CC oligonucleotides are also useful for treating: hyperproliferative  
CC disorders (e.g. cancer), psoriasis, fibrosis, atherosclerosis, or  
CC restenosis. The antisense oligonucleotides are also useful for modulating  
CC apoptosis, and for increasing expression of p21. The present DNA sequence  
CC represents a human mdm2 gene antisense oligonucleotide of the invention.  
CC The present sequence contains 2'-methoxyethoxy-residues and has a  
CC phosphorothioate backbone.  
XX  
XX Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;  
SQ  
Query Match 2.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 851 GGCTTCCTCCAAAGTCTGCGA 870  
DB 20 GGCTTCCTCCAAAGTCTGCGA 1  
RESULT 500  
ADD21677/c  
ID ADD21677 standard; DNA; 20 BP.  
XX  
XX ADD21677;  
AC  
XX  
XX 15-JAN-2004 (first entry)  
DT  
XX  
XX Human mdm2 antisense oligonucleotide #240.  
DE  
XX  
XX antisense oligonucleotide; human; mdm2; hyperproliferation;  
KM hyperproliferative disorder; cancer; psoriasis; fibrosis;  
KM atherosclerosis; restenosis; apoptosis modulation; p21; ss;  
KM 2'-methoxyethoxy-residue; phosphorothioate backbone.  
XX  
XX Homo sapiens.  
XX  
XX WO2003048315-A2.  
XX  
XX 12-JUN-2003.  
PD  
XX

PF 02-DEC-2002; 2002WO-US038281.  
XX  
XX 04-DEC-2001; 2001US-00005344.  
PR  
XX  
XX (ISIS-) ISIS PHARM INC.  
XX  
XX Miraglia LJ, Nero PS, Graham MJ, Monia BP, Koller E, Chiang MY,  
PI Manoharan M;  
XX  
XX WPI; 2003-577263/54.  
XX  
XX Novel antisense compound targeted to 5' untranslated region, coding  
PT region, or intron:exon junction of nucleic acid molecule encoding mdm2,  
PT useful for treating e.g. cancer, psoriasis or restenosis by inhibiting  
PT mdm2 expression.  
XX  
XX Example 9; SEQ ID NO 242; 289pp; English.  
XX  
XX The invention comprises antisense oligonucleotides which are targeted to  
CC the human mdm2 gene. The antisense oligonucleotides of the invention are  
CC useful for reducing hyperproliferation of human cells. The antisense  
CC oligonucleotides are also useful for treating: hyperproliferative  
CC disorders (e.g. cancer), psoriasis, fibrosis, atherosclerosis, or  
CC restenosis. The antisense oligonucleotides are also useful for modulating  
CC apoptosis, and for increasing expression of p21. The present DNA sequence  
CC represents a human mdm2 gene antisense oligonucleotide of the invention.  
CC The present sequence contains 2'-methoxyethoxy-residues and has a  
CC phosphorothioate backbone.  
XX  
XX Sequence 20 BP; 5 A; 7 C; 5 G; 3 T; 0 U; 0 Other;  
SQ  
Query Match 2.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 937 CTGTACCCAGCTGAGTG 956  
DB 20 CTGTACCCAGCTGAGTG 1  
RESULT 501  
ABZ97911  
ID ABZ97911 standard; DNA; 20 BP.  
XX  
XX ABZ97911;  
AC  
XX  
XX 17-OCT-2003 (first entry)  
DT  
XX  
XX Human RANTES oligonucleotide sequence.  
DE  
XX  
XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
KM antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KM antiaesthetic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KM antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KM adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KM lung inflammation; respiratory disease; ds.  
XX  
XX Homo sapiens.  
XX  
XX WO200285308-A2.  
XX  
XX 31-OCT-2002.  
PD  
XX  
XX 23-APR-2002; 2002WO-US013135.  
PF  
XX  
XX 24-APR-2001; 2001US-0286137P.  
PR  
XX  
XX (EPIC-) EPICGENESIS PHARM INC.  
XX  
XX Nyce JW, Li Y, Sandrasegura A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX  
XX WPI; 2003-229219/22.  
DR

XX Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ublquinone.  
XX  
PS Disclosure; SEQ ID NO 13153; 872pp; English.  
XX  
XX The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ublquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine or  
CC receptor, producing bronchodilation, increasing levels of ublquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 U; 0 Other;  
XX  
Query Match 2.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 732 AGCTGGACTACAGCGCCCC 751  
DB 1 AGCTGGACTACAGCGCCCC 20  
XX  
RESULT 502  
ABZ99076  
ID ABZ99076 standard; DNA; 20 BP.  
XX  
AC ABZ99076;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Human PDE4C oligonucleotide sequence.  
XX  
XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ublquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200285308-A2.  
XX  
PD 31-OCT-2002.  
XX  
PF 23-APR-2002; 2002WO-US013135.  
XX  
PR 24-APR-2001; 2001US-0286137P.  
XX  
PA (EPIG-) EPIGENESIS PHARM INC.  
XX  
PI NYce JW, Li Y, Sandrasagra A, Katz E, Fabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX  
DR WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ublquinone.  
XX  
PS Disclosure; SEQ ID NO 14318; 872pp; English.  
XX  
XX The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ublquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine or  
CC receptor, producing bronchodilation, increasing levels of ublquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;  
XX  
Query Match 2.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. NO. 1.1e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 379 TCAGCTCCCAAGTGTGG 398  
DB 1 TCAGCTCCCAAGTGTGG 20  
XX  
RESULT 503  
ABZ98014  
ID ABZ98014 standard; DNA; 20 BP.  
XX  
AC ABZ98014;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Human RANTES oligonucleotide sequence.  
XX  
XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ublquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200285308-A2.  
XX  
PD 31-OCT-2002.  
XX  
PF 23-APR-2002; 2002WO-US013135.  
XX  
PR 24-APR-2001; 2001US-0286137P.  
XX  
PA (EPIG-) EPIGENESIS PHARM INC.  
XX  
PI NYce JW, Li Y, Sandrasagra A, Katz E, Fabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX  
DR WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.  
 XX  
 PS Disclosure; SEQ ID NO 13256; 872bp; English.  
 XX  
 CC The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 20 BP; 3 A; 4 C; 10 G; 3 T; 0 U; 0 Other;  
 Query Match 2.0%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 646 AGGCTGAGTGCAGTGGCGC 665  
 Db 1 AGGCTGAGTGCAGTGGCGC 20  
 RESULT 504  
 ABZ99055 standard; DNA; 20 BP.  
 XX  
 AC ABZ99055;  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX  
 DE Human PDE4C oligonucleotide sequence.  
 XX  
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200285308-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 23-APR-2002; 2002WO-US013135.  
 XX  
 PR 24-APR-2001; 2001US-0286137P.  
 XX  
 PA (EPIG-) EPIGENESIS PHARM INC.  
 XX  
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D,  
 PI Miller S, Tang L, Shahabuddin S;  
 XX  
 DR WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.  
 XX  
 PS Disclosure; SEQ ID NO 14297; 872bp; English.  
 XX  
 CC The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 20 BP; 3 A; 5 C; 9 G; 3 T; 0 U; 0 Other;  
 Query Match 2.0%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 643 CCCAGGCTGAGTGCAGTGG 662  
 Db 1 CCCAGGCTGAGTGCAGTGG 20  
 RESULT 505  
 ABZ99075 standard; DNA; 20 BP.  
 XX  
 AC ABZ99075;  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX  
 DE Human PDE4C oligonucleotide sequence.  
 XX  
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200285308-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 23-APR-2002; 2002WO-US013135.  
 XX  
 PR 24-APR-2001; 2001US-0286137P.  
 XX  
 PA (EPIG-) EPIGENESIS PHARM INC.  
 XX  
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D,  
 PI Miller S, Tang L, Shahabuddin S;  
 XX  
 DR WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.

PS Disclosure; SEQ ID NO 14317; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 20 BP; 2 A; 12 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 369 TCACCTGCTCAGCCTCCC 388  
DB 1 TCACCTGCTCAGCCTCCC 20

RESULT 506  
AB292715  
ID AB292715 standard; DNA; 20 BP.

XX AB292715;

XX 17-OCT-2003 (first entry)

XX Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.

PS Disclosure; SEQ ID NO 7957; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 20 BP; 4 A; 9 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 540 GCCTCAGCTCCCAAGTAGC 559  
DB 1 GCCTCAGCTCCCAAGTAGC 20

RESULT 507  
AB292716  
ID AB292716 standard; DNA; 20 BP.

XX AB292716;

XX 17-OCT-2003 (first entry)

XX Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX WPI; 2003-229219/22.

XX	Pharmaceutical composition for treating ailments associated with impaired
PT	respiration, has oligo(s) antisense to specific gene(s) or its
PT	corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT	ubiquinone.
XX	
PS	Disclosure; SEQ ID NO 7958; 872pp; English.
XX	
CC	The invention relates to a novel pharmaceutical composition, which has a
CC	first active agent comprising an oligonucleotide antisense to the
CC	initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC	5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC	junctions of genes encoding a polypeptide associated with lung and/or
CC	nasal airway dysfunction and a second active agent comprising an
CC	antiinflammatory steroid and ubiquinone. A composition of the invention
CC	has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC	immunosuppressive, and cytostatic activity. The composition may have a
CC	use in antisense gene therapy. The composition is useful for treating or
CC	preventing a respiratory, lung or malignant disease or condition, also
CC	for enhancing the prophylactic or therapeutic respiratory effect of an
CC	antiinflammatory steroid in a subject, for reducing or depleting levels
CC	of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC	receptor, producing bronchodilatation, increasing levels of ubiquinone or
CC	lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC	lung inflammation, lung allergies, or a respiratory disease or condition.
CC	Note: The sequence data for this patent is not represented in the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences
CC	
SQ	Sequence 20 BP; 4 A; 7 C; 6 G; 3 T; 0 U; 0 Other;
Query Match	2.0%; Score 20; DB 1; Length 20;
Best Local Similarity	100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	546 GCCTCCCAAGTAGCTGGAC 565       1 GCCTCCCAAGTAGCTGGAC 20
Db	
RESULT 508	
ABZ99068	
ID	ABZ99068 standard; DNA; 20 BP.
XX	
AC	ABZ99068;
XX	
DT	17-OCT-2003 (first entry)
XX	
DE	Human PDB4C oligonucleotide sequence.
XX	
KW	Human; antisense; lung dysfunction; nasal airway dysfunction;
KW	antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW	antiasthmatic; hypotensive; immunosuppressive; cytotoxic; gene therapy;
KW	antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW	adenosine receptor; bronchodilatation; bronchoconstriction; lung allergy;
KW	lung inflammation; respiratory disease; ds.
XX	
OS	Homo sapiens.
XX	
PV	WO200285308-A2.
XX	
PD	31-OCT-2002.
XX	
PF	23-APR-2002; 2002WO-US013135.
XX	
PR	24-APR-2001; 2001US-0286137P.
XX	
PA	(EPIG-) EPIGENESIS PHARM INC.
XX	
PI	Nyce JM, Li Y, Sandrasagra A, Katz B, Pabalan J, Aguilar D;
PI	Miller S, Tang L, Shahabuddin S;
DR	WPI; 2003-229219/22.

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XX Pharmaceutical composition for treating ailments associated with impaired
XX respiration, has oligo(s) antisense to specific gene(s) or its
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX ubiquinone.
XX
XX PS Disclosure; SEQ ID NO 14310; 872pp; English.
XX
XX CC The invention relates to a novel pharmaceutical composition, which has a
XX CC first active agent comprising an oligonucleotide antisense to the
XX CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX CC junctions of genes encoding a polypeptide associated with lung and/or
XX CC nasal airway dysfunction and a second active agent comprising an
XX CC antiinflammatory steroid and ubiquinone. A composition of the invention
XX CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
XX CC immunosuppressive, and cytostatic activity. The composition may have a
XX CC use in antisense gene therapy. The composition is useful for treating or
XX CC preventing a respiratory, lung or malignant disease or condition, also
XX CC for enhancing the prophylactic or therapeutic respiratory effect of an
XX CC antiinflammatory steroid in a subject, for reducing or depleting levels
XX CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX CC receptor, producing bronchodilation, increasing levels of ubiquinone or
XX CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX CC lung inflammation, lung allergies, or a respiratory disease or condition.
XX CC Note: The sequence data for this patent is not represented in the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pat_sequences
XX
XX SQ Sequence 20 BP; 5 A; 0 C; 5 G; 10 T; 0 U; 0 Other;
XX
XX Query Match 2.0%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.1e+03;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 772 TTGTATTTTGTAGAGATG 791
XX |||||||||||||||
XX 1 TTGTATTTTGTAGAGATG 20
XX
XX Db
XX
XX RESULT 509
XX ABX94882
XX ID ABX94882 standard; cDNA; 20 BP.
XX
XX AC ABX94882;
XX
XX AT 13-AUG-2003 (first entry)
XX
XX DE Human MBH1K receptor P2Y34 PCR primer #4.
XX
XX XX Human; receptor; MBH1K receptor; P2Y34 receptor; chromosome 1;
XX XX G protein-coupled receptor; immunomodulatory; gastrointestinal;
XX XX antiinflammatory; cardiovascular; gene therapy; intestinal function;
XX XX blood pressure; blood flow; blood coagulation; haematopoiesis;
XX XX interleukin; prostaglandin; inflammation; neuronal function; cell growth;
XX XX differentiation; PCR; primer; ss.
XX
XX OS Homo sapiens.
XX
XX PN DE10142478-A1.
XX
XX PD 20-MAR-2003.
XX
XX PF 31-AUG-2001; 2001DE-01042478.
XX
XX PR 31-AUG-2001; 2001DE-01042478.
XX
XX XX (BRUE/) BRUES M.
XX XX (BOEN/) BOENISCH H.
XX XX (VKUE/) VON KUEGELGEN I.
XX
XX PT Brues M, Boenisch H, Von Kuegelgen I;
XX

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DR WPI; 2003-383212/37.  
XX New human gene P2Y34 and encoded G protein-coupled receptor, useful for  
PT treatment and diagnosis of receptor-associated diseases and for drug  
PT screening.  
XX  
XX Disclosure; Page 2; 6pp; German.  
XX  
XX This invention describes a novel human G protein-coupled receptor MBHBK  
CC type, designated P2Y34 which is located on chromosome 1. The product of  
CC the invention has immunomodulatory, gastrointestinal, anti-inflammatory  
CC and cardiovascular activity, and can be used for gene therapy. The  
CC receptor described in the disclosure may be implicated in regulation of  
CC intestinal function, blood pressure, blood flow through organs and  
CC regions of the body; blood coagulation, haematopoiesis and immune  
CC reactions; release of interleukins and prostaglandins, i.e. in  
CC inflammation; modulation of neuronal function and cell growth and  
CC differentiation. The polynucleotide of the invention which encodes a G  
CC protein-coupled receptor, and also its related cDNA, mRNA, protein,  
CC antibodies and oligonucleotides, are useful in the diagnosis and  
CC treatment of diseases associated with abnormal levels of P2Y34 expression  
CC in screening assays for modulators, potential therapeutic agents; and  
CC to produce transgenic animals, e.g. for identifying diseases associated  
CC with abnormal expression of P2Y34. This sequence represents a PCR primer  
CC used to amplify the gene encoding the human P2Y34 protein  
XX  
SQ Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;  
Query Match 2.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred.No. 1.1e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 379 TCAGCTCCCAAGTGTGG 398  
DB 1 TCAGCTCCCAAGTGTGG 20  
RESULT 510  
ADL25066/C  
ID ADL25066 standard; DNA; 20 BP.  
XX  
XX ADL25066;  
AC  
XX  
XX 20-MAY-2004 (first entry)  
DT  
XX  
XX Intestinal epithelium/peyer's patch M cell-associated PCR primer #211.  
DE  
XX Intestinal epithelium cell development; peyer's patch M cell development;  
XX inflammatory bowel disease; glutenenteropathy; infectious disease;  
XX autoimmune disease; haemolytic anaemia; rheumatoid arthritis; dermatitis;  
XX Grave's disease; multiple sclerosis; allergy; asthma; diabetic mellitus;  
XX immune system disorder; hypersensitivity; anaphylaxis;  
XX blood group incompatibility; ss; human; PCR; primer.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200280852-A2.  
PN  
XX  
XX 17-OCT-2002.  
PD  
XX  
XX 04-APR-2002; 2002WO-US010873.  
XX  
XX 04-APR-2001; 2001US-0281416P.  
PR  
XX  
XX (DIGIT-) DIGITAL GENE TECHNOLOGIES INC.  
PA  
XX  
XX Brayden DJ, Byrne D, O'mahony DJ, Evans CF, Mah SP, Lo DD;  
PI  
XX  
XX WPI; 2003-075470/07.  
DR  
XX  
XX Novel isolated or purified polypeptide encoded by genes associated with  
PT intestinal epithelium or M cell development, differentiation or function,  
PT useful for treating autoimmune diseases and infectious diseases.

XX  
XX Disclosure; SEQ ID NO 576; 152pp; English.  
PS  
XX  
XX The invention comprises DNA sequences which are associated with  
CC intestinal epithelium and peyer's patch M cells. The DNA sequences of the  
CC invention are useful for assessing, modifying, modulating or regulating  
CC intestinal epithelium or M cell development. The DNA sequences of the  
CC invention are also useful in the treatment of: inflammatory bowel  
CC disease, glutenenteropathy, infectious diseases, autoimmune diseases  
CC (e.g. haemolytic anaemia, rheumatoid arthritis, dermatitis, Grave's  
CC disease, multiple sclerosis, allergy, asthma and diabetic mellitus),  
CC diseases or disorders of the immune system, hypersensitivity,  
CC anaphylaxis, and blood group incompatibility. The present DNA sequence  
CC represents a PCR primer that was used to amplify an intestinal  
CC epithelium/peyer's patch M cell-associated DNA sequence of the invention.  
XX  
SQ Sequence 20 BP; 4 A; 9 C; 3 G; 4 T; 0 U; 0 Other;  
Query Match 2.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred.No. 1.1e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 864 GCTGGATTACAGCGCTGAG 883  
DB 20 GCTGGATTACAGCGCTGAG 1  
RESULT 511  
ADM65742  
ID ADM65742 standard; DNA; 20 BP.  
XX  
XX ADM65742;  
AC  
XX  
XX 03-JUN-2004 (first entry)  
DT  
XX  
XX Human Y chromosome non-recombining region polymorphic fragment #201.  
DE  
XX ethnic origin determination; polymorphic site determination;  
XX Y chromosome; paternity testing; forensic diagnosis;  
XX non-recombining region; human; NRY; polymorphic fragment; ds.  
XX  
XX Homo sapiens.  
OS  
XX  
XX US2003134285-A1.  
PN  
XX  
XX 17-JUL-2003.  
PD  
XX  
XX 01-NOV-2001; 2001US-00002623.  
XX  
XX 01-NOV-2000; 2000US-0245355P.  
XX  
XX (OEPN/) OEFNER P J.  
XX (UNDE/) UNDERHILL P A.  
PA  
XX  
XX Oefner PJ, Underhill PA;  
PI  
XX  
XX WPI; 2003-843259/78.  
DR  
XX  
XX Determining the ethnic origin of a male by obtaining a nucleic acid  
PT sample from the male and identifying at least two polymorphic markers in  
PT the nucleic acid sample indicative of the ethnic origin of the male.  
XX  
XX Claim 24; Page 65; 74pp; English.  
PS  
XX  
XX The invention describes a method of determining the ethnic origin of a  
CC male comprising obtaining a nucleic acid sample from the male, and  
CC identifying at least two polymorphic markers in the nucleic acid sample  
CC indicative of the ethnic origin of the male, using at least one primer  
CC pair from the primer pairs given in the specification. Also described is  
CC a method of: identifying polymorphic sites in a nucleic acid; a kit for  
CC determining the ethnic origin of an individual; determining the ethnic  
CC origin of a human male individual; an isolated nucleic acid segment of a  
CC human Y chromosome comprising at least 10 contiguous bases including at

CC least one of the polymorphic sites given in the specification; nucleic  
CC acid primer pairs for amplifying polymorphic regions of the Y chromosome  
CC given in the specification; and determining the paternity of a human male  
CC individual. The method is useful for determining the ethnic origin of a  
CC male, for paternity testing, for forensic studies or for diagnosis. This  
CC sequence represents a fragment of the non-recombining region of the human  
CC Y chromosome (NRY) comprising a polymorphism that can be used to  
CC determine ethnic origin of a male.

XX Sequence 20 BP; 6 A; 3 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 388 CAAAGTGTGGGATTACAGG 407  
DB 1 CAAAGTGTGGGATTACAGG 20

RESULT 512

ADM65739 standard; DNA; 20 BP.

XX ADM65739;

DT 03-JUN-2004 (first entry)

XX Human Y chromosome non-recombining region polymorphic fragment #300.

XX ethnic origin determination; polymorphic site determination;

KW Y chromosome; paternity testing; forensic; diagnosis;

KM non-recombining region; human; NRY; polymorphic fragment; ds.

XX Homo sapiens.

XX US2003134285-A1.

XX 17-JUL-2003.

XX 01-NOV-2001; 2001US-00002623.

XX 01-NOV-2000; 2000US-0245355P.

PA (OEFRN/) OEFRNER P J.

PI (UNDE/) UNDERHILL P A.

PI Oefner PJ, Underhill PA;

PI WPI; 2003-843259/78.

PT Determining the ethnic origin of a male by obtaining a nucleic acid  
PT sample from the male and identifying at least two polymorphic markers in  
PT the nucleic acid sample indicative of the ethnic origin of the male.

Claim 24; Page 64; 74pp; English.

CC The invention describes a method of determining the ethnic origin of a  
CC male comprising obtaining a nucleic acid sample from the male, and  
CC identifying at least two polymorphic markers in the nucleic acid sample  
CC indicative of the ethnic origin of the male, using at least one primer  
CC pair from the primer pairs given in the specification. Also described is  
CC a method of: identifying polymorphic sites in a nucleic acid; a kit for  
CC determining the ethnic origin of an individual; determining the ethnic  
CC origin of a human male individual; an isolated nucleic acid segment of a  
CC human Y chromosome comprising at least 10 contiguous bases including at  
CC least one of the polymorphic sites given in the specification; nucleic  
CC acid primer pairs for amplifying polymorphic regions of the Y chromosome  
CC given in the specification; and determining the paternity of a human male  
CC individual. The method is useful for determining the ethnic origin of a  
CC male, for paternity testing, for forensic studies or for diagnosis. This  
CC sequence represents a fragment of the non-recombining region of the human  
CC Y chromosome (NRY) comprising a polymorphism that can be used to

CC determine ethnic origin of a male.

XX Sequence 20 BP; 6 A; 3 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 388 CAAAGTGTGGGATTACAGG 407  
DB 1 CAAAGTGTGGGATTACAGG 20

RESULT 513

ADM65575/C standard; DNA; 20 BP.

XX ADM65575;

DT 03-JUN-2004 (first entry)

XX NRY polymorphism detection primer #489.

KW ethnic origin determination; polymorphic site determination;

KM Y chromosome; paternity testing; forensic; diagnosis;

XX non-recombining region; human; NRY; PCR; primer; ss.

XX Homo sapiens.

XX US2003134285-A1.

XX 17-JUL-2003.

XX 01-NOV-2001; 2001US-00002623.

XX 01-NOV-2000; 2000US-0245355P.

PA (OEFRN/) OEFRNER P J.

PI (UNDE/) UNDERHILL P A.

PI Oefner PJ, Underhill PA;

PI WPI; 2003-843259/78.

PT Determining the ethnic origin of a male by obtaining a nucleic acid  
PT sample from the male and identifying at least two polymorphic markers in  
PT the nucleic acid sample indicative of the ethnic origin of the male.

Claim 24; Page 54; 74pp; English.

CC The invention describes a method of determining the ethnic origin of a  
CC male comprising obtaining a nucleic acid sample from the male, and  
CC identifying at least two polymorphic markers in the nucleic acid sample  
CC indicative of the ethnic origin of the male, using at least one primer  
CC pair from the primer pairs given in the specification. Also described is  
CC a method of: identifying polymorphic sites in a nucleic acid; a kit for  
CC determining the ethnic origin of an individual; determining the ethnic  
CC origin of a human male individual; an isolated nucleic acid segment of a  
CC human Y chromosome comprising at least 10 contiguous bases including at  
CC least one of the polymorphic sites given in the specification; nucleic  
CC acid primer pairs for amplifying polymorphic regions of the Y chromosome  
CC given in the specification; and determining the paternity of a human male  
CC individual. The method is useful for determining the ethnic origin of a  
CC male, for paternity testing, for forensic studies or for diagnosis. This  
CC sequence represents a primer used to detect polymorphisms in the non-  
CC recombining region of the human Y chromosome (NRY).

XX Sequence 20 BP; 4 A; 7 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



KW ss; primer; antiinflammatory; cryopyrin; inflammation;  
 KW Familial cold urticaria; familial cold autoinflammatory syndrome;  
 KW Muckle Wells Syndrome.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003031639-A2.  
 XX  
 PD 17-APR-2003.  
 XX  
 PF 04-OCT-2002; 2002WO-US031502.  
 XX  
 PR 05-OCT-2001; 2001US-0327728P.  
 XX  
 PA (LUDWIG) LUDWIG INST CANCER RES.  
 XX  
 PI Hoffman H, Kolodner R;  
 XX  
 DR WPI; 2003-393448/37.  
 XX  
 PT New isolated cryopyrin protein and encoding nucleic acid, useful for  
 PT diagnosing and treating inflammatory disorders, in particular familial  
 PT cold urticaria, familial cold autoinflammatory syndrome and/or Muckle  
 PT Wells Syndrome.  
 XX  
 PS Example 2; SEQ ID NO 2; 36pp; English.  
 XX  
 CC The invention relates to a novel isolated protein (I) comprises the amino  
 CC acid sequence of wild type cryopyrin of 1034 amino acids, with the  
 CC proviso that amino acid 198 is not Val, amino acid 352 is not Ala, amino  
 CC acid 434 is not Ala, amino acid 627 is not Glu, or amino acid 703 is not  
 CC Glu. The methods are useful for determining the presence of a disorder,  
 CC treating inflammation, familial cold urticaria/familial cold  
 CC autoinflammatory syndrome (FCU/FCAS) or Muckle Wells Syndrome (MWS), and  
 CC identifying a substance useful in modulating binding of a cryopyrin  
 CC protein to a second protein. The oligonucleotide is useful in diagnosing  
 CC a disorder characterized by an aberrant CIAS1 gene. This sequence  
 CC corresponds to a primer used to amplify the cryopyrin gene of the  
 CC invention.  
 XX  
 SQ Sequence 20 BP; 6 A; 3 C; 7 G; 4 T; 0 U; 0 Other;  
 XX  
 Query Match 2.0%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 667 ATCTTGCTCACTGCACCT 686  
 Db 20 ATCTTGCTCACTGCACCT 1  
 XX  
 RESULT 517  
 ABB32099  
 ID ABB32099 standard; DNA; 20 BP.  
 XX  
 AC ABB32099;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE Human PDB4C-derived oligonucleotide SEQ ID 14310.  
 XX  
 KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
 KW surfactant depletion; inflammation; adenosine sensitivity; lung; cancer;  
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
 KW pulmonary transplantation rejection; ss; primer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200285309-A2.

XX  
 PD 31-OCT-2002.  
 XX  
 PF 23-APR-2002; 2002WO-US013143.  
 XX  
 PR 24-APR-2001; 2001US-0286036P.  
 XX  
 PA (EPIG-) EPIGENESIS PHARM INC.  
 XX  
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX  
 DR WPI; 2003-093058/08.  
 XX  
 PT Pharmaceutical composition for treating asthma, has antisense  
 PT oligonucleotide containing less percentage of adenosine, targeted to  
 PT nucleic acids associated with lung airway or lung dysfunction, and  
 PT bronchodilating agent.  
 XX  
 PS Claim 15; SEQ ID NO 14310; 763pp; English.  
 XX  
 CC This invention describes a novel composition (a) a first active agent,  
 CC comprising oligonucleotides, effective for alleviating allergies and  
 CC bronchoconstriction, respiratory tract inflammation, allergies and  
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
 CC surfactant depletion or hyposecretion, when administered to a mammal. The  
 CC oligonucleotides are derived from a gene encoding or regulating  
 CC expression of a target polypeptide associated with lung airway or lung  
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
 CC The invention also describes a kit, that comprises: (a) a delivery  
 CC device, in separate containers, (b) the oligonucleotides, (c)  
 CC instructions for adding a carrier and for use of the kit. The composition  
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,  
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
 CC beta-adrenergic agonist. The composition is useful for preventing or  
 CC treating a respiratory, lung or malignant disease. The administered  
 CC composition comprises oligo and is administered to reduce the production  
 CC or availability, or to increase the degradation of the target mRNA or to  
 CC reduce the amount of target polypeptide present in the lungs. The  
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
 CC inflammation, allergies and/or surfactant hypoproduction are associated  
 CC with a disease or condition such as pulmonary vasoconstriction,  
 CC inflammation, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
 CC The reduced adenosine content of the anti-sense oligos corresponding to  
 CC thymidines present in the target RNA serves to prevent the breakdown of  
 CC the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
 CC prevent any unwanted effects due to it  
 XX  
 SQ Sequence 20 BP; 5 A; 0 C; 5 G; 10 T; 0 U; 0 Other;  
 XX  
 Query Match 2.0%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 772 TTGATTTTGTAGTAGAGATG 791  
 Db 1 TTGATTTTGTAGTAGAGATG 20  
 XX  
 RESULT 518  
 ABB31045  
 ID ABB31045 standard; DNA; 20 BP.  
 XX  
 AC ABB31045;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE Human RANTES-derived oligonucleotide SEQ ID 13256.  
 XX

KW Human, antisense; bronchoconstriction; allergy; hyposecretion; pain;  
KM respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
KM surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;  
KM analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
KM beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
KM respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
KM emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
KM pulmonary transplantation rejection; ss; primer.  
XX  
XX Homo sapiens.  
OS  
XX WO200285309-A2.  
PN  
XX 31-OCT-2002.  
PD  
XX 23-APR-2002; 2002WO-US013143.  
PF  
XX 24-APR-2001; 2001US-0286036P.  
PR  
XX (EPIG-) EPIGENESIS PHARM INC.  
XX  
XX NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX  
XX WPI; 2003-093058/08.  
DR  
XX  
XX Pharmaceutical composition for treating asthma, has antisense  
PT oligonucleotide containing less percentage of adenosine, targeted to  
PT nucleic acids associated with lung airway or lung dysfunction, and  
PT bronchodilating agent.  
XX  
XX  
XX Claim 15; SEQ ID NO 13256; 763pp; English.  
PS  
XX This invention describes a novel composition (a) a first active agent,  
CC comprising oligonucleotides, effective for alleviating  
CC bronchoconstriction, respiratory tract inflammation, allergies and  
CC surfactant depletion or hyposecretion, when administered to a mammal. The  
CC oligonucleotides are derived from a gene encoding or regulating  
CC expression of a target polypeptide associated with lung airway or lung  
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
CC The invention also describes a kit, that comprises: (a) a delivery  
CC device, in separate containers, (b) the oligonucleotides, (c)  
CC instructions for adding a carrier and for use of the kit. The composition  
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,  
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
CC beta-adrenergic agonist. The composition is useful for preventing or  
CC treating a respiratory, lung or malignant disease. The administered  
CC composition comprises oligo and is administered to reduce the production  
CC or availability, or to increase the degradation of the target mRNA or to  
CC reduce the amount of target polypeptide present in the lungs. The  
CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
CC inflammation, allergies and/or surfactant hypoproduction are associated  
CC with a disease or condition such as pulmonary vasoconstriction,  
CC inflammation, allergies, asthma, impeded respiration, respiratory  
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
CC The reduced adenosine content of the anti-sense oligos corresponding to  
CC thymidines present in the target RNA serves to prevent the breakdown of  
CC the oligonucleotides into products that free adenosine into the system  
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
CC prevent any unwanted effects due to it  
XX  
XX Sequence 20 BP; 3 A; 4 C; 10 G; 3 T; 0 U; 0 Other;  
SQ  
XX  
XX Query Match 2.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 646 AGGCTGAGTGCAGTGGCGC 665  
DB 1 AGGCTGAGTGCAGTGGCGC 20

RESULT 519  
ABD30942  
ID ABD30942 standard; DNA; 20 BP.  
XX  
XX ABD30942;  
AC  
XX  
XX 29-JUL-2004 (first entry)  
DT  
XX  
XX Human RANTES-derived oligonucleotide SEQ ID 13153.  
DE  
XX  
XX Human, antisense; bronchoconstriction; allergy; hyposecretion; pain;  
KM respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
KM surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;  
KM analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
KM beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
KM respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
KM emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
KM pulmonary transplantation rejection; ss; primer.  
XX  
XX  
XX Homo sapiens.  
OS  
XX WO200285309-A2.  
PN  
XX 31-OCT-2002.  
PD  
XX 23-APR-2002; 2002WO-US013143.  
PF  
XX 24-APR-2001; 2001US-0286036P.  
PR  
XX (EPIG-) EPIGENESIS PHARM INC.  
XX  
XX NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX  
XX WPI; 2003-093058/08.  
DR  
XX  
XX Pharmaceutical composition for treating asthma, has antisense  
PT oligonucleotide containing less percentage of adenosine, targeted to  
PT nucleic acids associated with lung airway or lung dysfunction, and  
PT bronchodilating agent.  
XX  
XX  
XX Claim 15; SEQ ID NO 13153; 763pp; English.  
PS  
XX This invention describes a novel composition (a) a first active agent,  
CC comprising oligonucleotides, effective for alleviating  
CC bronchoconstriction, respiratory tract inflammation, allergies and  
CC surfactant depletion or hyposecretion, when administered to a mammal. The  
CC oligonucleotides are derived from a gene encoding or regulating  
CC expression of a target polypeptide associated with lung airway or lung  
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
CC The invention also describes a kit, that comprises: (a) a delivery  
CC device, in separate containers, (b) the oligonucleotides, (c)  
CC instructions for adding a carrier and for use of the kit. The composition  
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,  
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
CC beta-adrenergic agonist. The composition is useful for preventing or  
CC treating a respiratory, lung or malignant disease. The administered  
CC composition comprises oligo and is administered to reduce the production  
CC or availability, or to increase the degradation of the target mRNA or to  
CC reduce the amount of target polypeptide present in the lungs. The  
CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
CC inflammation, allergies and/or surfactant hypoproduction are associated  
CC with a disease or condition such as pulmonary vasoconstriction,  
CC inflammation, allergies, asthma, impeded respiration, respiratory  
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
CC The reduced adenosine content of the anti-sense oligos corresponding to  
CC thymidines present in the target RNA serves to prevent the breakdown of  
CC the oligonucleotides into products that free adenosine into the system

CC	e.g., lung, brain, heart, kidney, etc.	tissue environment and thereby, to
CC	prevent any unwanted effects due to it	
XX		
SQ	Sequence 20 BP, 4 A, 7 C, 2 T, 0 U, 0 Other;	

Query Match	2.0%	Score 20;	DB 1;	Length 20;
Best Local Similarly	100.0%	Pred. No. 1.1e+03;		
Matches 20; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

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QY      732 AGCTGGACTACAGGCGCC 751
          |||||
Db      1  AGCTGGACTACAGGCGCC 20

```

**RESULT 520**

ID ABD32107 standard; DNA; 20 BP.

AC ABD32107

DT 29-JUL-2004 (first entry)

Human PDE4C-derived oligonucleotide SEQ ID 14318.

KM Human; antitense; bronchoconstriction; allergy; hyposecretion; pain;  
 KM respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
 KM surfactant depletion; anti allergic; anti inflammatory; antiasthmatic;  
 KM analgesic; hypotensive; immunosuppressive; cystic; cystic fibrosis;  
 beta-adrenergic agonist; respiratory disease; pulmonary vasodilation;  
 KM respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
 KM emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
 KM pulmonary transplantation rejection; ss; primer.

OS Homo sapiens.

PN WO200285309-A2.

PD 31-OCT-2002.

23-APR-2002; 2002WO-US013143.

24-APR-2001; 2001US-0286036P.

PA (EPIG-) EPIGENESIS PHARM INC.

NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

[illegible]

REF: 2003-032020/00.  
XX

PT Pharmaceutical composition for treating asthma, has antisense  
PT oligonucleotide containing less percentage of adenosine, targeted to  
PT nucleic acids associated with lung airway or lung dysfunction, and  
PT bronchodilating agent.

PS Claim 15; SEQ ID NO 14318; 763pp; English.

CC This invention describes a novel composition (a) a first active agent,  
CC comprising oligonucleotides, effective for alleviating  
CC bronchoconstriction, respiratory tract inflammation, allergies and  
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
CC surfactant depletion or hyposecretion, when administered to a mammal. The  
CC oligonucleotides are derived from a gene encoding or regulating  
CC expression of a target polypeptide associated with lung airway or lung  
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
CC The invention also describes a kit that comprises: (a) a delivery  
CC device, in separate containers, (b) the oligonucleotides, (c)  
CC instructions for adding a carrier and for use of the kit. The composition  
CC of the invention has antiallergic, antiinflammatory, antiasmatic,  
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
CC beta-adrenergic agonist. The composition is useful for preventing or  
CC treating a respiratory, lung or malignant disease. The administered  
CC composition comprises oligo and is administered to reduce the production

or to increase the degradation of the target mRNA or to  
reduce the amount of target polypeptide present in the lungs. The  
mujomary obstruction. and/or bronchoconstriction and/or lung

CC inflammation, allergies and/or surfactant hypoproduction are associated  
CC with a disease or condition such as pulmonary vasoconstriction,  
CC inflammation, allergies, asthma, impaired respiration, respiratory  
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
CC The reduced adenosine content of the anti-sense oligos corresponding to  
CC thymidines present in the target RNA serves to prevent the breakdown of  
CC the oligonucleotides into products that free adenosine into the system  
CC e.g., lung, brain, heart, kidney, etc. tissue environment and thereby, to  
CC prevent any unwanted effects due to it

SQ Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;

Query Match	2.0%	Score 20;	DB 1;	Length 20;
Best Local Similarity	100.0%	Pred. No. 1.1e+03;		
Matches 20; Conservative	0;	Mismatches	0;	Indels 0;
				Gaps 0;

QY	379	TCAGCCTCCCAAGTGTGG	398
Db	1	TCAGCCTCCCAAGTGTGG	20

**RESULT 521**

ID ABD28946 standard; DNA; 20 BP.

AC ABD28946;

DT 29-JUL-2004 (first entry)

DE N58473-derived oligonucleotide SEQ ID 7958.

Human, atherosclerosis, bronchoconstriction, allergy, hyposecretion, pain, respiratory tract inflammation, adenosine sensitivity, lung, cancer, surfactant depletion, antiallergic, antinflammatory, antiaesthetic, analgesic, hypotensive, immunosuppressive, cytostatic, cystic fibrosis, beta-adrenergic agonist, respiratory disease, pulmonary vasodilation, respiratory distress syndrome, allergic rhinitis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease, cancer, bronchitis, pulmonary transplantation rejection, ss, primer.

**Homo sapiens.**

PN WO200285309-A2.

PD 31-OCT-2002

PF 23-APR-2002; 2002WO-US013143.

24-APR-2001; 2001US-0286036P.

PA (EPIG-) EPIGENESIS PHARM INC.

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

[illegible][illegible]

PT   Pharmaceutical composition for treating asthma, has antisense  
PT   oligonucleotide containing less percentage of adenosine, targeted to  
PT   nucleic acids associated with lung airway or lung dysfunction, and  
PT   bronchodilating agent.

Claim 15; SEQ ID NO 7958; 763pp; English

CC This invention describes a novel composition (a) a first active agent,  
CC comprising oligonucleotides, effective for alleviating  
CC bronchoconstriction, respiratory tract inflammation, allergies and  
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors

CC surfactant depletion or hyposecretion, when administered to a mammal. The  
CC oligonucleotides are derived from a gene encoding or regulating  
CC expression of a target polypeptide associated with lung airway or lung  
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
CC The invention also describes a kit that comprises: (a) a delivery  
CC device, in separate containers, (b) the oligonucleotides, (c)  
CC instructions for adding a carrier and for use of the kit. The composition  
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,  
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
CC beta-adrenergic agonist. The composition is useful for preventing or  
CC treating a respiratory, lung or malignant disease. The administered  
CC composition comprises oligo and is administered to reduce the production  
CC or availability, or to increase the degradation of the target mRNA or to  
CC reduce the amount of target polypeptide present in the lungs. The  
CC pulmonary obstruction, and/or surfactant hypoproduction are associated  
CC inflammation, allergies and/or surfactant hypoproduction are associated  
CC with a disease or condition such as pulmonary vasoconstriction,  
CC inflammation, allergies, asthma, impeded respiration, respiratory  
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
CC The reduced adenosine content of the anti-sense oligos corresponding to  
CC thymidines present in the target RNA serves to prevent the breakdown of  
CC the oligonucleotides into products that free adenosine into the system  
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
CC prevent any unwanted effects due to it  
XX  
XX Sequence 20 BP; 4 A; 7 C; 6 G; 3 T; 0 U; 0 Other;  
XX  
XX Query Match 2.0%; Score 20; DB 1; Length 20;  
XX Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 546 GCCTCCCAAGTAGCTGGGAC 565  
DB 1 GCCTCCCAAGTAGCTGGGAC 20  
RESULT 522  
ABD32106 standard; DNA; 20 BP.  
ID ABD32106  
AC ABD32106;  
XX  
XX 29-JUL-2004 (first entry)  
XX  
XX Human PDB4C-derived oligonucleotide SEQ ID 14317.  
XX  
XX Human; anti-sense; bronchoconstriction; allergy; hyposecretion; pain;  
XX respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
XX surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;  
XX analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
XX beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
XX emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
XX pulmonary transplantation rejection; ss; primer.  
XX  
XX Homo sapiens.  
XX  
XX WO200285309-A2.  
XX  
XX 31-OCT-2002.  
XX  
XX 23-APR-2002; 2002WO-US013143.  
XX  
XX 24-APR-2001; 2001US-0286036P.  
XX  
XX (EPIG-) EPIGENESIS PHARM INC.  
XX  
XX NYCE JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D,  
XX PI Miller S, Tang L, Shahabuddin S;  
XX  
XX WPI; 2003-093058/08.

XX pharmaceutical composition for treating asthma, has anti-sense  
XX oligonucleotide containing less percentage of adenosine, targeted to  
XX nucleic acids associated with lung airway or lung dysfunction, and  
XX bronchodilating agent.  
XX  
XX Claim 15; SEQ ID NO 14317; 763pp; English.  
XX  
XX This invention describes a novel composition (a) a first active agent,  
XX comprising oligonucleotides, effective for alleviating  
XX bronchoconstriction, respiratory tract inflammation, allergies and  
XX reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
XX surfactant depletion or hyposecretion, when administered to a mammal. The  
XX oligonucleotides are derived from a gene encoding or regulating  
XX expression of a target polypeptide associated with lung airway or lung  
XX dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
XX The invention also describes a kit, that comprises: (a) a delivery  
XX device, in separate containers, (b) the oligonucleotides, (c)  
XX instructions for adding a carrier and for use of the kit. The composition  
XX of the invention has anti-allergic, anti-inflammatory, antiasthmatic,  
XX analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
XX beta-adrenergic agonist. The composition is useful for preventing or  
XX treating a respiratory, lung or malignant disease. The administered  
XX composition comprises oligo and is administered to reduce the production  
XX or availability, or to increase the degradation of the target mRNA or to  
XX reduce the amount of target polypeptide present in the lungs. The  
XX pulmonary obstruction, and/or surfactant hypoproduction are associated  
XX inflammation, allergies and/or surfactant hypoproduction are associated  
XX with a disease or condition such as pulmonary vasoconstriction,  
XX inflammation, allergies, asthma, impeded respiration, respiratory  
XX distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
XX hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
XX transplantation rejection, pulmonary infections, bronchitis or cancer.  
XX The reduced adenosine content of the anti-sense oligos corresponding to  
XX thymidines present in the target RNA serves to prevent the breakdown of  
XX the oligonucleotides into products that free adenosine into the system  
XX e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
XX prevent any unwanted effects due to it  
XX  
XX Sequence 20 BP; 2 A; 12 C; 2 G; 4 T; 0 U; 0 Other;  
XX  
XX Query Match 2.0%; Score 20; DB 1; Length 20;  
XX Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 369 TCACCTGCTCAGCTCCC 388  
DB 1 TCACCTGCTCAGCTCCC 20  
RESULT 523  
ABD32086 standard; DNA; 20 BP.  
ID ABD32086  
AC ABD32086;  
XX  
XX 29-JUL-2004 (first entry)  
XX  
XX Human PDB4C-derived oligonucleotide SEQ ID 14297.  
XX  
XX Human; anti-sense; bronchoconstriction; allergy; hyposecretion; pain;  
XX respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
XX surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;  
XX analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
XX beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
XX emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
XX pulmonary transplantation rejection; ss; primer.  
XX  
XX Homo sapiens.  
XX  
XX WO200285309-A2.



PD	31-0CT-2002.
XX	23-APR-2002; 2002WO-US013143.
PF	23-APR-2002; 2002WO-US013143.
XX	24-APR-2001; 2001US-0286036P.
PR	24-APR-2001; 2001US-0286036P.
XX	(EPIC-) EPIGENESIS PHARM INC.
PA	(EPIC-) EPIGENESIS PHARM INC.
XX	Nyce JW, Li Y, Sandrasegura A, Katz E, Pabalan J, Aguilar D;
PI	Miller S, Tang L, Shahabuddin S;
XX	WPI, 2003-093058/08.
XX	Pharmaceutical composition for treating asthma, has antienase
PT	oligonucleotide containing less percentage of adenosine, targeted to
PT	nucleic acids associated with lung airway or lung dysfunction, and
PT	bronchodilating agent.
PS	Claim 15; SEQ ID NO 14297; 763bp; English.
XX	This invention describes a novel composition (a) a first active agent,
CC	comprising oligonucleotides, effective for alleviating
CC	bronchoconstriction, respiratory tract inflammation, allergies and
CC	reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC	surfactant depletion or hyposecretion, when administered to a mammal. The
CC	oligonucleotides are derived from a gene encoding or regulating
CC	expression of a target polypeptide associated with lung airway or lung
CC	dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC	The invention also describes a kit, that comprises: (a) a delivery
CC	device, in separate containers, (b) the oligonucleotides, (c)
CC	instructions for adding a carrier and for use of the kit. The composition
CC	of the invention has anti-allergic, anti-inflammatory, antiallstatic,
CC	analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC	beta-adrenergic agonist. The composition is useful for preventing or
CC	treating a respiratory, lung or malignant disease. The administered
CC	composition comprises oligo and is administered to reduce the production
CC	or availability, or to increase the degradation of the target mRNA or to
CC	reduce the amount of target polypeptide present in the lungs. The
CC	pulmonary obstruction, and/or bronchoconstriction and/or lung
CC	inflammation, allergies and/or surfactant hypoproduction are associated
CC	with a disease or condition such as pulmonary vasoconstriction,
CC	inflammation, allergies, asthma, impeded respiration, respiratory
CC	distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC	hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC	transplantation rejection, pulmonary infections, bronchitis or cancer.
CC	The reduced adenosine content of the anti-sense oligos corresponding to
CC	thymidines present in the target RNA serves to prevent the breakdown of
CC	the oligonucleotides into products that free adenosine into the system
CC	e.g., lung, brain, heart, kidney, etc. tissue environment and thereby, to
CC	prevent any unwanted effects due to it
CC	
SQ	Sequence 20 BP; 3 A; 5 C; 9 G; 3 T; 0 U; 0 Other;
Query Match	2.0%; Score 20; DB 1; Length 20;
Best Local Similarity	100.0%; Pred.No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0.	
QY	643 CCCAGCCTGGAGTGCAGTGG 662
DB	1 CCCAGCCTGGAGTGCAGTGG 20
RESULT 524	
ID	ABD28945
AC	ABD28945 standard; DNA; 20 BP.
XX	ABD28945;
XX	29-JUL-2004 (first entry)
DE	N58473-derived oligonucleotide SEQ ID 7957.
XX	Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW	

XX respiratory tract inflammation; adenosine sensitivity; lung cancer;  
 XX surfactant depletion; anti-allergic; anti-inflammatory; anti-asthmatic;  
 XX analgesic; hypotensive; immunosuppressive; cyclostatic; cystic fibrosis;  
 XX beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
 XX respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
 XX emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
 XX pulmonary transplantation rejection; ssf, primer.  
 XX  
 XX Homo sapiens.  
 OS  
 PN WO200285309-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 23-APR-2002; 2002WO-US013143.  
 XX  
 PR 24-APR-2001; 2001US-0286036P.  
 XX  
 PA (EPIC-) EPIGENESIS PHARM INC.  
 XX  
 PI Nyce JM, Li Y, Sandrasegura A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX  
 DR WPI; 2003-093056/08.  
 XX  
 PT Pharmaceutical composition for treating asthma, has antisense  
 PT oligonucleotide containing less percentage of adenosine, targeted to  
 PT nucleic acids associated with lung airway or lung dysfunction, and  
 PT bronchodilating agent.  
 XX  
 XX Claim 15; SEQ ID NO 7957; 763pp; English.  
 XX  
 XX This invention describes a novel composition (a) a first active agent,  
 CC comprising oligonucleotides, effective for alleviating  
 CC bronchoconstriction, respiratory tract inflammation, allergies and  
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
 CC surfactant depletion or hyposecretion, when administered to a mammal. The  
 CC oligonucleotides are derived from a gene encoding or regulating  
 CC expression of a target polypeptide associated with lung airway or lung  
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
 CC The invention also describes a kit, that comprises: (a) a delivery  
 CC device, in separate containers, (b) the oligonucleotides, (c)  
 CC instructions for adding a carrier and for use of the kit. The composition  
 CC of the invention has anti-allergic, anti-inflammatory, anti-asthmatic,  
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
 CC beta-adrenergic agonist. The composition is useful for preventing or  
 CC treating a respiratory, lung or malignant disease. The administered  
 CC composition comprises oligo and is administered to reduce the production  
 CC or availability, or to increase the degradation of the target mRNA or to  
 CC reduce the amount of target polypeptide present in the lungs. The  
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
 CC inflammation, allergies and/or surfactant hypoproduction are associated  
 CC with a disease or condition such as pulmonary vasoconstriction,  
 CC inflammation, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
 CC hypertranson, emphysema, chronic obstructive pulmonary disease, pulmonary  
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
 CC The reduced adenosine content of the anti-sense oligos corresponding to  
 CC thymidines present in the target RNA serves to prevent the breakdown of  
 CC the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
 CC prevent any unwanted effects due to it  
 XX  
 SO Sequence 20 BP; 4 A; 9 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Prid. No. 1.1e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

540 GCGTCAGCCTCCCAAGTAGC 559  
 |||||  
 1 GCGTCAGCCTCCCAAGTAGC 20



RESULT 525  
AD180086/c  
ID AD180086 standard; DNA; 20 BP.  
XX  
XX  
AC AD180086;  
XX  
XX  
DT 22-APR-2004 (first entry)  
DE Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 87.  
XX  
XX  
XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
XX  
XX cytosolic; neurotrophic; neuroprotective; immunosuppressive;  
XX  
XX hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
XX  
XX immune; ss; human.  
XX  
OS Homo sapiens.  
XX  
PN US2004006030-A1.  
XX  
PD 08-JAN-2004.  
XX  
PF 02-JUL-2002; 2002US-00189267.  
XX  
PR 02-JUL-2002; 2002US-00189267.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Freier SM, Dobie KW;  
XX  
DR WPI; 2004-081742/08.  
XX  
PT New compounds, particularly antisense oligonucleotides targeted to a  
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
PT neurodegenerative disorder, or a disease involving hyperactivation of  
PT immune response.  
XX  
PS Example 15; SEQ ID NO 87; 135bp; English.  
XX  
XX The invention relates to a novel antisense compound of 8-80 nucleobases  
XX in length targeted to, and which specifically hybridizes with, a nucleic  
XX acid molecule encoding transforming growth factor (TGF)-beta 2, and  
XX inhibits the expression of TGF-beta 2. The invention further relates to:  
XX a compound 8-80 nucleobases in length that specifically hybridizes with  
XX at least an 8-nucleobase portion of an active site on a nucleic acid  
XX molecule encoding TGF-beta 2; a composition comprising the compound and a  
XX carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
XX tissues by contacting the cells or tissues with the compound so that  
XX expression of TGF-beta 2 is inhibited; treating an animal having a  
XX disease or condition associated with TGF-beta 2 by administering to the  
XX animal a therapeutic or prophylactic amount of the compound so that  
XX expression of TGF-beta 2 is inhibited; and screening an antisense  
XX compound. The antisense compound has cytosolic, neurotrophic,  
XX neuroprotective, and immunosuppressive activities. The compound,  
XX composition, and methods are useful for treating a disease or condition  
XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.,  
XX cancer, a neurodegenerative disorder, or a disease or condition involving  
XX hyperactivation of an immune response. This polynucleotide sequence  
XX represents an antisense oligonucleotide of the invention.  
XX  
SQ Sequence 20 BP; 3 A; 7 C; 7 G; 3 T; 0 U; 0 Other;  
XX  
XX  
Query Match 2.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1,1e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 850 CGGCTCCCAAGTGTGG 869  
DB 20 CGGCTCCCAAGTGTGG 1  
XX  
XX  
RESULT 526  
AD180222

ID AD180222 standard; DNA; 20 BP.  
XX  
XX  
AC AD180222;  
XX  
XX  
DT 22-APR-2004 (first entry)  
DE Human transforming growth factor-beta 2 target DNA region, SEQ ID No 223.  
XX  
XX  
XX antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;  
XX  
XX cytosolic; neurotrophic; neuroprotective; immunosuppressive;  
XX  
XX hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;  
XX  
XX immune; ss; human.  
XX  
OS Homo sapiens.  
XX  
PN US2004006030-A1.  
XX  
PD 08-JAN-2004.  
XX  
PF 02-JUL-2002; 2002US-00189267.  
XX  
PR 02-JUL-2002; 2002US-00189267.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Freier SM, Dobie KW;  
XX  
DR WPI; 2004-081742/08.  
XX  
PT New compounds, particularly antisense oligonucleotides targeted to a  
PT nucleic acid encoding TGF-beta 2, useful for treating cancer, a  
PT neurodegenerative disorder, or a disease involving hyperactivation of  
PT immune response.  
XX  
PS Example 16; SEQ ID NO 223; 135bp; English.  
XX  
XX The invention relates to a novel antisense compound of 8-80 nucleobases  
XX in length targeted to, and which specifically hybridizes with, a nucleic  
XX acid molecule encoding transforming growth factor (TGF)-beta 2, and  
XX inhibits the expression of TGF-beta 2. The invention further relates to:  
XX a compound 8-80 nucleobases in length that specifically hybridizes with  
XX at least an 8-nucleobase portion of an active site on a nucleic acid  
XX molecule encoding TGF-beta 2; a composition comprising the compound and a  
XX carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or  
XX tissues by contacting the cells or tissues with the compound so that  
XX expression of TGF-beta 2 is inhibited; treating an animal having a  
XX disease or condition associated with TGF-beta 2 by administering to the  
XX animal a therapeutic or prophylactic amount of the compound so that  
XX expression of TGF-beta 2 is inhibited; and screening an antisense  
XX compound. The antisense compound has cytosolic, neurotrophic,  
XX neuroprotective, and immunosuppressive activities. The compound,  
XX composition, and methods are useful for treating a disease or condition  
XX associated with TGF-beta 2, such as a hyperproliferative disorder e.g.,  
XX cancer, a neurodegenerative disorder, or a disease or condition involving  
XX hyperactivation of an immune response. This polynucleotide sequence  
XX represents a preferred target DNA region of TGF-beta 2 of the invention.  
XX  
SQ Sequence 20 BP; 4 A; 4 C; 8 G; 4 T; 0 U; 0 Other;  
XX  
XX  
Query Match 2.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1,1e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 866 TGGATTACAGCGGTGACC 885  
DB 1 TGGATTACAGCGGTGACC 20  
XX  
XX  
RESULT 527  
AD180087/c  
ID AD180087 standard; DNA; 20 BP.  
XX  
XX  
AC AD180087;  
XX



KW 2'-O-methoxyethyl sugar moiety; 5-methylcytosine; autoimmune disorder;  
KW Alzheimer's disease; immunosuppressive; nootropic; neuroprotective.  
XX  
XX Homo sapiens.  
OS  
XX US2004023382-A1.  
PN  
XX  
XX 05-FEB-2004.  
PD  
XX  
XX 31-JUL-2002; 2002US-00210723.  
PF  
XX  
XX 31-JUL-2002; 2002US-00210723.  
PR  
XX  
XX (ISIS-) ISIS PHARM INC.  
PA  
XX Dean NM, Bennett CF, Dobie KW;  
PI  
XX WPI; 2004-142663/14.  
DR  
XX  
XX New compounds, particularly antisense oligonucleotides targeted to a  
PT nucleic acid encoding PPP3CB, useful for treating an autoimmune disorder,  
PT or Alzheimer's disease.  
XX  
XX Example 15; SEQ ID NO 78; 91pp, English.  
PS  
XX The invention relates to an antisense oligonucleotide targeted to a  
CC nucleic acid encoding the human PPP3CB polypeptide and inhibits  
CC expression of the PPP3CB polypeptide. The antisense oligonucleotide  
CC comprises at least one modified internucleoside linkage, i.e. a  
CC phosphorothioate linkage, at least one modified sugar moiety, preferably  
CC a 2'-O-methoxyethyl sugar moiety, or at least one modified nucleobase  
CC comprising a 5-methylcytosine. The antisense oligonucleotides are useful  
CC for inhibiting expression of the PPP3CB polypeptide and in preparation of  
CC a composition for treating autoimmune disorders or Alzheimer's disease.  
CC This sequence represents an antisense oligonucleotide of the invention.  
XX  
XX SQ Sequence 20 BP; 4 A; 9 C; 3 G; 4 T; 0 U; 0 Other;  
XX  
XX Query Match 2.0%; Score 20; DB 1; Length 20;  
XX Best Local Similarity 100.0%; Pred. No. 1.1e+03; Indels 0; Gaps 0;  
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 541 CCTCAGCCTCCCAAGTAGCT 560  
XX |||||  
Db 1 CCTCAGCCTCCCAAGTAGCT 20  
XX  
XX RESULT 530  
XX ADJ53600/c  
XX ID ADJ53600 standard; DNA; 20 BP.  
XX  
XX AC ADJ53600;  
XX  
XX XX 06-MAY-2004 (first entry)  
XX  
XX DE Human PPP3CB DNA antisense oligonucleotide target region #51.  
XX  
XX KW Human; PPP3CB; sg; antisense oligonucleotide; phosphorothioate linkage;  
KW 2'-O-methoxyethyl sugar moiety; 5-methylcytosine; autoimmune disorder;  
KW Alzheimer's disease; immunosuppressive; nootropic; neuroprotective.  
XX  
XX OS Homo sapiens.  
XX  
XX XX US2004023382-A1.  
XX  
XX PN 05-FEB-2004.  
XX  
XX PD 31-JUL-2002; 2002US-00210723.  
XX  
XX PF 31-JUL-2002; 2002US-00210723.  
XX  
XX PR 31-JUL-2002; 2002US-00210723.  
XX  
XX PA (ISIS-) ISIS PHARM INC.  
XX

PI Dean NM, Bennett CF, Dobie KW;  
XX WPI; 2004-142663/14.  
XX  
XX DR  
XX New compounds, particularly antisense oligonucleotides targeted to a  
PT nucleic acid encoding PPP3CB, useful for treating an autoimmune disorder,  
PT or Alzheimer's disease.  
XX  
XX Example 15; SEQ ID NO 136; 91pp, English.  
PS  
XX The invention relates to an antisense oligonucleotide targeted to a  
CC nucleic acid encoding the human PPP3CB polypeptide and inhibits  
CC expression of the PPP3CB polypeptide. The antisense oligonucleotide  
CC comprises at least one modified internucleoside linkage, i.e. a  
CC phosphorothioate linkage, at least one modified sugar moiety, preferably  
CC a 2'-O-methoxyethyl sugar moiety, or at least one modified nucleobase  
CC comprising a 5-methylcytosine. The antisense oligonucleotides are useful  
CC for inhibiting expression of the PPP3CB polypeptide and in preparation of  
CC a composition for treating autoimmune disorders or Alzheimer's disease.  
CC This sequence represents an antisense oligonucleotide target region of  
CC the invention.  
XX  
XX SQ Sequence 20 BP; 4 A; 3 C; 9 G; 4 T; 0 U; 0 Other;  
XX  
XX Query Match 2.0%; Score 20; DB 1; Length 20;  
XX Best Local Similarity 100.0%; Pred. No. 1.1e+03; Indels 0; Gaps 0;  
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 541 CCTCAGCCTCCCAAGTAGCT 560  
XX |||||  
Db 20 CCTCAGCCTCCCAAGTAGCT 1  
XX  
XX RESULT 531  
XX ADJ60953  
XX ID ADJ60953 standard; DNA; 20 BP.  
XX  
XX AC ADJ60953;  
XX  
XX DT 06-MAY-2004 (first entry)  
XX  
XX DE Oligonucleotide associated to PDE4C #19.  
XX  
XX KW Interleukin; IL-4 receptor; IL-5 receptor; lung disease;  
KW airway inflammation; allergy; asthma; impeded respiration;  
KW cystic fibrosis; acute respiratory distress syndrome;  
KW pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;  
KW sg.  
XX  
XX OS Homo sapiens.  
XX  
XX OS WO2004011613-A2.  
XX  
XX PN 05-FEB-2004.  
XX  
XX PD 25-JUL-2003; 2003WO-US023509.  
XX  
XX PF 29-JUL-2002; 2002US-0339076P.  
XX  
XX PR (EPIC-) EPIGENESIS PHARM INC.  
XX  
XX PA Nyce JW, Tang L, Sandrasagra A, Aguilar D, Miller S;  
XX PI Shahbuddin S, Lu H, Cong H;  
XX  
XX DR WPI; 2004-203534/19.  
XX  
XX PT Novel single or multiple target oligonucleotide anti-sense to e.g.  
PT initiation codons and introns of respiratory disease-relevant genes e.g.,  
PT CCR1, RANTES, MCP4, useful for prophylaxis or treating respiratory  
PT disease e.g., asthma.  
XX  
XX PS Claim 2; SEQ ID NO 1809; 85pp; English.  
XX

CC The present invention relates to an oligonucleotide anti-sense to e.g.,  
CC initiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-  
CC end of nucleic acid target comprising gene(s) chosen from e.g.  
CC interleukin (IL)-4 receptor, IL-5 receptor or salts of the  
CC oligonucleotide and optionally surfactant operatively linked to the  
CC oligonucleotide. The method is useful for preventing or treating a  
CC respiratory or lung disease, which involves administering to the airways  
CC of a subject an effective amount of an inhibitor. The oligonucleotide is  
CC useful for production of a medicament for the prevention and/or treatment  
CC of a respiratory or lung disease. The respiratory or lung disease is  
CC chosen from airway inflammation, allergy(ies), asthma, impeded  
CC respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases  
CC (COPD), allergic rhinitis (AR), acute respiratory distress syndrome  
CC (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway  
CC obstruction. The present sequence represents an oligonucleotide of the  
CC invention.

SQ Sequence 20 BP; 5 A; 0 C; 5 G; 10 T; 0 U; 0 Other;  
Query Match 2.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 772 TTGATTTTGTAGAGATG 791  
|||||  
1 TTGTATTTTGTAGAGATG 20

DB 1 TTGTATTTTGTAGAGATG 20

RESULT 532  
ADJ60960  
ID ADJ60960 standard; DNA; 20 BP.  
XX  
AC ADJ60960;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Oligonucleotide associated to PDEAC #26.  
XX  
KW interleukin; IL-4 receptor; IL-5 receptor; lung disease;  
XX airway inflammation; allergy; asthma; impeded respiration;  
XX cystic fibrosis; acute respiratory distress syndrome;  
XX pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;  
XX ss.  
OS Homo sapiens.  
XX  
XX WO2004011613-A2.  
XX  
XX 05-FEB-2004.  
XX  
XX 25-JUL-2003; 2003WO-US023509.  
XX  
XX 29-JUL-2002; 2002US-0399076P.  
XX  
XX (EPIG-) EPIGENESIS PHARM INC.  
XX  
XX Nyce JW, Tang L, Sandrasagra A, Aguilar D, Miller S;  
XX Shahabuddin S, Lu H, Cong H;  
XX WPI, 2004-203534/19.  
XX  
XX Novel single or multiple target oligonucleotide anti-sense to e.g.,  
XX initiation codons and introns of respiratory disease-relevant genes e.g.,  
XX CCR1, RANTES, MCP4, useful for prophylaxis or treating respiratory  
XX disease e.g., asthma.  
XX  
XX Claim 2; SEQ ID NO 1816; 85pp; English.  
XX  
XX The present invention relates to an oligonucleotide anti-sense to e.g.,  
XX initiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-  
XX end of nucleic acid target comprising gene(s) chosen from e.g.,  
XX interleukin (IL)-4 receptor, IL-5 receptor or salts of the  
XX oligonucleotide and optionally surfactant operatively linked to the  
XX respiratory or lung disease, which involves administering to the airways  
XX of a subject an effective amount of an inhibitor. The oligonucleotide is  
XX useful for production of a medicament for the prevention and/or treatment  
XX of a respiratory or lung disease. The respiratory or lung disease is

CC oligonucleotide. The method is useful for preventing or treating a  
CC respiratory or lung disease, which involves administering to the airways  
CC of a subject an effective amount of an inhibitor. The oligonucleotide is  
CC useful for production of a medicament for the prevention and/or treatment  
CC of a respiratory or lung disease. The respiratory or lung disease is  
CC chosen from airway inflammation, allergy(ies), asthma, impeded  
CC respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases  
CC (COPD), allergic rhinitis (AR), acute respiratory distress syndrome  
CC (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway  
CC obstruction. The present sequence represents an oligonucleotide of the  
CC invention.

SQ Sequence 20 BP; 2 A; 12 C; 2 G; 4 T; 0 U; 0 Other;  
Query Match 2.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 369 TCCACCTGCTCAGCTGCC 388  
|||||  
1 TCCACCTGCTCAGCTGCC 20

DB 1 TCCACCTGCTCAGCTGCC 20

RESULT 533  
ADJ59879  
ID ADJ59879 standard; DNA; 20 BP.  
XX  
AC ADJ59879;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Oligonucleotide associated to RANTES #128.  
XX  
KW interleukin; IL-4 receptor; IL-5 receptor; lung disease;  
XX airway inflammation; allergy; asthma; impeded respiration;  
XX cystic fibrosis; acute respiratory distress syndrome;  
XX pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;  
XX ss.  
OS Homo sapiens.  
XX  
XX WO2004011613-A2.  
XX  
XX 05-FEB-2004.  
XX  
XX 25-JUL-2003; 2003WO-US023509.  
XX  
XX 29-JUL-2002; 2002US-0399076P.  
XX  
XX (EPIG-) EPIGENESIS PHARM INC.  
XX  
XX Nyce JW, Tang L, Sandrasagra A, Aguilar D, Miller S;  
XX Shahabuddin S, Lu H, Cong H;  
XX WPI, 2004-203534/19.  
XX  
XX Novel single or multiple target oligonucleotide anti-sense to e.g.,  
XX initiation codons and introns of respiratory disease-relevant genes e.g.,  
XX CCR1, RANTES, MCP4, useful for prophylaxis or treating respiratory  
XX disease e.g., asthma.  
XX  
XX Claim 2; SEQ ID NO 735; 85pp; English.  
XX  
XX The present invention relates to an oligonucleotide anti-sense to e.g.,  
XX initiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-  
XX end of nucleic acid target comprising gene(s) chosen from e.g.,  
XX interleukin (IL)-4 receptor, IL-5 receptor or salts of the  
XX oligonucleotide and optionally surfactant operatively linked to the  
XX respiratory or lung disease, which involves administering to the airways  
XX of a subject an effective amount of an inhibitor. The oligonucleotide is  
XX useful for production of a medicament for the prevention and/or treatment  
XX of a respiratory or lung disease. The respiratory or lung disease is

CC Chosen from airway inflammation, allergy(ies), asthma, impeded  
CC respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases  
CC (COPD), allergic rhinitis (AR), acute respiratory distress syndrome  
CC (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway  
CC obstruction. The present sequence represents an oligonucleotide of the  
CC invention.  
XX  
SQ Sequence 20 BP; 3 A; 4 C; 10 G; 3 T; 0 U; 0 Other;  
Query Match 2.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 646 AGCGCTGAGTGCAGTGGCGC 665  
DB 1 AGCGCTGAGTGCAGTGGCGC 20  
RESULT 534  
ADJ60940  
ID ADJ60940 standard; DNA; 20 BP.  
XX  
AC ADJ60940;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Oligonucleotide associated to PDE4C #6.  
XX  
KM interleukin; IL-4 receptor; IL-5 receptor; lung disease;  
KM airway inflammation; allergy; asthma; impeded respiration;  
KM cystic fibrosis; acute respiratory distress syndrome;  
KM pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;  
KM ss.  
XX  
OS Homo sapiens.  
OS  
XX  
PN WO2004011613-A2.  
XX  
PD 05-FEB-2004.  
XX  
PF 25-JUL-2003; 2003WO-US023509.  
XX  
PR 29-JUL-2002; 2002US-0399076P.  
XX  
PA (EPIC-) EPIGENESIS PHARM INC.  
XX  
PI Nyce JW, Tang L, Sandrasagra A, Aguilar D, Miller S;  
PI Shahbuddin S, Lu H, Cong H;  
XX  
DR WPI; 2004-203534/19.  
XX  
PT Novel single or multiple target oligonucleotide anti-sense to e.g.  
PT initiation codons and introns of respiratory disease-relevant genes e.g.,  
PT CCR1, RANTES, MCP4, useful for prophylaxis or treating respiratory  
PT disease e.g., asthma.  
XX  
PS Claim 2; SEQ ID NO 1796; 85pp; English.  
XX  
CC The present invention relates to an oligonucleotide anti-sense to e.g.,  
CC initiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-  
CC end of nucleic acid target comprising gene(s) chosen from e.g.,  
CC interleukin (IL)-4 receptor, IL-5 receptor or salts of the  
CC oligonucleotide and optionally surfactant operatively linked to the  
CC oligonucleotide. The method is useful for preventing or treating a  
CC respiratory or lung disease, which involves administering to the airways  
CC of a subject an effective amount of an inhibitor. The oligonucleotide is  
CC useful for production of a medicament for the prevention and/or treatment  
CC of a respiratory or lung disease. The respiratory or lung disease is  
CC chosen from airway inflammation, allergy(ies), asthma, impeded  
CC respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases  
CC (COPD), allergic rhinitis (AR), acute respiratory distress syndrome  
CC (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway  
CC obstruction. The present sequence represents an oligonucleotide of the

CC invention.  
XX  
SQ Sequence 20 BP; 3 A; 5 C; 9 G; 3 T; 0 U; 0 Other;  
QY 643 CCCAGCTGAGTGCAGTGG 662  
DB 1 CCCAGCTGAGTGCAGTGG 20  
RESULT 535  
ADJ60961  
ID ADJ60961 standard; DNA; 20 BP.  
XX  
AC ADJ60961;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Oligonucleotide associated to PDE4C #27.  
XX  
KM interleukin; IL-4 receptor; IL-5 receptor; lung disease;  
KM airway inflammation; allergy; asthma; impeded respiration;  
KM cystic fibrosis; acute respiratory distress syndrome;  
KM pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;  
KM ss.  
XX  
OS Homo sapiens.  
OS  
XX  
PN WO2004011613-A2.  
XX  
PD 05-FEB-2004.  
XX  
PF 25-JUL-2003; 2003WO-US023509.  
XX  
PR 29-JUL-2002; 2002US-0399076P.  
XX  
PA (EPIC-) EPIGENESIS PHARM INC.  
XX  
PI Nyce JW, Tang L, Sandrasagra A, Aguilar D, Miller S;  
PI Shahbuddin S, Lu H, Cong H;  
XX  
DR WPI; 2004-203534/19.  
XX  
PT Novel single or multiple target oligonucleotide anti-sense to e.g.  
PT initiation codons and introns of respiratory disease-relevant genes e.g.,  
PT CCR1, RANTES, MCP4, useful for prophylaxis or treating respiratory  
PT disease e.g., asthma.  
XX  
PS Claim 2; SEQ ID NO 1817; 85pp; English.  
XX  
CC The present invention relates to an oligonucleotide anti-sense to e.g.,  
CC initiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-  
CC end of nucleic acid target comprising gene(s) chosen from e.g.,  
CC interleukin (IL)-4 receptor, IL-5 receptor or salts of the  
CC oligonucleotide and optionally surfactant operatively linked to the  
CC oligonucleotide. The method is useful for preventing or treating a  
CC respiratory or lung disease, which involves administering to the airways  
CC of a subject an effective amount of an inhibitor. The oligonucleotide is  
CC useful for production of a medicament for the prevention and/or treatment  
CC of a respiratory or lung disease. The respiratory or lung disease is  
CC chosen from airway inflammation, allergy(ies), asthma, impeded  
CC respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases  
CC (COPD), allergic rhinitis (AR), acute respiratory distress syndrome  
CC (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway  
CC obstruction. The present sequence represents an oligonucleotide of the  
XX  
SQ Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;  
Query Match 2.0%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 379 TCAGCTCCCAAGCTCG 398  
DB 1 TCAGCTCCCAAGCTCG 20

## RESULT 536

ADJ59776  
ID ADJ59776 standard; DNA; 20 BP.

AC ADJ59776;

DT 06-MAY-2004 (first entry)

DE Oligonucleotide associated to RANTES #25.

KM interleukin; IL-4 receptor; IL-5 receptor; lung disease;

KM airway inflammation; allergy; asthma; impeded respiration;

KM cystic fibrosis; acute respiratory distress syndrome;

KM pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;

KM ss.

OS Homo sapiens.

PN WO2004011613-A2.

PD 05-FEB-2004.

PF 25-JUL-2003; 2003WO-US023509.

PR 29-JUL-2002; 2002US-0399076P.

XX (EPG-) EPGENESIS PHARM INC.

PI Myce JW, Tang L, Sandrasagra A, Aguilar D, Miller S;

PI Shababuddin S, Lu H, Cong H;

DR WPI; 2004-203534/19.

XX Novel single or multiple target oligonucleotide anti-sense to e.g.

PT initiation codons and introns of respiratory disease-relevant genes e.g.,

PT CCRI, RANTES, MCP4, useful for prophylaxis or treating respiratory

PT disease e.g., asthma.

PS Claim 2; SEQ ID NO 632; 85bp; English.

XX The present invention relates to an oligonucleotide anti-sense to e.g.,

CC initiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-

CC end of nucleic acid target comprising gene(s) chosen from e.g.

CC interleukin (IL)-4 receptor, IL-5 receptor or salts of the

CC oligonucleotide. The method is useful for preventing or treating a

CC respiratory or lung disease, which involves administering to the always

CC of a subject an effective amount of an inhibitor. The oligonucleotide is

CC useful for production of a medicament for the prevention and/or treatment

CC of a respiratory or lung disease. The respiratory or lung disease is

CC chosen from airway inflammation, allergy(ies), asthma, impeded

CC respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases

CC (COPD), allergic rhinitis (AR), acute respiratory distress syndrome

CC (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway

CC obstruction. The present sequence represents an oligonucleotide of the

CC invention.

XX Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 U; 0 Other;

QY Query Match 2.0%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 732 AGCTGGACTACAGCGCCC 751

QY |||||

DB 1 AGCTGGACTACAGCGCCC 20

## RESULT 537

ADL23339  
ID ADL23339 standard; DNA; 20 BP.

AC ADL23339;

DT 20-MAY-2004 (first entry)

DE Primer #1 for amplification of D6S105.

KM ss; primer; diagnosis; cervical intraepithelial neoplasia; CIN;

KM allelic deletion; FHIT; fragile histidine triad gene; PR;

KM progesterone receptor; DLEC1; deleted in lung and oesophageal cancer 1;

KM TRIM29; tripartite motif-containing 29; microsatellite; D3S1300; D3S1260;

KM D1S35; D1S528.

OS Homo sapiens.

OS Synthetic.

PN WO2004018711-A2.

PD 04-MAR-2004.

PF 20-AUG-2003; 2003WO-GB003637.

PR 24-AUG-2002; 2002GB-00019890.

PR 26-AUG-2002; 2002US-0405717P.

XX (UNLO ) UNIV COLLEGE LONDON.

PI Ming-Qing D;

DR WPI; 2004-226867/21.

XX Diagnosing cervical intraepithelial neoplasia comprising detecting an

PT allelic deletion in genes selected from FHIT, PR, DLEC1- or TRIM 29 by

PT comparing the FHIT, PR, DLEC1 and/or TRIM 29 polynucleotides or proteins

PT present in the samples.

PS Disclosure; SEQ ID NO 21; 56bp; English.

XX This sequence represents a primer which was used in the method of the

CC invention for diagnosing susceptibility to persistence or progression of

CC cervical intraepithelial neoplasia (CIN) in an individual suffering from

CC the disease. The method comprises detecting an allelic deletion in one or

CC more genes selected from FHIT (fragile histidine triad gene), PR

CC (progesterone receptor), DLEC1 (deleted in lung and oesophageal cancer 1)

CC or TRIM29 (tripartite motif-containing 29) by comparing the FHIT, PR,

CC DLEC1 and/or TRIM29 polynucleotides or proteins present in the samples

CC derived from non-dyskaryotic and dyskaryotic samples, respectively. The

CC method is carried out using a kit comprising a panel of two or more pairs

CC of primers, where each pair of primers is suitable for amplifying a

CC microsatellite DNA marker selected from D3S1300, D3S1260, D1S35 or

CC D1S528, or a panel of two or more specific binding agents, where each

CC binding agent is capable of distinguishing between the normal and allelic

CC deletion forms of a polynucleotide or protein selected from FHIT, PR,

CC TRIM29 or DLEC1. The method is useful for diagnosing susceptibility to

CC persistence or progression of cervical intraepithelial neoplasia in an

XX individual suffering from the disease.

XX Sequence 20 BP; 6 A; 4 C; 6 G; 4 T; 0 U; 0 Other;

QY Query Match 2.0%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 387 CCAAGTCTGGATTACAG 406

QY |||||



```
PH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
PN WO2004028458-A2.
PD 08-APR-2004.
PF 25-SEP-2003; 2003WO-US030374.
PR 25-SEP-2002; 2002US-0413549P.
PA (PHAA ) PHARMACIA CORP.
PI Gierse JK;
PX MPI; 2004-305094/28.
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.
XX Claim 4; SEQ ID NO 581; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin H2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mPGES-1, which specifically hybridize with the nucleic acid mPGES-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytostatic,
XX antiinflammatory, immunomodulator, cardiant, neuroprotective,
XX antiinflammatory, neuroprotective, nocotropic, antiarthritic, vasotropic,
XX ophthalmological, immunomodulatory and cardiovascular activities, and can
XX be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX can be used for preparing a composition for treating a disease or
XX condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX disease, arthritis, diabetes, cancer, ischemia or reperfusion injury, or
XX ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 2.0%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.1e+03;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 851 GGCTTCCCAAGTGTGGGA 870
XX | | | | | | | | | |
XX Db 20 GGCTTCCCAAGTGTGGGA 1
XX
XX RESULT 541
XX ADM14746/c
XX ID ADM14746 standard; DNA; 20 BP.
XX
XX ADM14746;
XX
XX 01-JUL-2004 (first entry)
```

```
XX
XX Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:933.
DE
XX chimeric; antisense oligonucleotide; phosphorothioate; human;
XX microsomal prostaglandin H2 synthase; mPGES-1; mPGES-1 inhibitor;
XX microsomal prostaglandin H2 synthase inhibitor; cytosolic; antiinflammatory;
XX immunomodulator; cardiant; neuroprotective; antiinflammatory;
XX neuroprotective; nocotropic; antiarthritic; vasotropic; ophthalmological;
XX immunomodulatory; cardiovascular; gene therapy; inflammation;
XX Alzheimer's disease; arthritis; diabetes; cancer; ischemia;
XX reperfusion injury; ophthalmic disorder; immunological disorder;
XX cardiovascular disorder; neurological disorder; ss.
XX
XX Homo sapiens.
OS Synthetic.
OS
XX
XX Key Location/Qualifiers
FT modified_base 1..20
FT /tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
PN WO2004028458-A2.
PD 08-APR-2004.
PF 25-SEP-2003; 2003WO-US030374.
PR 25-SEP-2002; 2002US-0413549P.
PA (PHAA ) PHARMACIA CORP.
PI Gierse JK;
PX MPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.
XX Claim 4; SEQ ID NO 933; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin H2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mPGES-1, which specifically hybridize with the nucleic acid mPGES-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytostatic,
XX antiinflammatory, neuroprotective, cardiant, neuroprotective,
XX antiinflammatory, neuroprotective, nocotropic, antiarthritic, vasotropic,
XX ophthalmological, immunomodulatory and cardiovascular activities, and can
XX be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX can be used for preparing a composition for treating a disease or
XX condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX disease, arthritis, diabetes, cancer, ischemia or reperfusion injury, or
XX ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX Sequence 20 BP; 4 A; 6 C; 6 G; 4 T; 0 U; 0 Other;
```



```
Query Match      2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      382 GCCTCCCAAGTCTGGGAT 401
      |||
      20 GCCTCCCAAGTCTGGGAT 1

RESULT 542
ADM14277/c
ID      ADM14277 standard; DNA; 20 BP.
AC      ADM14277;
XX
XX
XX      01-JUL-2004 (first entry)
DE      Human mPGEs-1 chimeric antisense oligonucleotide SEQ ID NO:464.
XX
XX      chimeric; antisense oligonucleotide; phosphorothioate; human;
KW      microsomal prostaglandin E2 synthase; mPGEs-1; mPGEs-1 inhibitor;
KW      microsomal prostaglandin E2 synthase inhibitor; cyclooxygenase; antidiabetic;
KW      immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW      neuroprotective; neurotropic; antiarthritic; vasotrophic; ophthalmological;
KW      immunomodulatory; cardiovascular; gene therapy; inflammation;
KW      Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW      reperfusion injury; ophthalmic disorder; immunological disorder;
KW      cardiovascular disorder; neurological disorder; ss.
XX
XX      Homo sapiens.
OS      Synthetic.
XX
XX      Key
FH      modified_base
FT      1..20
      Location/Qualifiers
      +tag= b
      /mod_base= OTHER
      /note= "phosphorothioate linkages and all cytidine
      residues are 5-methylcytidines"
FT      modified_base
FT      1..5
      +tag= a
      /mod_base= OTHER
      /note= "2'-O-methoxyethyls"
FT      modified_base
FT      16..20
      +tag= c
      /mod_base= OTHER
      /note= "2'-O-methoxyethyls"
XX
XX      WO2004028458-A2.
PN
XX
XX      08-APR-2004.
PD
XX
XX      25-SEP-2003; 2003WO-US030374.
PF
XX
XX      25-SEP-2002; 2002US-0413549P.
PR
XX
XX      (PHAA ) PHARMACIA CORP.
PA
XX
XX      Gierse JK;
PI
XX
XX      WPI; 2004-305094/28.
DR
XX
XX      New antisense compound, having a sequence targeted to a nucleic acid
PT      encoding mPGEs-1, useful for preparing a composition for treating e.g.,
PT      inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT      lechemia.
XX
XX      Claim 4; SEQ ID NO 464; 132pp; English.
XX
XX      The present sequence represents a chimeric antisense oligonucleotide
CC      targeted to human microsomal prostaglandin E2 synthase (mPGEs-1). The
CC      human mPGEs-1 gene is located on chromosome 9, more specifically to
CC      9q34.3. The present invention also describes: (1) antisense compounds,
CC      having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
```

```
CC      mPGEs-1, which specifically hybridise with the nucleic acid mPGEs-1 and
CC      inhibits its expression; (2) a method of inhibiting the expression of
CC      mPGEs-1 in cells or tissues; and (3) a method of treating an animal
CC      having a disease or condition associated with mPGEs-1. mPGEs-1 chimeric
CC      antisense oligonucleotides and antisense compounds have cytostatic,
CC      antidiabetic, immunomodulator, cardiant, neuroprotective,
CC      antiinflammatory, neuroprotective, neurotropic, antiarthritic, vasotrophic,
CC      ophthalmological, immunomodulatory and cardiovascular activities, and can
CC      be used as mPGEs-1 inhibitors and in gene therapy. The antisense compound
CC      can be used for preparing a composition for treating a disease or
CC      condition associated with mPGEs-1 e.g., inflammation, Alzheimer's
CC      disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC      ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX      Sequence 20 BP; 3 A; 7 C; 7 G; 3 T; 0 U; 0 Other;
SQ
XX
XX      Query Match      2.0%; Score 20; DB 1; Length 20;
XX      Best Local Similarity 100.0%; Pred. No. 1.1e+03;
XX      Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      850 CGGCTCCCAAGTCTGGG 869
      |||
      20 CGGCTCCCAAGTCTGGG 1

RESULT 543
ADM14482/c
ID      ADM14482 standard; DNA; 20 BP.
AC      ADM14482;
XX
XX
XX      01-JUL-2004 (first entry)
DE      Human mPGEs-1 chimeric antisense oligonucleotide SEQ ID NO:669.
XX
XX      chimeric; antisense oligonucleotide; phosphorothioate; human;
KW      microsomal prostaglandin E2 synthase; mPGEs-1; mPGEs-1 inhibitor;
KW      microsomal prostaglandin E2 synthase inhibitor; cyclooxygenase; antidiabetic;
KW      immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW      neuroprotective; neurotropic; antiarthritic; vasotrophic; ophthalmological;
KW      immunomodulatory; cardiovascular; gene therapy; inflammation;
KW      Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW      reperfusion injury; ophthalmic disorder; immunological disorder;
KW      cardiovascular disorder; neurological disorder; ss.
XX
XX      Homo sapiens.
OS      Synthetic.
XX
XX      Key
FH      modified_base
FT      1..20
      Location/Qualifiers
      +tag= b
      /mod_base= OTHER
      /note= "phosphorothioate linkages and all cytidine
      residues are 5-methylcytidines"
FT      modified_base
FT      1..5
      +tag= a
      /mod_base= OTHER
      /note= "2'-O-methoxyethyls"
FT      modified_base
FT      16..20
      +tag= c
      /mod_base= OTHER
      /note= "2'-O-methoxyethyls"
XX
XX      WO2004028458-A2.
PN
XX
XX      08-APR-2004.
PD
XX
XX      25-SEP-2003; 2003WO-US030374.
PF
XX
XX      25-SEP-2002; 2002US-0413549P.
PR
XX
XX      (PHAA ) PHARMACIA CORP.
PA
XX
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PI Gierse JK;
XX
XX WPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
PT encoding mPGEs-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT ischemia.
XX
XX Claim 4; SEQ ID NO 669; 132bp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsomal prostaglandin E2 synthase (mPGEs-1). The
CC human mPGEs-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGEs-1, which specifically hybridize with the nucleic acid mPGEs-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGEs-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGEs-1. mPGEs-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytostatic,
CC antidiabetic, immunomodulator, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, neurotropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGEs-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGEs-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX Sequence 20 BP; 4 A; 6 C; 7 G; 3 T; 0 U; 0 Other;
SQ
Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 849 TCGGCTCCCAAGTCTGG 868
DB 20 TCGGCTCCCAAGTCTGG 1
RESULT 544
ADM15309/C
ID ADM15309 standard; DNA; 20 BP.
XX
XX ADM15309;
AC
XX
XX 01-JUL-2004 (first entry)
DT
XX
XX Human mPGEs-1 chimeric antisense oligonucleotide SEQ ID NO:1496.
DE
XX
XX chimeric; antisense oligonucleotide; phosphorothioate; human;
XX microsomal prostaglandin E2 synthase; mPGEs-1; mPGEs-1 inhibitor;
XX microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
XX immunomodulator; cardiant; neuroprotective; antiinflammatory;
XX neuroprotective; neurotropic; antiarthritic; vasotropic; ophthalmological;
XX immunomodulatory; cardiovascular; gene therapy; inflammation;
XX Alzheimer's disease; arthritis; diabetes; cancer; ischemia;
XX reperfusion injury; ophthalmic disorder; immunological disorder;
XX cardiovascular disorder; neurological disorder; ss.
XX
XX Homo sapiens.
OS
XX
XX Synthetic.
FH
XX
XX Key location/Qualifiers
FT 1. .20
FT /tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT 1. .5
FT /tag= a
FT /mod_base= OTHER

```

```

FT /note= "2'-O-methoxyethyls"
FT modified_base 16. .20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX
XX WO2004028458-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Gierse JK;
XX
XX WPI; 2004-305094/28.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsomal prostaglandin E2 synthase (mPGEs-1). The
CC human mPGEs-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGEs-1, which specifically hybridize with the nucleic acid mPGEs-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGEs-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGEs-1. mPGEs-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytostatic,
CC antidiabetic, immunomodulator, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, neurotropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGEs-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGEs-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
XX Sequence 20 BP; 12 A; 4 C; 0 G; 4 T; 0 U; 0 Other;
SQ
Query Match 2.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 769 TTTTGTATTTTGTAGAG 788
DB 20 TTTTGTATTTTGTAGAG 1
RESULT 545
ADM15160/C
ID ADM15160 standard; DNA; 20 BP.
XX
XX ADM15160;
AC
XX
XX 01-JUL-2004 (first entry)
DT
XX
XX Human mPGEs-1 chimeric antisense oligonucleotide SEQ ID NO:1347.
DE
XX
XX chimeric; antisense oligonucleotide; phosphorothioate; human;
XX microsomal prostaglandin E2 synthase; mPGEs-1; mPGEs-1 inhibitor;
XX microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
XX immunomodulator; cardiant; neuroprotective; antiinflammatory;
XX neuroprotective; neurotropic; antiarthritic; vasotropic; ophthalmological;
XX immunomodulatory; cardiovascular; gene therapy; inflammation;

```

XX	Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW	reperfusion injury; ophthalmic disorder; immunological disorder;
KW	cardiovascular disorder; neurological disorder; ss.
OS	Homo sapiens.
OS	Synthetic.
XX	
FH	Key
FT	modified_base
FT	location/Qualifiers
FT	1..20
FT	/+tag= b
FT	/mod_base= OTHER
FT	/note= "phosphorothioate linkages and all cytidine residues are 5-methylcytidines"
FT	modified_base
FT	1..5
FT	/+tag= a
FT	/mod_base= OTHER
FT	/note= "2'-O-methoxyethyls"
FT	modified_base
FT	16..20
FT	/+tag= c
FT	/mod_base= OTHER
FT	/note= "2'-O-methoxyethyls"
XX	
PN	WO2004028458-A2.
XX	
PD	08-APR-2004.
XX	
PE	25-SEP-2003; 2003WO-US030374.
XX	
PR	25-SEP-2002; 2002US-0413549P.
XX	
PA	(PHAA ) PHARMACIA CORP.
XX	
PI	Gierse JK;
XX	
DRI	WPT: 2004-305094/28.
XX	
PT	New antisense compound, having a sequence targeted to a nucleic acid
PT	mpgs-1, useful for preparing a composition for treating e.g.,
PT	inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT	ischemia.
XX	
PS	Claim 4; SEQ ID NO 1347; 132pp; English.
XX	
CC	The present sequence represents a chimeric antisense oligonucleotide
CC	targeted to human microsomal prostaglandin E2 synthase (mpgs-1). The
CC	human mpgs-1 gene is located on chromosome 9, more specifically to
CC	qg4.3. The present invention also describes: (1) antisense compounds,
CC	having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC	mpgs-1, which specifically hybridise with the nucleic acid mpgs-1 and
CC	inhibits its expression; (2) a method of inhibiting the expression of
CC	mpgs-1 in cells or tissues; and (3) a method of treating an animal
CC	having a disease or condition associated with mpgs-1. Mpgs-1 chimeric
CC	antisense oligonucleotides and antisense compounds have cytostatic,
CC	antidiabetic, immunomodulator, cardiant, neuroprotective,
CC	antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC	ophthalmological, immunomodulatory, and cardiovascular activities, and can
CC	be used as mpgs-1-inhibitors and in gene therapy. The antisense compound
CC	can be used for preparing a composition for treating a disease or
CC	condition associated with mpgs-1 e.g., inflammation, Alzheimer's
CC	disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC	ophthalnic, immunological, cardiovascular or neurological disorder.
XX	
SQ	Sequence 20 BP; 4 A; 4 C; 9 G; 3 T; 0 U; 0 Other;
XX	
QY	Query Match 2.0%; Score 20; DB 1; Length 20;
DB	Best Local Similarity 100.0%; Pred.No. 1.le+03;
	Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	CCTCGGCGCTCCCAAGTGCT 666
	CCTGGCGCTCCCAAGTGCT 1

	RESULT	546
ID	ADM14957/C	
XZ	ADM14957 standard; DNA;	20 BP.
AC	ADM14957;	
D7	01-JUL-2004	(first entry)
XX	Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:1144.	
KW	chimeric; antisense oligonucleotide; phosphorothioate; human;	
KM	micosomal prostaglandin E2 synthase; mPGES-1; inhibitor;	
KW	microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;	
KM	immunomodulator; cardiant; neuroprotective; anti-inflammatory;	
KX	neuroprotective; nootropic; antiarthritic; vasotrophic; ophthalmological;	
KV	immunomodulatory; cardiovascular; gene therapy; inflammation;	
KH	Alzheimer's disease; arthritis; diabetes; cancer; ischemia;	
KJ	reperfusion injury; ophthalmic disorder; immunological disorder;	
KL	cardiovascular disorder; neurological disorder; ss.	
OS	Homo sapiens.	
XS	Synthetic.	
FH	Key	location/qualifiers
FT	modified_base	1..20
FT	/tag= b	/mod_base= OTHER
FT	/note= "phosphorothioate linkages and all cyclidine residues are 5-methylcytidines"	1..5
FT	modified_base	1..5
FT	/tag= a	/mod_base= OTHER
FT	/note= "2'-O-methoxyethyls"	16..20
FT	modified_base	16..20
FT	/tag= c	/mod_base= OTHER
FT	/note= "2'-O-methoxyethyls"	
FN	WO2004028458-A2.	
PN	08-APR-2004.	
PD	25-SEP-2003; 2003WO-US030374.	
PE	25-SEP-2003; 2003US-0413549P.	
PR	25-SEP-2002; 2002US-0413549P.	
PA	{PHNA } PHARMACIA CORP.	
Gierse JK:		
WPt:	2004-305094/28.	
New antisense compound,	having a sequence targeted to a nucleic acid	
targeting mPGES-1, useful for preparing a composition for treating e.g.,		
inflammation, Alzheimer's disease, arthritis, diabetes, cancer or		
ischemia.		
Claim 4; SEQ ID NO 1144; 132pp; English.		
The present sequence represents a chimeric antisense oligonucleotide		
targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The		
human mPGES-1 gene is located on chromosome 9, more specifically to		
9q34.3. The present invention also describes: (1) antisense compounds,		
having a sequence comprising 8-30 bp targeted to a nucleic acid encoding		
mPGES-1, which specifically hybridize with the nucleic acid mPGES-1 and		
inhibits its expression; (2) a method of inhibiting the expression of		
mPGES-1 in cells or tissues; and (3) a method of treating an animal		
having a disease or condition associated with mPGES-1. mPGES-1 chimeric		
antisense oligonucleotides and antisense compounds have cytostatic,		
antibiotic, immunomodulator, cardiact, neuroprotective,		
antiinflammatory, neuroprotective, nootropic, antiarthritis, vasotrophic,		
ophthalmologicall, immunomodulatory and cardiovascular activities, and can		
be used as mPGES-1 inhibitors and in gene therapy. The antisense compound		

CC can be used for preparing a composition for treating a disease or  
CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's  
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or  
CC ophthalmic, immunological, cardiovascular or neurological disorder.

XX Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 720 AGCCTCTGAGTAGCTGGGA 739

Db 20 AGCCTCTGAGTAGCTGGGA 1

RESULT 547  
ADM1553/c  
ID ADM1553 standard; DNA; 20 BP.

AC ADM1553;

DT 01-JUL-2004 (first entry)

DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:1740.

XX chimeric; antisense oligonucleotide; phosphorothioate; human;  
XX microsome prostaglandin E2 synthase inhibitor; mPGES-1 inhibitor;  
XX immunomodulator; cardiant; neuroprotective; antidiabetic;  
XX neuroprotective; nocotropic; antiarthritic; vasotropic; ophthalmological;  
XX immunomodulatory; cardiovascular; gene therapy; inflammation;  
XX Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;  
XX reperfusion injury; ophthalmic disorder; immunological disorder;  
XX cardiovascular disorder; neurological disorder; ss.

OS Homo sapiens.  
XX Synthetic.

FT Key Location/Qualifiers  
FT modified\_base 1..20

FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "phosphorothioate linkages and all cytidine  
FT residues are 5-methylcytidines"

FT modified\_base 1..5

FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "2'-O-methoxyethyls"  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "2'-O-methoxyethyls"

FT WO2004028458-A2.

XX 08-APR-2004.

XX 25-SEP-2003; 2003WO-US030374.

XX 25-SEP-2002; 2002US-0413549P.

XX (PHAA ) PHARMACIA CORP.

XX Gierse JK;

XX WPI; 2004-305094/28.

XX New antisense compound, having a sequence targeted to a nucleic acid  
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,  
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or  
XX ischemia.

PS Claim 4; SEQ ID NO 1740; 132pp; English.

XX The present sequence represents a chimeric antisense oligonucleotide  
XX targeted to human microsome prostaglandin E2 synthase (mPGES-1). The  
XX human mPGES-1 gene is located on chromosome 9, more specifically to  
XX 9q34.3. The present invention also describes: (1) antisense compounds,  
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding  
XX mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and  
XX inhibits its expression; (2) a method of inhibiting the expression of  
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal  
XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric  
XX antisense oligonucleotides and antisense compounds have cytostatic,  
XX antidiabetic, immunomodulator, cardiant, neuroprotective,  
XX antiinflammatory, neuroprotective, nocotropic, antiarthritic, vasotropic,  
XX ophthalmological, immunomodulatory and cardiovascular activities, and can  
XX be used as mPGES-1 inhibitors and in gene therapy. The antisense compound  
XX can be used for preparing a composition for treating a disease or  
XX condition associated with mPGES-1 e.g., inflammation, Alzheimer's  
XX disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or  
XX ophthalmic, immunological, cardiovascular or neurological disorder.

XX Sequence 20 BP; 11 A; 4 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 770 TTTTGATTTTATTAGAGAGA 789

Db 20 TTTTGATTTTATTAGAGAGA 1

RESULT 548  
ADM15081/c

ID ADM15081 standard; DNA; 20 BP.

AC ADM15081;

DT 01-JUL-2004 (first entry)

DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:1268.

XX chimeric; antisense oligonucleotide; phosphorothioate; human;  
XX microsome prostaglandin E2 synthase inhibitor; mPGES-1 inhibitor;  
XX immunomodulator; cardiant; neuroprotective; antidiabetic;  
XX neuroprotective; nocotropic; antiarthritic; vasotropic; ophthalmological;  
XX immunomodulatory; cardiovascular; gene therapy; inflammation;  
XX Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;  
XX reperfusion injury; ophthalmic disorder; immunological disorder;  
XX cardiovascular disorder; neurological disorder; ss.

OS Homo sapiens.  
XX Synthetic.

FT Key Location/Qualifiers  
FT modified\_base 1..20

FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "phosphorothioate linkages and all cytidine  
FT residues are 5-methylcytidines"

FT modified\_base 1..5

FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "2'-O-methoxyethyls"  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "2'-O-methoxyethyls"

FT WO2004028458-A2.

XX 08-APR-2004.

XX 25-SEP-2003; 2003WO-US030374.  
PF  
XX  
XX 25-SEP-2002; 2002US-0413549P.  
PR  
XX  
PA (PHAA ) PHARMACIA CORP.  
XX  
XX  
PI Gierse JK;  
XX  
DR MPI; 2004-305094/28.  
XX  
PT New antisense compound, having a sequence targeted to a nucleic acid  
XX encoding mpGES-1, useful for preparing a composition for treating e.g.,  
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or  
PT ischemia.  
XX  
PS Claim 4; SEQ ID NO 1268; 132pp; English.  
XX  
XX The present sequence represents a chimeric antisense oligonucleotide  
CC targeted to human microsomal prostaglandin E2 synthase (mpGES-1). The  
CC human mpGES-1 gene is located on chromosome 9, more specifically to  
CC 9q34.3. The present invention also describes: (1) antisense compounds,  
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding  
CC mpGES-1, which specifically hybridize with the nucleic acid mpGES-1 and  
CC inhibits its expression; (2) a method of inhibiting the expression of  
CC mpGES-1 in cells or tissues; and (3) a method of treating an animal  
CC having a disease or condition associated with mpGES-1. MPGES-1 chimeric  
CC antisense oligonucleotides and antisense compounds have cytostatic,  
CC anti-diabetic, immunomodulator, cardiant, neuroprotective,  
CC anti-inflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,  
CC ophthalmological, immunomodulatory and cardiovascular activities, and can  
CC be used as mpGES-1 inhibitors and in gene therapy. The antisense compound  
CC can be used for preparing a composition for treating a disease or  
CC condition associated with mpGES-1 e.g., inflammation, Alzheimer's  
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or  
CC ophthalmic, immunological, cardiovascular or neurological disorder.  
XX  
SQ Sequence 20 BP; 4 A; 7 C; 6 G; 3 T; 0 U; 0 Other;  
XX  
Query Match 2.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
Oy 719 CAGCCTCCTGAGTAGCTGGG 738  
Db 20 CAGCCTCCTGAGTAGCTGGG 1  
XX  
RESULT 549  
ADM15268/c  
ID ADM15268 standard; DNA; 20 BP.  
XX  
AC ADM15268;  
XX  
XX 01-JUL-2004 (first entry)  
XX  
DE Human mpGES-1 chimeric antisense oligonucleotide SEQ ID NO:1455.  
XX  
XX chimeric; antisense oligonucleotide; phosphorothioate; human;  
KW microsomal prostaglandin E2 synthase; mpGES-1; mpGES-1 inhibitor;  
KW microsomal prostaglandin E2 synthase inhibitor; cytostatic; anti-diabetic;  
KW immunomodulator; cardiant; neuroprotective; anti-inflammatory;  
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;  
KW immunomodulatory; cardiovascular; gene therapy; inflammation;  
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;  
KW reperfusion injury; ophthalmic disorder; immunological disorder;  
KW cardiovascular disorder; neurological disorder; se.  
XX  
XX Homo sapiens.  
OS Synthetic.  
OS  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..20

FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "phosphorothioate linkages and all cytidine  
FT residues are 5-methylcytidines"  
FT modified\_base 1..5  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "2'-O-methoxyethyls"  
FT modified\_base 16..20  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "2'-O-methoxyethyls"  
XX  
XX MO2004028458-A2.  
XX  
XX 08-APR-2004.  
XX  
XX 25-SEP-2003; 2003WO-US030374.  
XX  
XX 25-SEP-2002; 2002US-0413549P.  
XX  
XX (PHAA ) PHARMACIA CORP.  
XX  
XX Gierse JK;  
XX  
XX MPI; 2004-305094/28.  
XX  
XX New antisense compound, having a sequence targeted to a nucleic acid  
PT encoding mpGES-1, useful for preparing a composition for treating e.g.,  
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or  
PT ischemia.  
XX  
XX Claim 4; SEQ ID NO 1455; 132pp; English.  
XX  
XX The present sequence represents a chimeric antisense oligonucleotide  
CC targeted to human microsomal prostaglandin E2 synthase (mpGES-1). The  
CC human mpGES-1 gene is located on chromosome 9, more specifically to  
CC 9q34.3. The present invention also describes: (1) antisense compounds,  
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding  
CC mpGES-1, which specifically hybridize with the nucleic acid mpGES-1 and  
CC inhibits its expression; (2) a method of inhibiting the expression of  
CC mpGES-1 in cells or tissues; and (3) a method of treating an animal  
CC having a disease or condition associated with mpGES-1. MPGES-1 chimeric  
CC antisense oligonucleotides and antisense compounds have cytostatic,  
CC anti-diabetic, immunomodulator, cardiant, neuroprotective,  
CC anti-inflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,  
CC ophthalmological, immunomodulatory and cardiovascular activities, and can  
CC be used as mpGES-1 inhibitors and in gene therapy. The antisense compound  
CC can be used for preparing a composition for treating a disease or  
CC condition associated with mpGES-1 e.g., inflammation, Alzheimer's  
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or  
CC ophthalmic, immunological, cardiovascular or neurological disorder.  
XX  
SQ Sequence 20 BP; 3 A; 5 C; 9 G; 3 T; 0 U; 0 Other;  
XX  
Query Match 2.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
Oy 846 GCCTCGGCTCCCAAGTGC 865  
Db 20 GCCTCGGCTCCCAAGTGC 1  
XX  
RESULT 550  
ADM14958/c  
ID ADM14958 standard; DNA; 20 BP.  
XX  
AC ADM14958;  
XX  
XX 01-JUL-2004 (first entry)  
XX  
DE Human mpGES-1 chimeric antisense oligonucleotide SEQ ID NO:1455.



CC respiratory or lung disease is associated with hyper-responsiveness to  
CC and/or increased levels of, adenosine and/or levels of adenosine A  
CC receptor(s), and/or asthma and/or lung allergies associated with  
CC inflammation or an inflammatory disease. The respiratory or lung disease  
CC is chosen from allergy inflammation, allergy, asthma, impeded respiration,  
CC allergic fibrosis (CF), chronic obstructive pulmonary disease (COPD),  
CC allergic rhinitis, acute respiratory distress syndrome, pulmonary  
CC hypertension, lung inflammation, bronchitis, airway obstruction or  
CC bronchoconstriction. This sequence represents an oligonucleotide of the  
CC invention.

XX SQ Sequence 20 BP, 3 A; 4 C; 10 G; 3 T; 0 U; 0 Other;

XX Query Match 2.0%; Score 20; DB 1; Length 20;

XX Best Local Similarity 100.0%; Pred. No. 1.1e+03;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 646 AGGCTGAGTGCAGTGGCGC 665

DB 1 AGGCTGAGTGCAGTGGCGC 20

RESULT 552

AD046429 standard; DNA; 20 BP.

AC ADO46429;

XX 15-JUL-2004 (first entry)

DE Human oligonucleotide #1795.

XX Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;  
KM CCR1, CCR3; Eotaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;  
KM tryptase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease;  
KM lung disease; hyper-responsiveness; adenosine; adenosine A receptor;  
KM asthma; lung allergy; inflammation; inflammatory disease;  
KM airway inflammation; allergy; impeded respiration; cystic fibrosis; CF;  
KM chronic obstructive pulmonary disease; COPD; allergic rhinitis;  
KM acute respiratory distress syndrome; pulmonary hypertension;  
KM lung inflammation; bronchitis; airway obstruction; bronchoconstriction.

XX Homo sapiens.

PN US2004049022-A1.

XX 11-MAR-2004.

XX 25-JUL-2003; 2003US-00627930.

XX 23-APR-2002; 2002WO-US013135.

XX 23-APR-2002; 2002WO-US013143.

XX (NYCE/) NYCE J W.

XX (SAND/) SANDRASAGRA A.

XX (TANG/) TANG L.

XX (AGUT/) AGUTLAR D.

XX (MILL/) MILLER S.

XX (SHAH/) SHAHABUDDIN S.

XX (LUTH/) LUT H.

XX (CONG/) CONG H.

PI NYCE JW, Sandrasagra A, Tang L, Aguilar D, Miller S;

XX Shahabuddin S, Lu H, Cong H;

XX WPI; 2004-293804/27.

XX Novel single or multiple target oligonucleotide anti-sense to e.g.

XX initiation codon, intion of respiratory disease-relevant gene e.g. CCR1,

XX RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.

XX asthma.

XX Claim 2; SEQ ID NO 1796; 174pp; English.

XX The invention relates to oligonucleotides anti-sense to an initiation  
CC codon, coding region, 5' or 3' intron-exon junction, intron or region  
CC with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target  
CC chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)  
CC -5 receptor, CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,  
CC tryptase a, tryptase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention  
CC also relates to a method of screening a candidate compound that binds to  
CC one or more nucleic acid target(s) or expressed product(s), for the  
CC prevention and/or treatment of a respiratory or lung disease. The  
CC oligonucleotides are useful for reducing or inhibiting expression of a  
CC gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,  
CC CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, tryptase a,  
CC tryptase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are  
CC useful for preventing or treating a respiratory or lung disease. The  
CC respiratory or lung disease is associated with hyper-responsiveness to  
CC and/or increased levels of, adenosine and/or levels of adenosine A  
CC receptor(s), and/or asthma and/or lung allergies associated with  
CC inflammation or an inflammatory disease. The respiratory or lung disease  
CC is chosen from allergy inflammation, allergy, asthma, impeded respiration,  
CC allergic fibrosis (CF), chronic obstructive pulmonary disease (COPD),  
CC allergic rhinitis, acute respiratory distress syndrome, pulmonary  
CC hypertension, lung inflammation, bronchitis, airway obstruction or  
CC bronchoconstriction. This sequence represents an oligonucleotide of the  
CC invention.

XX SQ Sequence 20 BP, 3 A; 5 C; 9 G; 3 T; 0 U; 0 Other;

XX Query Match 2.0%; Score 20; DB 1; Length 20;

XX Best Local Similarity 100.0%; Pred. No. 1.1e+03;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 643 CCCAGGCTGAGTGCAGTGG 662

DB 1 CCCAGGCTGAGTGCAGTGG 20

RESULT 553

AD046442 standard; DNA; 20 BP.

AC ADO46442;

XX 15-JUL-2004 (first entry)

DE Human oligonucleotide #1808.

XX Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;  
KM CCR1, CCR3; Eotaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;  
KM tryptase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease;  
KM lung disease; hyper-responsiveness; adenosine; adenosine A receptor;  
KM asthma; lung allergy; inflammation; inflammatory disease;  
KM airway inflammation; allergy; impeded respiration; cystic fibrosis; CF;  
KM chronic obstructive pulmonary disease; COPD; allergic rhinitis;  
KM acute respiratory distress syndrome; pulmonary hypertension;  
KM lung inflammation; bronchitis; airway obstruction; bronchoconstriction.

XX Homo sapiens.

PN US2004049022-A1.

XX 11-MAR-2004.

XX 25-JUL-2003; 2003US-00627930.

XX 23-APR-2002; 2002WO-US013135.

XX 23-APR-2002; 2002WO-US013143.

XX (NYCE/) NYCE J W.

XX (SAND/) SANDRASAGRA A.

XX (TANG/) TANG L.

XX (AGUT/) AGUTLAR D.

XX (MILL/) MILLER S.

PA (SHAH/) SHAHABUDDIN S.  
 PA (LUHH/) LU H.  
 PA (CONG/) CONG H.  
 XX  
 PI Nyce JW, Sandrasagra A, Tang L, Aguilar D, Miller S,  
 PI Shahabuddin S, Lu H, Cong H;  
 XX  
 DR WPI; 2004-293804/27.  
 XX  
 PT Novel single or multiple target oligonucleotide anti-sense to e.g.  
 PT initiation codon, intron of respiratory disease-relevant gene e.g. CCRI,  
 PT RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.  
 PT asthma.  
 XX  
 PS Claim 2; SEQ ID NO 1809; 174pp; English.  
 XX  
 CC The invention relates to oligonucleotides anti-sense to an initiation  
 CC codon, coding region, 5' or 3' intron-exon junction, intron or region  
 CC with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target  
 CC chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)  
 CC -5 receptor, CCRI, CCR3, Botaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,  
 CC tryptase a, tryptase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention  
 CC also relates to a method of screening a candidate compound that binds to  
 CC one or more nucleic acid target(s) or expressed product(s), for the  
 CC prevention and/or treatment of a respiratory or lung disease. The  
 CC oligonucleotides are useful for reducing or inhibiting expression of a  
 CC gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,  
 CC CCRI, CCR3, Botaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, tryptase a,  
 CC tryptase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are  
 CC useful for preventing or treating a respiratory or lung disease. The  
 CC respiratory or lung disease is associated with hyper-responsiveness to  
 CC and/or increased levels of, adenosine and/or levels of adenosine A  
 CC receptor(s), and/or asthma and/or lung allergies associated with  
 CC inflammation or an inflammatory disease. The respiratory or lung disease  
 CC is chosen from airway inflammation, allergy, asthma, impeded respiration,  
 CC cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),  
 CC allergic rhinitis, acute respiratory distress syndrome, pulmonary  
 CC hypertension, lung inflammation, bronchitis, airway obstruction or  
 CC bronchoconstriction. This sequence represents an oligonucleotide of the  
 CC invention.  
 XX  
 SQ Sequence 20 BP; 5 A; 0 C; 5 G; 10 T; 0 U; 0 Other;  
 XX  
 Query Match 2.0%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 772 TTGATTTTACTAGAGATG 791  
 DB 1 TTGTATTTTACTAGAGATG 20  
 RESULT 554  
 ADO45266  
 ID ADO45266 standard; DNA; 20 BP.  
 XX  
 AC ADO45266;  
 XX  
 DT 15-JUL-2004 (first entry)  
 XX  
 DE Human oligonucleotide #632.  
 XX  
 KW Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;  
 KW CCR1; CCR3; Botaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;  
 KW tryptase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease;  
 KW lung disease; hyper-responsiveness; adenosine A receptor;  
 KW asthma; lung allergy; inflammation; inflammatory disease;  
 KW airway inflammation; allergy; impeded respiration; cystic fibrosis; CF;  
 KW chronic obstructive pulmonary disease; COPD; allergic rhinitis;  
 KW acute respiratory distress syndrome; pulmonary hypertension;  
 KW lung inflammation; bronchitis; airway obstruction; bronchoconstriction.  
 XX  
 OS Homo sapiens.

XX US2004049022-A1.  
 PN  
 XX 11-MAR-2004.  
 XX  
 PD 25-JUL-2003; 2003US-00627930.  
 XX  
 PF 23-APR-2002; 2002WO-US013135.  
 XX  
 PR 23-APR-2002; 2002WO-US013143.  
 XX  
 PA (NYCE/) NYCE J W.  
 PA (SAND/) SANDRASAGRA A.  
 PA (TANG/) TANG L.  
 PA (AGUI/) AGUILAR D.  
 PA (MILL/) MILLER S.  
 PA (SHAH/) SHAHABUDDIN S.  
 PA (LUHH/) LU H.  
 PA (CONG/) CONG H.  
 XX  
 PI Nyce JW, Sandrasagra A, Tang L, Aguilar D, Miller S;  
 PI Shahabuddin S, Lu H, Cong H;  
 XX  
 DR WPI; 2004-293804/27.  
 XX  
 PT Novel single or multiple target oligonucleotide anti-sense to e.g.  
 PT initiation codon, intron of respiratory disease-relevant gene e.g. CCRI,  
 PT RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.  
 PT asthma.  
 XX  
 PS Claim 2; SEQ ID NO 632; 174pp; English.  
 XX  
 CC The invention relates to oligonucleotides anti-sense to an initiation  
 CC codon, coding region, 5' or 3' intron-exon junction, intron or region  
 CC with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target  
 CC chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)  
 CC -5 receptor, CCRI, CCR3, Botaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,  
 CC tryptase a, tryptase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention  
 CC also relates to a method of screening a candidate compound that binds to  
 CC one or more nucleic acid target(s) or expressed product(s), for the  
 CC prevention and/or treatment of a respiratory or lung disease. The  
 CC oligonucleotides are useful for reducing or inhibiting expression of a  
 CC gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,  
 CC CCRI, CCR3, Botaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, tryptase a,  
 CC tryptase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are  
 CC useful for preventing or treating a respiratory or lung disease. The  
 CC respiratory or lung disease is associated with hyper-responsiveness to  
 CC and/or increased levels of, adenosine and/or levels of adenosine A  
 CC receptor(s), and/or asthma and/or lung allergies associated with  
 CC inflammation or an inflammatory disease. The respiratory or lung disease  
 CC is chosen from airway inflammation, allergy, asthma, impeded respiration,  
 CC cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),  
 CC allergic rhinitis, acute respiratory distress syndrome, pulmonary  
 CC hypertension, lung inflammation, bronchitis, airway obstruction or  
 CC bronchoconstriction. This sequence represents an oligonucleotide of the  
 CC invention.  
 XX  
 SQ Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 U; 0 Other;  
 XX  
 Query Match 2.0%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 732 AGCTGGACTACAGCGGCC 751  
 DB 1 AGCTGGACTACAGCGGCC 20  
 RESULT 555  
 ADO46449  
 ID ADO46449 standard; DNA; 20 BP.  
 XX  
 AC ADO46449;  
 XX



DT 15-JUL-2004 (first entry)  
 XX Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 DE Mismatches 20; Conservative 0; Indels 0; Gaps 0;  
 XX Human oligonucleotide #1815.  
 XX Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;  
 KM CCR1; CCR3; Eotaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;  
 KM tryptase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease;  
 KM lung disease; hyper-responsiveness; adenosine A receptor;  
 KM asthma; lung allergy; inflammation; inflammatory disease;  
 KM airway inflammation; allergy; impeded respiration; cystic fibrosis; CF;  
 KM chronic obstructive pulmonary disease; COPD; allergic rhinitis;  
 KM acute respiratory distress syndrome; pulmonary hypertension;  
 KM lung inflammation; bronchitis; airway obstruction; bronchoconstriction.  
 XX Homo sapiens.  
 OS US2004049022-A1.  
 XX 11-MAR-2004.  
 PD 25-JUL-2003; 2003US-00627930.  
 PF 23-APR-2002; 2002WO-US013135.  
 PR 23-APR-2002; 2002WO-US013143.  
 PA (NYCE/) NYCE J W.  
 PA (SAND/) SANDRASAGRA A.  
 PA (TANG/) TANG L.  
 PA (AGUI/) AGUILAR D.  
 PA (MILL/) MILLER S.  
 PA (SHAH/) SHAHABUDDIN S.  
 PA (LUHH/) LU H.  
 PA (CONG/) CONG H.  
 XX Nyce JW, Sandrasagra A, Tang L, Aguilar D, Miller S;  
 PI Shahabuddin S, Lu H, Cong H;  
 XX WPI; 2004-293804/27.  
 DR Novel single or multiple target oligonucleotide anti-sense to e.g.  
 PT initiation codon, intron of respiratory disease-relevant gene e.g. CCR1,  
 PT RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.  
 PT asthma.  
 PS Claim 2; SEQ ID NO 1816; 174pp; English.  
 XX The invention relates to oligonucleotides anti-sense to an initiation  
 CC codon, coding region, 5' or 3' intron-exon junction, intron or region  
 CC with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target  
 CC chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)  
 CC -5 receptor, CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,  
 CC tryptase a, tryptase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention  
 CC also relates to a method of screening a candidate compound that binds to  
 CC one or more nucleic acid target(s) or expressed product(s), for the  
 CC prevention and/or treatment of a respiratory or lung disease. The  
 CC oligonucleotides are useful for reducing or inhibiting expression of a  
 CC gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,  
 CC CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, tryptase a,  
 CC tryptase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are  
 CC useful for preventing or treating a respiratory or lung disease. The  
 CC respiratory or lung disease is associated with hyper-responsiveness to  
 CC and/or increased levels of, adenosine and/or levels of adenosine A  
 CC receptor(s), and/or asthma and/or lung allergies associated with  
 CC inflammation or an inflammatory disease. The respiratory or lung disease  
 CC is chosen from airway inflammation, allergy, asthma, impeded respiration,  
 CC cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),  
 CC allergic rhinitis, acute respiratory distress syndrome, pulmonary  
 CC hyperextension, lung inflammation, bronchitis, airway obstruction or  
 CC bronchoconstriction. This sequence represents an oligonucleotide of the  
 CC invention.  
 XX Sequence 20 BP; 2 A; 12 C; 2 G; 4 T; 0 U; 0 Other;  
 SQ

Query Match 2.0%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 369 TCACCTGCTCAGCTCCC 388  
 Db 1 TCACCTGCTCAGCTCCC 20  
 RESULT 556  
 ADO46450  
 ID ADO46450 standard; DNA; 20 BP.  
 AC ADO46450;  
 XX 15-JUL-2004 (first entry)  
 XX Human oligonucleotide #1816.  
 DE Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;  
 KM CCR1; CCR3; Eotaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;  
 KM tryptase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease;  
 KM lung disease; hyper-responsiveness; adenosine A receptor;  
 KM asthma; lung allergy; inflammation; inflammatory disease;  
 KM airway inflammation; allergy; impeded respiration; cystic fibrosis; CF;  
 KM chronic obstructive pulmonary disease; COPD; allergic rhinitis;  
 KM acute respiratory distress syndrome; pulmonary hypertension;  
 KM lung inflammation; bronchitis; airway obstruction; bronchoconstriction.  
 XX Homo sapiens.  
 OS US2004049022-A1.  
 XX 11-MAR-2004.  
 PD 25-JUL-2003; 2003US-00627930.  
 PF 23-APR-2002; 2002WO-US013135.  
 PR 23-APR-2002; 2002WO-US013143.  
 PA (NYCE/) NYCE J W.  
 PA (SAND/) SANDRASAGRA A.  
 PA (TANG/) TANG L.  
 PA (AGUI/) AGUILAR D.  
 PA (MILL/) MILLER S.  
 PA (SHAH/) SHAHABUDDIN S.  
 PA (LUHH/) LU H.  
 PA (CONG/) CONG H.  
 XX Nyce JW, Sandrasagra A, Tang L, Aguilar D, Miller S;  
 PI Shahabuddin S, Lu H, Cong H;  
 XX WPI; 2004-293804/27.  
 DR Novel single or multiple target oligonucleotide anti-sense to e.g.  
 PT initiation codon, intron of respiratory disease-relevant gene e.g. CCR1,  
 PT RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.  
 PT asthma.  
 PS Claim 2; SEQ ID NO 1817; 174pp; English.  
 XX The invention relates to oligonucleotides anti-sense to an initiation  
 CC codon, coding region, 5' or 3' intron-exon junction, intron or region  
 CC with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target  
 CC chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)  
 CC -5 receptor, CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,  
 CC tryptase a, tryptase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention  
 CC also relates to a method of screening a candidate compound that binds to  
 CC one or more nucleic acid target(s) or expressed product(s), for the  
 CC prevention and/or treatment of a respiratory or lung disease. The  
 CC oligonucleotides are useful for reducing or inhibiting expression of a  
 CC gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,  
 CC CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, tryptase a,  
 CC tryptase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are  
 CC useful for preventing or treating a respiratory or lung disease. The  
 CC respiratory or lung disease is associated with hyper-responsiveness to  
 CC and/or increased levels of, adenosine and/or levels of adenosine A  
 CC receptor(s), and/or asthma and/or lung allergies associated with  
 CC inflammation or an inflammatory disease. The respiratory or lung disease  
 CC is chosen from airway inflammation, allergy, asthma, impeded respiration,  
 CC cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),  
 CC allergic rhinitis, acute respiratory distress syndrome, pulmonary  
 CC hyperextension, lung inflammation, bronchitis, airway obstruction or  
 CC bronchoconstriction. This sequence represents an oligonucleotide of the  
 CC invention.  
 XX Sequence 20 BP; 2 A; 12 C; 2 G; 4 T; 0 U; 0 Other;  
 SQ

CC tryptase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are  
 CC useful for preventing or treating a respiratory or lung disease. The  
 CC respiratory or lung disease is associated with hyper-responsiveness to  
 CC and/or increased levels of, adenosine and/or levels of adenosine A  
 CC receptor(s), and/or asthma and/or lung allergies associated with  
 CC inflammation or an inflammatory disease. The respiratory or lung disease  
 CC is chosen from airway inflammation, allergy, asthma, impeded respiration,  
 CC cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),  
 CC allergic rhinitis, acute respiratory distress syndrome, pulmonary  
 CC hypertension, lung inflammation, bronchitis, airway obstruction or  
 CC bronchoconstriction. This sequence represents an oligonucleotide of the  
 CC invention.

CC Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+03; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 379 TCAGCCTCCCAAGTGTGG 398  
 |||||  
 1 TCAGCCTCCCAAGTGTGG 20

RESULT 557

ADO81016/C

ID ADO81016 standard; DNA; 20 BP.

XX ADO81016;

DT 29-JUL-2004 (first entry)

XX Human prion protein microsatellite locus primer #12.

DE gene typing; polymorphic microsatellite loci; PMU;

KM disease predisposition; microsatellite marker; prion disease;

KW cystic fibrosis; malignant hyperthermia syndrome; metabolic disease;

KM milk protein; hormone; transcription factor; pT7-blue-vector; human;

KW microsatellite; PCR; primer; ss.

XX Homo sapiens.

OS DE10236711-A1.

XX 26-FEB-2004.

PD 09-AUG-2002; 2002DE-01036711.

XX 09-AUG-2002; 2002DE-01036711.

PR (UYHO-) UNIV HOHENHEIM.

XX Geldermann H, Preuss S, Han Y;

PI WPI; 2004-215730/21.

XX Typing genes that contain polymorphic microsatellite loci, useful for

PT identifying predisposition to disease, by amplification and determining

PT length of amplicons.

XX Example 3; Page 34; 64pp; German.

XX The invention describes a method of typing (M1) a gene (I) that has one

CC or more polymorphic microsatellite loci (PMU). The method comprises: PCR

CC amplification of at least one DNA region of (I) that includes PMU, using

CC as template a DNA sample containing at least one segment of (I); and

CC determining the length of the resulting amplicon(s). Also described are:

CC a method of determining (M2) microsatellite markers (MM) for

CC predisposition to a disease, associated with a gene that includes one or

CC more PMU; and diagnosis (M3) of diseases associated with gene that

CC include PMU. The method is used to identify microsatellite markers, in a

CC disease-related gene, that are associated with a predisposition to

CC diseases and for diagnosis of such diseases, especially prion diseases

CC but also cystic fibrosis, malignant hyperthermia syndrome in pigs and  
 CC metabolic diseases; also to type genes that encode milk proteins,  
 CC hormones or transcription factors. The method is simpler, quicker and  
 CC particularly less expensive than known methods based on sequencing. This  
 CC sequence represents a primer used to genotype a region of the human prion  
 CC protein (PrP) comprising a polymorphic microsatellite locus.

CC Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+03; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 725 CCTGAGTAGCTGGAGCTACA 744  
 |||||  
 DB 20 CCTGAGTAGCTGGAGCTACA 1

RESULT 558

ADO52209

ID ADO52209 standard; DNA; 20 BP.

XX ADO52209;

DT 12-AUG-2004 (first entry)

XX Human inhibitor of apoptosis-like antisense oligonucleotide seqid 83.

DE cytosolic; gene therapy; inhibitors of apoptosis-like; IAP-like;

KW IAP-like modulator; IAP-like associated disorder;

KW hyperproliferative disorder; human; antisense oligonucleotide;

KW antisense technology; ss.

XX Homo sapiens.

OS modified\_base

FT Key Location/Qualifiers

FT modified\_base 1..20

FT /\*tag= b

FT /mod\_base= OTHER

FT /note= "OTHER= Phosphorothioate backbone. All cytidines

FT are 5-methylcytidines"

FT modified\_base 1..5

FT /\*tag= a

FT /mod\_base= OTHER

FT /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"

FT modified\_base 15..20

FT /\*tag= c

FT /mod\_base= OTHER

FT /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"

XX US2004102395-A1.

XX 27-MAY-2004.

XX 22-NOV-2002; 2002US-00303325.

XX 22-NOV-2002; 2002US-00303325.

XX (ISIS-) ISIS PHARM INC.

XX Bennett CF, Dobie KW;

XX WPI; 2004-399725/37.

XX New compound targeted to a nucleic acid molecule encoding inhibitors of

XX apoptosis (IAP)-like and inhibits expression of IAP-like, useful for

XX PT modulating the expression of IAP-like or for treating, e.g.

XX PT hyperproliferative disorder.

XX Example 14; SEQ ID NO 83; 58pp; English.

XX The invention describes a compound 8-80 nucleobases in length targeted to

XX a nucleic acid molecule encoding inhibitors of apoptosis (IAP)-like,

XX

CC

CC where the compound specifically hybridizes with the nucleic acid molecule  
CC encoding IAP-like comprising 1600 bp (SEQ ID NO. 4) and inhibits the  
CC expression of IAP-like. Also described are: inhibiting the expression of  
CC IAP-like in cells or tissues; screening for a modulator of IAP-like; a  
CC diagnostic method for identifying a disease state comprising identifying  
CC the presence of IAP-like in a sample using at least one of the primers  
CC selected from 2 sequences comprising SEQ ID NO. 5 or 6, or the probe  
CC comprising SEQ ID NO. 7; a kit or assay device comprising the compound,  
CC and treating an animal having a disease or condition associated with IAP-  
CC like. The compound is useful for modulating the expression of IAP-like.  
CC It is also useful for diagnosing or treating diseases associated with  
CC expression of IAP-like, e.g. a hyperproliferative disorder. This sequence  
CC represents a human inhibitor of apoptosis (IAP)-like antisense  
CC oligonucleotide.  
XX  
SQ Sequence 20 BP; 3 A; 9 C; 3 G; 5 T; 0 U; 0 Other;  
Query Match 2.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.le+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 969 CTCGGCTCACTGCACTCT 988  
DB 1 CTCGGCTCACTGCACTCT 20  
RESULT 559  
AD052273/C  
ID AD052273 standard; DNA; 20 BP.  
XX  
XX AD052273;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Human inhibitor of apoptosis-like antisense oligonucleotide seqid 149.  
XX  
XX cytosolic; gene therapy; inhibitors of apoptosis-like; IAP-like;  
XX IAP-like modulator; IAP-like associated disorder;  
XX hyperproliferative disorder; human; antisense oligonucleotide;  
XX antisense technology; ss.  
XX  
XX Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT 1..20  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "OTHER= Phosphorothioate backbone. All cytidines  
FT are 5-methylcytidines"  
FT 1..5  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"  
FT 15..20  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"  
XX  
XX US2004102395-A1.  
XX  
XX 27-MAY-2004.  
XX  
XX 22-NOV-2002; 2002US-00303325.  
XX  
XX 22-NOV-2002; 2002US-00303325.  
XX  
XX (ISIS-) ISIS PHARM INC.  
XX  
XX Bennett CF, Dobie KW;  
XX  
XX WPI; 2004-399725/37.  
XX  
XX New compound targeted to a nucleic acid molecule encoding inhibitors of

PT apoptosis (IAP)-like and inhibits expression of IAP-like, useful for  
PT modulating the expression of IAP-like or for treating, e.g.  
PT hyperproliferative disorder.  
XX  
XX Example 14; SEQ ID NO 147; 58bp; English.  
XX  
XX The invention describes a compound 8-80 nucleobases in length targeted to  
XX a nucleic acid molecule encoding inhibitors of apoptosis (IAP)-like,  
XX where the compound specifically hybridizes with the nucleic acid molecule  
XX encoding IAP-like comprising 1600 bp (SEQ ID NO. 4) and inhibits the  
XX expression of IAP-like. Also described are: inhibiting the expression of  
XX IAP-like in cells or tissues; screening for a modulator of IAP-like; a  
XX diagnostic method for identifying a disease state comprising identifying  
XX the presence of IAP-like in a sample using at least one of the primers  
XX selected from 2 sequences comprising SEQ ID NO. 5 or 6, or the probe  
XX comprising SEQ ID NO. 7; a kit or assay device comprising the compound,  
XX and treating an animal having a disease or condition associated with IAP-  
XX like. The compound is useful for modulating the expression of IAP-like.  
XX It is also useful for diagnosing or treating diseases associated with  
XX expression of IAP-like, e.g. a hyperproliferative disorder. This sequence  
XX represents a human inhibitor of apoptosis (IAP)-like antisense  
XX oligonucleotide.  
XX  
SQ Sequence 20 BP; 5 A; 3 C; 9 G; 3 T; 0 U; 0 Other;  
Query Match 2.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.le+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 969 CTCGGCTCACTGCACTCT 988  
DB 20 CTCGGCTCACTGCACTCT 1  
RESULT 560  
AAV27991/C  
ID AAV27991 standard; DNA; 21 BP.  
XX  
XX AAV27991;  
XX  
DT 25-SEP-1998 (first entry)  
XX  
DE Ataxia telangiectasia exon 17 primer 2.  
XX  
XX ss; PCR; primer; amplification; ataxia telangiectasia; diagnosis; human;  
XX radiation; breast cancer.  
XX  
XX Synthetic.  
XX Homo sapiens.  
XX WO9822621-A1.  
XX  
XX 28-MAY-1998.  
XX  
XX 17-NOV-1997; 97WO-US020953.  
XX  
XX 20-NOV-1996; 96US-00753147.  
XX  
XX (VIRG-) VIRGINIA MASON RES CENT.  
XX  
XX Concannon P;  
XX  
XX WPI; 1998-312503/27.  
XX  
XX Method of detecting ataxia telangiectasia - comprises use of primers  
XX based on intron-exon boundaries, useful for diagnosing disease in  
XX heterozygotes.  
XX  
XX Claim 6; Page 6; 47pp; English.  
XX  
XX The primers AAV27964-V28066 are used to amplify ataxia telangiectasia  
XX (ATM) exons and their adjacent splice junction sites. These can be used  
XX as a method of detecting a mutation in the ATM gene by comparing the PCR

CC products of amplification from a sample from a patient suspected of  
CC having an ATM mutation with a sample from a non-mutated ATM patient. This  
CC method is especially useful for diagnosing ataxia telangiectasia in  
CC heterozygotes and can be used to locate the positions of the mutation.  
CC The diagnosis of ataxia telangiectasia in patients needing therapeutic  
CC radiation will prevent fatal radiation burns and the development of  
CC breast cancer which can occur

XX  
SQ Sequence 21 BP; 3 A; 10 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 643 CCCAGGCTGAGTGCAGTGG 662  
|||  
DB 21 CCCAGGCTGAGTGCAGTGG 2

RESULT 561  
AAZ25145  
ID AAZ25145 standard; DNA; 21 BP.

XX AAZ25145;  
XX  
DT 13-DEC-1999 (first entry)

DE Human short interspersed repetitive element PCR primer #3.

XX Human; short interspersed repetitive element; SINE; PCR; primer;  
XX Oncohychnus; restriction primer; short interspersed repeated sequence;  
XX eukaryote; restricted polymerase chain reaction fingerprinting;  
XX identification; DNA specimen; discrimination; ss.

XX Synthetic.  
XX Homo sapiens.

XX JP2913035-B1.

XX 28-JUN-1999.

XX 10-JUL-1998; 98JP-00195692.

XX 10-JUL-1998; 98JP-00195692.

XX (NORQ) NORINSUISANSO SUIANCHO YOSHOKU KENKYUSHOCHO.

XX WPI; 1999-583348/50.

XX Restriction primer for distinguishing individuals with short interspersed  
XX repeated sequence of eukaryotes by restricted polymerase chain reaction  
XX fingerprinting.

XX Claim 6; Page 3; 17pp; Japanese.

XX The present invention describes a restriction primer for eukaryotic short  
XX interspersed repeated sequences (SINE), which has one or more additional  
XX bases that are a mismatch to, or are unrelated to, the 3'-terminal end of  
XX the SINE. The annealing temperature of the primer to the DNA sequence is  
XX kept higher than the fusion temperature of the primer during polymerase  
XX chain reaction (PCR). The PCR fragments obtained are subjected to  
XX electrophoresis to obtain a fingerprint. By comparing the polymorphs from  
XX the electrophoresis band pattern, eukaryotic individuals are  
XX distinguished. The primer is used for amplifying a eukaryotic  
XX deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by  
XX polymerase chain reaction (PCR) fingerprinting. In particular it may be  
XX used individual identification of humans for medical and legal  
XX applications and ecological studies. DNA specimens in traces  
XX (approximately 10 ng in mass) can be used for individual discrimination  
XX of eukaryotes using the primer in a polymerase chain reaction (PCR).

XX AAZ25143 to AAZ25191 represent specifically claimed examples of primers  
XX from the present invention

SQ Sequence 21 BP; 5 A; 5 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 20; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 868 GGATTACAGCGGTAGCCAC 887  
|||  
DB 1 GGATTACAGCGGTAGCCAC 20

RESULT 562

AAZ25143  
ID AAZ25143 standard; DNA; 21 BP.

XX AAZ25143;  
XX

DT 13-DEC-1999 (first entry)

DE Human short interspersed repetitive element PCR primer #1.

XX Human; short interspersed repetitive element; SINE; PCR; primer;  
XX Oncohychnus; restriction primer; short interspersed repeated sequence;  
XX eukaryote; restricted polymerase chain reaction fingerprinting;  
XX identification; DNA specimen; discrimination; ss.

XX Synthetic.  
XX Homo sapiens.

XX JP2913035-B1.

XX 28-JUN-1999.

XX 10-JUL-1998; 98JP-00195692.

XX 10-JUL-1998; 98JP-00195692.

XX (NORQ) NORINSUISANSO SUIANCHO YOSHOKU KENKYUSHOCHO.

XX WPI; 1999-583348/50.

XX Restriction primer for distinguishing individuals with short interspersed  
XX repeated sequence of eukaryotes by restricted polymerase chain reaction  
XX fingerprinting.

XX Claim 6; Page 3; 17pp; Japanese.

XX The present invention describes a restriction primer for eukaryotic short  
XX interspersed repeated sequences (SINE), which has one or more additional  
XX bases that are a mismatch to, or are unrelated to, the 3'-terminal end of  
XX the SINE. The annealing temperature of the primer to the DNA sequence is  
XX kept higher than the fusion temperature of the primer during polymerase  
XX chain reaction (PCR). The PCR fragments obtained are subjected to  
XX electrophoresis to obtain a fingerprint. By comparing the polymorphs from  
XX the electrophoresis band pattern, eukaryotic individuals are  
XX distinguished. The primer is used for amplifying a eukaryotic  
XX deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by  
XX polymerase chain reaction (PCR) fingerprinting. In particular it may be  
XX used individual identification of humans for medical and legal  
XX applications and ecological studies. DNA specimens in traces  
XX (approximately 10 ng in mass) can be used for individual discrimination  
XX of eukaryotes using the primer in a polymerase chain reaction (PCR).

XX AAZ25143 to AAZ25191 represent specifically claimed examples of primers  
XX from the present invention

SQ Sequence 21 BP; 6 A; 5 C; 7 G; 3 T; 0 U; 0 Other;  
Query Match 2.0%; Score 20; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 868 GGATTACAGCGGTAGCCAC 887  
|||

DB 1 GGATTACAGCGGTAGCCAC 20

RESULT 563

AAZ25144

ID AAZ25144 standard; DNA; 21 BP.

XX

AC AAZ25144;

XX

DT 13-DEC-1999 (first entry)

XX

DE Human short interspersed repetitive element PCR primer #2.

XX

KW Human; short interspersed repetitive element; SINE; PCR; primer;

XX

KW Oncohychnus; restriction primer; short interspersed repeated sequence;

KW eukaryote; restricted polymerase chain reaction fingerprinting;

KW identification; DNA specimen; discrimination; ss.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN JP2913035-B1.

XX

PD 28-JUN-1999.

XX

PF 10-JUL-1998; 98JP-00195692.

XX

PR 10-JUL-1998; 98JP-00195692.

XX

PR (NORO) NORINSUISANSO SUIANCHO YOSHOKU KENKYUSHOCHO.

XX

PA WPI; 1999-58348/50.

XX

DR Restriction primer for distinguishing individuals with short interspersed

PT repeated sequence of eukaryotes by restricted polymerase chain reaction

PT fingerprinting.

XX

PS Claim 6; Page 3; 17pp; Japanese.

XX

CC The present invention describes a restriction primer for eukaryotic short

CC interspersed repeated sequences (SINE), which has one or more additional

CC bases that are a mismatch to, or are unrelated to, the 3'-terminal end of

CC the SINE. The annealing temperature of the primer to the DNA sequence is

CC kept higher than the fusion temperature of the primer during polymerase

CC chain reaction (PCR). The PCR fragments obtained are subjected to

CC electrophoresis to obtain a fingerprint. By comparing the polymorphs from

CC the electrophoresis band pattern, eukaryotic individuals are

CC distinguished. The primer is used for amplifying a eukaryotic

CC deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by

CC polymerase chain reaction (PCR) fingerprinting. In particular it may be

CC used in individual identification of humans for medical and legal

CC applications and ecological studies. DNA specimens in traces

CC (approximately 10 ng in mass) can be used for individual discrimination

CC of eukaryotes using the primer in a polymerase chain reaction (PCR).

CC AAZ25143 to AAZ25191 represent specifically claimed examples of primers

CC from the present invention

XX

SQ Sequence 21 BP; 5 A; 5 C; 8 G; 3 T; 0 U; 0 Other;

XX

Query Match 2.0%; Score 20; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 868 GGATTACAGCGGTAGCCAC 887

DB 1 GGATTACAGCGGTAGCCAC 20

RESULT 564

ADG70428/c

ID ADG70428 standard; DNA; 21 BP.

XX

AC ADG70428;

XX

DT 11-MAR-2004 (first entry)

XX

DE REN-34 SNP binding area oligo #2.

XX

XX

KW ANGE; CLUD8; CLUD7; ANGE-CLUD8; ANGE-CLUD7; CLUD7-CLUD8;

KW ANGE-CLUD8-CLUD7; antiallergic; antiallergic; dermatological;

KW antipyretic; antiinflammatory; gene therapy; IGE-mediated disease;

KW REN-34; ss.

XX

OS Unidentified.

OS

PN WO2003000727-A2.

XX

PD 03-JAN-2003.

XX

PF 21-JUN-2002; 2002WO-GB002859.

XX

PR 21-JUN-2001; 2001GB-00015211.

PR 21-JUN-2001; 2001GB-00015212.

PR 21-JUN-2001; 2001GB-00015213.

XX

PA (ISIS-) ISIS INNOVATIONS LTD.

XX

PI Zhang Y, Moffatt M, Cookson W, Tinsley J;

XX

DR WPI; 2003-201405/19.

XX

PT New nucleic acid sequence comprising an ANGE, CLUD8 or CLUD7 mRNA, or

PT their hybrid, useful for screening agents for treating IGE-mediated

PT diseases, e.g. asthma, atopy, hay fever, eczema, atopic dermatitis, or

PT allergic rhinitis.

XX

PS Disclosure; Page 429; 429pp; English.

XX

CC The invention relates to a novel isolated or recombinant nucleic acid

CC sequence comprising an ANGE, CLUD8 or CLUD7 mRNA, or ANGE-CLUD8, ANGE-

CC CLUD7, CLUD7-CLUD8, or ANGE-CLUD8-CLUD7 hybrid mRNA sequence, its

CC complement, homologue or fragment. The novel nucleic acid sequences have

CC the following activities: antiallergic, antiallergic, dermatological,

CC antipyretic, and antiinflammatory. The nucleic acids of the invention may

CC be used in gene therapy to treat disorders. The nucleic acid sequences

CC are useful for screening agents that inhibit or enhance activity of an

CC ANGE, CLUD8 or CLUD7 gene. The agent or antibody is useful for treating

CC IGE-mediated diseases, such as asthma, atopy, hay fever, eczema, atopic

CC dermatitis, allergic rhinitis or non-atopic asthma. The antibody is

CC useful in an assay detecting or measuring the polypeptide in the sample.

CC The host cell is useful for producing, regulating and analyzing the

CC polypeptide. The splice variant of ANGE, CLUD8, or CLUD7 is useful for

CC diagnosing an IGE-mediated disease, atopy, a form of atopic disease or

CC non-atopic asthma, or predicting the severity, or predisposition to a

CC disease. This polynucleotide sequence represents an REN-34 SNP binding

CC oligo relating to the invention.

XX

SQ Sequence 21 BP; 5 A; 5 C; 9 G; 2 T; 0 U; 0 Other;

XX

Query Match 2.0%; Score 20; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 685 CTCTGCTCCCGGTTCAAG 704

DB 21 CTCTGCTCCCGGTTCAAG 2

RESULT 565

ADG70427

ID ADG70427 standard; DNA; 21 BP.

XX

AC ADG70427;

XX

DT 11-MAR-2004 (first entry)

DE REN-34 SNP binding area oligo #1.  
 XX  
 KW ANGE: CLD8; CLD7; ANGE-CLD8; ANGE-CLD7; CLD7-CLD8;  
 KW ANGE-CLD8-CLD7; antiallergic; antiasthmatic; dermatological;  
 KW antipyretic; antiinflammatory; gene therapy; IGE-mediated disease;  
 KW REN-34; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN WO2003000727-A2.  
 XX  
 PD 03-JAN-2003.  
 XX  
 PF 21-JUN-2002; 2002WO-GB002859.  
 XX  
 PR 21-JUN-2001; 2001GB-00015211.  
 PR 21-JUN-2001; 2001GB-00015212.  
 PR 21-JUN-2001; 2001GB-00015213.  
 XX  
 PA (ISIS-) ISIS INNOVATIONS LTD.  
 XX  
 PI Zhang Y, Moffatt M, Cookson W, Tinsley J;  
 XX  
 DR WPI; 2003-201405/19.  
 XX  
 PS New nucleic acid sequence comprising an ANGE, CLD8 or CLD7 mRNA, or  
 PT their hybrid, useful for screening agents for treating IGE-mediated  
 PT diseases, e.g. asthma, atopy, hay fever, eczema, atopic dermatitis, or  
 PT allergic rhinitis.  
 XX  
 PS Disclosure; Page 429; 429pp; English.  
 XX  
 CC The invention relates to a novel isolated or recombinant nucleic acid  
 CC sequence comprising an ANGE, CLD8 or CLD7 mRNA, or ANGE-CLD8, ANGE-  
 CC CLD7, CLD7-CLD8, or ANGE-CLD8-CLD7 hybrid mRNA sequence, its  
 CC complement, homologue or fragment. The novel nucleic acid sequences have  
 CC the following activities: antiallergic, antiasthmatic, dermatological,  
 CC antipyretic, and antiinflammatory. The nucleic acids of the invention may,  
 CC be used in gene therapy to treat disorders. The nucleic acid sequences  
 CC are useful for screening agents that inhibit or enhance activity of an  
 CC ANGE, CLD8 or CLD7 gene. The agent or antibody is useful for treating  
 CC IGE-mediated diseases, such as asthma, atopy, hay fever, eczema, atopic  
 CC dermatitis, allergic rhinitis or non-atopic asthma. The antibody is  
 CC useful in an assay detecting or measuring the polypeptide in the sample.  
 CC The host cell is useful for producing, regulating and analyzing the  
 CC polypeptide. The splice variant of ANGE, CLD8, or CLD7 is useful for  
 CC diagnosing an IGE-mediated disease, atopy, a form of atopic disease or  
 CC non-atopic asthma, or predicting the severity, or predisposition to a  
 CC disease. This polynucleotide sequence represents an REN-34 SNP binding  
 CC oligo relating to the invention.  
 XX  
 SO Sequence 21 BP; 2 A; 9 C; 5 G; 5 T; 0 U; 0 Other;  
 Query Match 2.0%; Score 20; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 685 CTCTGCTCCCGGTTCAAG 704  
 DB 1 CTCTGCTCCCGGTTCAAG 20  
 RESULT 566  
 AD011941/c  
 ID AD011941 standard; DNA; 21 BP.  
 XX  
 AC AD011941;  
 XX  
 DT 15-JUL-2004 (first entry)  
 DE Single multiplex PCR primer #1313.  
 XX  
 KW ss; primer; simultaneous amplification;

KW single multiplex polymerase chain reaction; multifactorial disease;  
 KW genetic alteration; pharmacogenetic reaction; genotyping; polymorphism;  
 KW gene expression profiling.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2004033649-A2.  
 XX  
 PD 22-APR-2004.  
 XX  
 PF 07-OCT-2003; 2003WO-US031874.  
 XX  
 PR 07-OCT-2002; 2002US-0417009P.  
 XX  
 PA (UNNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.  
 XX  
 PI Li H, Li J;  
 XX  
 DR WPI; 2004-340914/31.  
 XX  
 PS Designing primers for simultaneous amplification of target DNA fragments  
 PT in a single multiplex polymerase chain reaction, for high throughput  
 PT multiplex DNA sequence amplification, comprises aligning two primers.  
 XX  
 PS Disclosure; Page 39; 120pp; English.  
 XX  
 CC The invention relates to a method of designing primers for simultaneous  
 CC amplification of target DNA fragments in a single multiplex polymerase  
 CC chain reaction by aligning a first primer and a second primer. The method  
 CC comprises: (a) aligning a first primer and a second primer; and (b)  
 CC selecting the first primer where the first primer at its 3' end does not  
 CC contain four or more bases that are perfectly matching to the 3' end  
 CC sequence of the first primer or a second primer, the first primer at its  
 CC 3' end does not contain seven or more bases that are perfectly matching  
 CC except one mismatch to the 3' end sequence of the first primer or the  
 CC second primer, the first primer at its 3' end does not contain six or  
 CC more bases that are perfectly matching to a sequence anywhere of the  
 CC first primer or the second primer, and the first primer at its 3' end  
 CC does not contain eleven or more bases that are perfectly matching except  
 CC one mismatch to a sequence anywhere of the first primer or the second  
 CC primer. The method is useful for designing primers for simultaneous  
 CC amplification of target DNA fragments in a single multiplex polymerase  
 CC chain reaction. It is also useful in the identification of multiple genes  
 CC related to multifactorial diseases, the genome-scale detection of genetic  
 CC alterations, the studies in pharmacogenetic reactions, the genotyping  
 CC genetic polymorphisms in a large population, the gene expression  
 CC profiling in various samples and high throughput genotyping technologies.  
 CC This sequence corresponds to an example of a primer of the invention.  
 XX  
 SO Sequence 21 BP; 4 A; 6 C; 6 G; 5 T; 0 U; 0 Other;  
 Query Match 2.0%; Score 20; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 545 AGCCTCCCAAGTAGCTGGGA 564  
 DB 20 AGCCTCCCAAGTAGCTGGGA 1  
 RESULT 567  
 AA225153  
 ID AA225153 standard; DNA; 22 BP.  
 XX  
 AC AA225153;  
 XX  
 DT 13-DEC-1999 (first entry)  
 DE Human short interspersed repetitive element PCR primer #11.  
 XX  
 KW Human; short interspersed repetitive element; SINE; PCR; primer;  
 KW OncoRhynchus; restriction primer; short interspersed repeated sequence;  
 KW eukaryote; restricted polymerase chain reaction fingerprinting;

```
KW identification; DNA specimen; discrimination; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX JP2913035-B1.
XX
XX 28-JUN-1999.
XX
XX 10-JUL-1998; 98UP-00195692.
XX
XX 10-JUL-1998; 98UP-00195692.
XX
XX (NORQ ) NORINSUISANSHO SUIANCHO YOSHOKU KENKYUSHOCHO.
XX
XX WPI; 1999-583348/50.
XX
XX Restriction primer for distinguishing individuals with short interspersed
XX repeated sequence of eukaryotes by restricted polymerase chain reaction
XX fingerprinting.
XX
XX Claim 6; Page 3; 17pp; Japanese.
XX
XX The present invention describes a restriction primer for eukaryotic short
XX interspersed repeated sequences (SINE), which has one or more additional
XX bases that are a mismatch to, or are unrelated to, the 3'-terminal end of
XX the SINE. The annealing temperature of the primer to the DNA sequence is
XX kept higher than the fusion temperature of the primer during polymerase
XX chain reaction (PCR). The PCR fragments obtained are subjected to
XX electrophoresis to obtain a fingerprint. By comparing the polymorphs from
XX the electrophoresis band pattern, eukaryotic individuals are
XX distinguished. The primer is used for amplifying a eukaryotic
XX deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by
XX polymerase chain reaction (PCR) fingerprinting. In particular it may be
XX used individual identification of humans for medical and legal
XX applications and ecological studies. DNA specimens in traces
XX (approximately 10 ng in mass) can be used for individual discrimination
XX of eukaryotes using the primer in a polymerase chain reaction (PCR).
XX AA25143 to AA25191 represent specifically claimed examples of primers
XX from the present invention
XX
SQ Sequence 22 BP; 5 A; 5 C; 7 G; 5 T; 0 U; 0 Other;
XX
Query Match 2.0%; Score 20; DB 1; Length 22;
Best Local Similarity 100.0%; Pred No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 868 GGATTACAGGCGTGAGCCAC 887
DB 1 GGATTACAGGCGTGAGCCAC 20
XX
RESULT 568
AA25148
ID AA25148 standard; DNA; 22 BP.
XX
XX AA25148;
XX
XX 13-DEC-1999 (first entry)
XX
XX Human short interspersed repetitive element PCR primer #6.
XX
XX Human short interspersed repetitive element; SINE; PCR; primer;
XX Oncothychnus; restriction primer; short interspersed repeated sequence;
XX eukaryote; restricted polymerase chain reaction fingerprinting;
XX identification; DNA specimen; discrimination; ss.
XX
XX Synthetic.
XX OS Homo sapiens.
XX
XX JP2913035-B1.
XX
XX 28-JUN-1999.
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XX
XX 10-JUL-1998; 98UP-00195692.
XX
XX 10-JUL-1998; 98UP-00195692.
XX
XX (NORQ ) NORINSUISANSHO SUIANCHO YOSHOKU KENKYUSHOCHO.
XX
XX WPI; 1999-583348/50.
XX
XX Restriction primer for distinguishing individuals with short interspersed
XX repeated sequence of eukaryotes by restricted polymerase chain reaction
XX fingerprinting.
XX
XX Claim 6; Page 3; 17pp; Japanese.
XX
XX The present invention describes a restriction primer for eukaryotic short
XX interspersed repeated sequences (SINE), which has one or more additional
XX bases that are a mismatch to, or are unrelated to, the 3'-terminal end of
XX the SINE. The annealing temperature of the primer to the DNA sequence is
XX kept higher than the fusion temperature of the primer during polymerase
XX chain reaction (PCR). The PCR fragments obtained are subjected to
XX electrophoresis to obtain a fingerprint. By comparing the polymorphs from
XX the electrophoresis band pattern, eukaryotic individuals are
XX distinguished. The primer is used for amplifying a eukaryotic
XX deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by
XX polymerase chain reaction (PCR) fingerprinting. In particular it may be
XX used individual identification of humans for medical and legal
XX applications and ecological studies. DNA specimens in traces
XX (approximately 10 ng in mass) can be used for individual discrimination
XX of eukaryotes using the primer in a polymerase chain reaction (PCR).
XX AA25143 to AA25191 represent specifically claimed examples of primers
XX from the present invention
XX
SQ Sequence 22 BP; 6 A; 6 C; 7 G; 3 T; 0 U; 0 Other;
XX
Query Match 2.0%; Score 20; DB 1; Length 22;
Best Local Similarity 100.0%; Pred No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 868 GGATTACAGGCGTGAGCCAC 887
DB 1 GGATTACAGGCGTGAGCCAC 20
XX
RESULT 569
AA25154
ID AA25154 standard; DNA; 22 BP.
XX
XX AA25154;
XX
XX 13-DEC-1999 (first entry)
XX
XX Human short interspersed repetitive element PCR primer #12.
XX
XX Human short interspersed repetitive element; SINE; PCR; primer;
XX Oncothychnus; restriction primer; short interspersed repeated sequence;
XX eukaryote; restricted polymerase chain reaction fingerprinting;
XX identification; DNA specimen; discrimination; ss.
XX
XX Synthetic.
XX OS Homo sapiens.
XX
XX JP2913035-B1.
XX
XX 28-JUN-1999.
XX
XX 10-JUL-1998; 98UP-00195692.
XX
XX 10-JUL-1998; 98UP-00195692.
XX
XX (NORQ ) NORINSUISANSHO SUIANCHO YOSHOKU KENKYUSHOCHO.
XX
XX WPI; 1999-583348/50.
XX
```

XX Restriction primer for distinguishing individuals with short interspersed  
PT repeated sequence of eukaryotes by restricted polymerase chain reaction  
PT fingerprinting.  
PS Claim 6, Page 3, 17pp; Japanese.  
XX The present invention describes a restriction primer for eukaryotic short  
CC interspersed repeated sequences (SINE), which has one or more additional  
CC bases that are a mismatch to, or are unrelated to, the 3'-terminal end of  
CC the SINE. The annealing temperature of the primer to the DNA sequence is  
CC kept higher than the fusion temperature of the primer during polymerase  
CC chain reaction (PCR). The PCR fragments obtained are subjected to  
CC electrophoresis to obtain a fingerprint. By comparing the polymorphs from  
CC the electrophoresis band pattern, eukaryotic individuals are  
CC distinguished. The primer is used for amplifying a eukaryotic  
CC deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by  
CC polymerase chain reaction (PCR) fingerprinting. In particular it may be  
CC used for individual identification of humans for medical and legal  
CC applications and ecological studies. DNA specimens in traces  
CC (approximately 10 ng in mass) can be used for individual discrimination  
CC of eukaryotes using the primer in a polymerase chain reaction (PCR).  
CC AA25143 to AA25191 represent specifically claimed examples of primers  
CC from the present invention  
XX  
SQ Sequence 22 BP; 5 A; 6 C; 7 G; 4 T; 0 U; 0 Other;  
  
Query Match 2.0%; Score 20; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 868 GGATTACAGCGCTGAGCCAC 887  
DB 1 GGATTACAGCGCTGAGCCAC 20  
  
RESULT 570  
AA25150  
ID AA25150 standard; DNA; 22 BP.  
XX  
AC AA25150;  
XX  
DT 13-DEC-1999 (first entry)  
XX  
DE Human short interspersed repetitive element PCR primer #8.  
XX  
KM Human; short interspersed repetitive element; SINE; PCR; primer;  
KM Oncorhynchus; restriction primer; short interspersed repeated sequence;  
KM eukaryote; restricted polymerase chain reaction fingerprinting;  
KM identification; DNA specimen; discrimination; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN JP2913035-B1.  
XX  
PD 28-JUN-1999.  
XX  
PF 10-JUL-1998; 98JP-00195692.  
XX  
PR 10-JUL-1998; 98JP-00195692.  
XX  
PS (NORQ) NORINSUISANSO SUISANCHO YOSHOKU KENKYUSHOCHO.  
XX  
DR WPI; 1999-583348/50.  
XX  
PT Restriction primer for distinguishing individuals with short interspersed  
PT repeated sequence of eukaryotes by restricted polymerase chain reaction  
PT fingerprinting.  
XX  
PS Claim 6, Page 3, 17pp; Japanese.  
XX  
CC The present invention describes a restriction primer for eukaryotic short

CC interspersed repeated sequences (SINE), which has one or more additional  
CC bases that are a mismatch to, or are unrelated to, the 3'-terminal end of  
CC the SINE. The annealing temperature of the primer to the DNA sequence is  
CC kept higher than the fusion temperature of the primer during polymerase  
CC chain reaction (PCR). The PCR fragments obtained are subjected to  
CC electrophoresis to obtain a fingerprint. By comparing the polymorphs from  
CC the electrophoresis band pattern, eukaryotic individuals are  
CC distinguished. The primer is used for amplifying a eukaryotic  
CC deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by  
CC polymerase chain reaction (PCR) fingerprinting. In particular it may be  
CC used for individual identification of humans for medical and legal  
CC applications and ecological studies. DNA specimens in traces  
CC (approximately 10 ng in mass) can be used for individual discrimination  
CC of eukaryotes using the primer in a polymerase chain reaction (PCR).  
CC AA25143 to AA25191 represent specifically claimed examples of primers  
CC from the present invention  
XX  
SQ Sequence 22 BP; 5 A; 5 C; 8 G; 4 T; 0 U; 0 Other;  
  
Query Match 2.0%; Score 20; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 868 GGATTACAGCGCTGAGCCAC 887  
DB 1 GGATTACAGCGCTGAGCCAC 20  
  
RESULT 571  
AA25151  
ID AA25151 standard; DNA; 22 BP.  
XX  
AC AA25151;  
XX  
DT 13-DEC-1999 (first entry)  
XX  
DE Human short interspersed repetitive element PCR primer #9.  
XX  
KM Human; short interspersed repetitive element; SINE; PCR; primer;  
KM Oncorhynchus; restriction primer; short interspersed repeated sequence;  
KM eukaryote; restricted polymerase chain reaction fingerprinting;  
KM identification; DNA specimen; discrimination; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN JP2913035-B1.  
XX  
PD 28-JUN-1999.  
XX  
PF 10-JUL-1998; 98JP-00195692.  
XX  
PR 10-JUL-1998; 98JP-00195692.  
XX  
PS (NORQ) NORINSUISANSO SUISANCHO YOSHOKU KENKYUSHOCHO.  
XX  
DR WPI; 1999-583348/50.  
XX  
PT Restriction primer for distinguishing individuals with short interspersed  
PT repeated sequence of eukaryotes by restricted polymerase chain reaction  
PT fingerprinting.  
XX  
PS Claim 6, Page 3, 17pp; Japanese.  
XX  
CC The present invention describes a restriction primer for eukaryotic short  
CC interspersed repeated sequences (SINE), which has one or more additional  
CC bases that are a mismatch to, or are unrelated to, the 3'-terminal end of  
CC the SINE. The annealing temperature of the primer to the DNA sequence is  
CC kept higher than the fusion temperature of the primer during polymerase  
CC chain reaction (PCR). The PCR fragments obtained are subjected to  
CC electrophoresis to obtain a fingerprint. By comparing the polymorphs from  
CC the electrophoresis band pattern, eukaryotic individuals are  
CC distinguished. The primer is used for amplifying a eukaryotic



CC deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by  
CC polymerase chain reaction (PCR) fingerprinting. In particular it may be  
CC used individual identification of humans for medical and legal  
CC applications and ecological studies. DNA specimens in traces  
CC (approximately 10 ng in mass) can be used for individual discrimination  
CC of eukaryotes using the primer in a polymerase chain reaction (PCR).  
CC AA25143 to AA25191 represent specifically claimed examples of primers  
CC from the present invention  
XX  
SQ Sequence 22 BP; 5 A; 6 C; 8 G; 3 T; 0 U; 0 Other;  
  
Query Match 2.0%; Score 20; DB 1; Length 22;  
Best local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 868 GGATTACAGCGCTGAGCCAC 887  
DB 1 GGATTACAGCGCTGAGCCAC 20  
  
RESULT 572  
AA25147  
ID AA25147 standard; DNA; 22 BP.  
XX  
AC AA25147;  
XX  
DT 13-DEC-1999 (first entry)  
DE Human short interspersed repetitive element PCR primer #5.  
XX  
XX Human; short interspersed repetitive element; SINE; PCR; primer;  
XX Oncochrysis; restriction primer; short interspersed repeated sequence;  
KW eukaryote; restriction polymerase chain reaction fingerprinting;  
KW identification; DNA specimen; discrimination; ss.  
XX  
XX Synthetic.  
OS Homo sapiens.  
XX  
XX JP2913035-B1.  
PN  
XX 28-JUN-1999.  
PD  
XX 10-JUL-1998; 98JP-00195692.  
PF  
XX 10-JUL-1998; 98JP-00195692.  
PR  
XX 10-JUL-1998; 98JP-00195692.  
XX  
PA (NORO) NORINSUISANSO SUISANCHO YOSHOKU KENKUSHOCHO.  
XX  
XX WPI; 1999-583348/50.  
DR  
XX  
PT Restriction primer for distinguishing individuals with short interspersed  
PT repeated sequence of eukaryotes by restricted polymerase chain reaction  
PT fingerprinting.  
XX  
XX Claim 6; Page 3; 17p; Japanese.  
XX  
CC The present invention describes a restriction primer for eukaryotic short  
CC interspersed repeated sequences (SINE), which has one or more additional  
CC bases that are a mismatch to, or are unrelated to, the 3'-terminal end of  
CC the SINE. The annealing temperature of the primer to the DNA sequence is  
CC kept higher than the fusion temperature of the primer during polymerase  
CC chain reaction (PCR). The PCR fragments obtained are subjected to  
CC electrophoresis to obtain a fingerprint. By comparing the polymorphs from  
CC the electrophoresis band pattern, eukaryotic individuals are  
CC distinguished. The primer is used for amplifying a eukaryotic  
CC deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by  
CC polymerase chain reaction (PCR) fingerprinting. In particular it may be  
CC used individual identification of humans for medical and legal  
CC applications and ecological studies. DNA specimens in traces  
CC (approximately 10 ng in mass) can be used for individual discrimination  
CC of eukaryotes using the primer in a polymerase chain reaction (PCR).  
CC AA25143 to AA25191 represent specifically claimed examples of primers  
CC from the present invention

XX  
SQ Sequence 22 BP; 6 A; 5 C; 7 G; 4 T; 0 U; 0 Other;  
  
Query Match 2.0%; Score 20; DB 1; Length 22;  
Best local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 868 GGATTACAGCGCTGAGCCAC 887  
DB 1 GGATTACAGCGCTGAGCCAC 20  
  
RESULT 573  
ABL55369  
ID ABL55369 standard; DNA; 24 BP.  
XX  
AC ABL55369;  
XX  
DT 23-JUL-2002 (first entry)  
DE Human leucine zipper protein 11.99 RT-PCR primer, SEQ ID NO:3.  
XX  
XX Human; leucine zipper protein 11.99; recombinant production; tumour;  
KW cancer; embryonic development disorder; cytostatic; gene therapy;  
KW reverse transcription-PCR; RT-PCR; primer; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX CN1331194-A.  
PN  
XX 16-JAN-2002.  
PD  
XX 30-JUN-2000; 2000CN-00116898.  
PF  
XX 30-JUN-2000; 2000CN-00116898.  
PR  
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
XX  
XX Mao Y, Xie Y;  
XX  
XX WPI; 2002-292862/34.  
DR  
XX  
PT Polypeptide-human leucine zipper protein 11.99 and polynucleotide for  
PT coding it.  
XX  
XX Example 2; Page 19 (Disclosure); 35p; Chinese.  
XX  
CC The invention relates to human leucine zipper protein 11.99 (AA049285)  
CC and to nucleic acids encoding it (ABL55368). The protein has a molecular  
CC weight of 12 kD. The invention also relates to a method for the  
CC recombinant production of the protein, an antagonist of the protein, and  
CC the use of the protein, gene and antagonist in therapeutic applications.  
CC Leucine zipper protein 11.99 can be used in the treatment of a variety of  
CC diseases such as embryonic development disorders and tumours. Sequences  
CC ABL55369-ABL55370 represent reverse transcription-PCR (RT-PCR) primers  
CC used in an exemplification of the invention to isolate human leucine  
CC zipper protein 11.99 cDNA  
XX  
SQ Sequence 24 BP; 4 A; 5 C; 10 G; 5 T; 0 U; 0 Other;  
  
Query Match 2.0%; Score 20; DB 1; Length 24;  
Best local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 943 CCCAGGCTGAGTGCATGG 962  
DB 1 CCCAGGCTGAGTGCATGG 20  
  
RESULT 574  
ADC56863/c  
ID ADC56863 standard; DNA; 24 BP.  
XX

```

AC ADC56863;
XX
DT 18-DEC-2003 (first entry)
XX
XX RT-PCR primer Seq ID3 related to human protein 8-91.
DE
XX human; protein 8-91; diabetes; cancer; PCR; primer; RT-PCR;
KM reverse transcription PCR; ss.
XX
OS Homo sapiens.
XX
XX CN1381492-A.
XX
XX 27-NOV-2002.
PD
XX
XX 18-APR-2001; 2001CN-00112644.
XX
XX 18-APR-2001; 2001CN-00112644.
XX
XX (BIOM-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
XX Mao Y, Xie Y;
XX
XX WPI; 2003-249017/25.
XX
XX Polypeptide-human ribosomal protein -8.91 and polynucleotide for coding
XX it.
XX
XX Example 3; SEQ ID NO 3; 30pp; Chinese.
XX
XX This invention relates to a novel protein, human protein 8-91, and the
CC DNA sequence encoding it. The protein of the invention may be useful for
CC the treatment of diseases such as diabetes and cancer. The present
CC sequence is that of an RT-PCR primer which was used in the
CC exemplification of the invention.
XX
XX Sequence 24 BP; 4 A; 8 C; 6 G; 6 T; 0 U; 0 Other;
XX
XX
XX Query Match 2.0%; Score 20; DB 1; Length 24;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+03;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 868 GGATTACAGCGGTGAGCCAC 887
DB 24 GGATTACAGCGGTGAGCCAC 5
XX
XX
XX RESULT 575
XX AAH77599
XX ID AAH77599 standard; DNA; 25 BP.
XX
XX AAH77599;
XX
XX 22-OCT-2001 (first entry)
XX
XX Human dihydropyrrrole-5-carboxylate reductase 30 PCR primer 2.
DE
XX Human; dihydropyrrrole-5-carboxylate reductase 30; cancer; cytosolic;
KM human immunodeficiency virus; HIV; infection; immunological disease;
KM inflammatory disease; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX CN1298002-A.
XX
XX 06-JUN-2001.
XX
XX 24-NOV-1999; 99CN-00124090.
XX
XX 24-NOV-1999; 99CN-00124090.
XX
XX (SHAN-) SHANGHAI BORONG GENE DEV CO LTD.
XX

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PI Mao Y, Xie Y;
XX
XX WPI; 2001-483680/54.
XX
XX Human dihydropyrrrole-5-carboxylate reductase 30 as one new kind of
PT polypeptide and polynucleotides encoding this polypeptide.
XX
XX Example 3; Page 16 (disclosure); 26pp; Chinese.
XX
XX The invention relates to a novel polypeptide, human dihydropyrrrole-5-
CC carboxylate reductase 30, polynucleotides encoding this polypeptide and a
CC DNA recombination process to produce the polypeptide. The polypeptide is
CC useful for treating various diseases, such as malignant tumours,
CC nosohaemia, HIV infection, immunological diseases and inflammatory
CC diseases. The invention also provides an antibody against the
CC polypeptide. The present sequence is a primer used to amplify a
CC polynucleotide encoding the polypeptide of the invention
XX
XX Sequence 25 BP; 7 A; 1 C; 5 G; 12 T; 0 U; 0 Other;
XX
XX
XX Query Match 2.0%; Score 20; DB 1; Length 25;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+03;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 770 TTTTGTATTTTGTAGTAGAGA 789
DB 6 TTTTGTATTTTGTAGTAGAGA 25
XX
XX
XX RESULT 576
XX AAF74080
XX ID AAF74080 standard; DNA; 23 BP.
XX
XX AAF74080;
XX
XX 30-APR-2001 (first entry)
XX
XX Primer #14.
XX
XX Solute carrier family 6 neurotransmitter transporter; serotonin 4; SLC6A4;
KM genotyping; allele specific oligonucleotide; ss.
XX
XX Homo sapiens.
XX
XX WO200109161-A1.
XX
XX 08-FEB-2001.
XX
XX 31-JUL-2000; 2000WO-US020638.
XX
XX 29-JUL-1999; 99US-0146290P.
XX
XX (GENA-) GENA1SSANCE PHARM INC.
XX
XX Denton RR, Duda A, Nandabalan K, Sanchis A, Stephens JC;
XX
XX WPI; 2001-123317/13.
XX
XX New isolated polynucleotide comprising a polymorphic variant for the
PT solute carrier family 6 neurotransmitter transporter, serotonin member 4
PT gene for identifying drugs for treating disorders related to expression
PT of the protein.
XX
XX Example 1; Page 33; 152pp; English.
XX
XX The present invention relates to a polymorphic variant of a reference
CC sequence for the solute carrier family 6 neurotransmitter transporter,
CC serotonin member 4 (SLC6A4) gene or a fragment of it or a sequence
CC complementary to the first sequence. The invention is used in producing a
CC recombinant organism that can be used to express SLC6A4 for protein
CC structure analysis and binding studies. A composition comprising a
CC genotyping oligonucleotide is used to detect a polymorphism in the SLC6A4
CC gene

```

XX SQ Sequence 23 BP; 5 A; 3 C; 10 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 19.8; DB 1; Length 23;

Best Local Similarity 91.3%; Pred. No. 1.2e+03; Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 862 GTGCTGGATTACAGCGCTGAGC 864  
DB 1 GTGCTGGATTAGAGCGTGAAC 23

RESULT 577

ADCT9601  
ID ADC79601 standard; DNA; 23 BP.

AC ADC79601;

DT 01-JAN-2004 (first entry)

DE Human p53 forward RT-PCR primer.

XX cytoplasmic; cancer; chemotherapy; carcinoma; tumour; RT-PCR; ss;  
KW primer; primer.

OS Homo sapiens.

PN MO2003035894-A2.

PD 01-MAY-2003.

PF 28-OCT-2002; 2002MO-US034397.

PR 26-OCT-2001; 2001US-0330669P.

PR 04-APR-2002; 2002US-0369945P.

XX (IMMU-) IMMUNIVEST CORP.

PI O'hara SM, Zweitzig D, Foulk B;

DR WPI; 2003-482052/45.

XX Extracting intact cytoplasmic biomolecules e.g. proteins, nucleic acids  
PT from cells, by treating sample comprising cells containing target cells  
PT with permeabilizing agents to release biomolecules and recovering them.

XX Example 10; Page 59; 119pp; English.

XX The invention relates to a novel method for extracting intact cytoplasmic  
CC biomolecules from cells. The method of the invention is useful for  
CC extracting or acquiring cytoplasmic biomolecules such as proteins or  
CC nucleic acids which include cytoplasmic RNA, nuclear and mitochondrial  
CC RNA, nuclear and mitochondrial DNA, cytoplasmic mRNA, or their  
CC combinations from cells. The method is useful in cancer screening,  
CC selecting and monitoring for chemotherapy treatment or cancer recurrence.  
CC This type of cell analysis is useful in cancer diagnostics. The method is  
CC useful in profiling cells isolated from tissues or body fluids and serves  
CC as an adjunct to clinical diagnosis of diverse carcinomas including early  
CC stage detection and classification of circulating tumour cells. The  
CC present sequence is used in the exemplification of the invention.

XX Sequence 23 BP; 3 A; 9 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 19.8; DB 1; Length 23;

Best Local Similarity 91.3%; Pred. No. 1.2e+03; Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 538 CTGCTCAGCTCCCAAGTAGCT 560  
DB 1 CTGCTCAGCTCCGAGTAGCT 23

RESULT 578

ADE44542.  
ID ADE44542 standard; DNA; 23 BP.

AC ADE44542;

DT 29-JAN-2004 (first entry)

DE Primer #1 to amplify the p53 gene for cancer-detection method.

XX ss; primer; diagnosis; cancer; epithelial cell; immunomagnetic particle;  
KW prostate cancer; breast cancer; colon cancer apudoma; choristoma;  
KW branchioma; malignant carcinoid syndrome; carcinoid heart disease;  
KW carcinoma.

OS Homo sapiens.

PN MO2003035895-A2.

PD 01-MAY-2003.

PF 28-OCT-2002; 2002MO-US034570.

PR 26-OCT-2001; 2001US-0330669P.

PR 04-APR-2002; 2002US-0369945P.

XX (IMMU-) IMMUNIVEST CORP.

PI O'hara SM, Zweitzig D, Foulk B;

DR WPI; 2003-421425/39.

XX Diagnosing severity of disease in a test subject, by mixing the sample  
PT comprising cancer cells with immunomagnetic particles and separating cell  
PT fraction to diagnose enriched fraction for the presence of cancer cells.

XX Example 10; Page 59; 105pp; English.

XX The invention relates to a method of diagnosing the severity of a disease  
CC in a test subject, by obtaining a sample having a mixed cell population  
CC suspected of containing cancer cells of epithelial origin, mixing the  
CC sample with immunomagnetic particles which bind specifically to the  
CC cancer cells, subjecting the mixture to produce a separated cell  
CC fraction, and assaying the enriched fraction for the presence of a  
CC cancer cells. The method is useful for diagnosing the severity of a  
CC disease in a test subject. The test subject is for assessment of a  
CC presence of circulating cancer cells. The test subject response to cancer  
CC eradication procedures and is assessed by the presence of circulating  
CC cancer cells. The test subject has been diagnosed with a cancer selected  
CC from prostate cancer, breast cancer, colon cancer apudoma, choristoma,  
CC branchioma, malignant carcinoid syndrome, carcinoid heart disease, and  
CC carcinoma e.g. Walker, basal cell, basosquamous, Brown-Pearce, ductal,  
CC Ehrlich tumor, Krebs 2, Merkel cells, mucinous, and non-small cell lung.  
CC This sequence represents a primer used to amplify a specific gene cDNA  
CC sequence in the method of the invention.

XX Sequence 23 BP; 3 A; 9 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 19.8; DB 1; Length 23;

Best Local Similarity 91.3%; Pred. No. 1.2e+03; Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 538 CTGCTCAGCTCCCAAGTAGCT 560  
DB 1 CTGCTCAGCTCCGAGTAGCT 23

RESULT 579

ADO47348  
ID ADO47348 standard; DNA; 23 BP.

AC ADO47348;

DT 15-JUL-2004 (first entry)

XX Human SORBS1 gene sequencing primer #54.  
 DE ITR sequence; pentanucleotide tandem repeat; stutter artifact;  
 XX ITR sequence; pentanucleotide tandem repeat; stutter artifact;  
 XX DNA typing; DNA profiling; linkage analysis; criminal justice;  
 XX paternity testing; animal lineage analysis; microsatellite loci;  
 XX polymorphism detection; PCR primer; ss.  
 XX Synthetic.  
 OS Homo sapiens.  
 XX OS Homo sapiens.  
 XX W09940194-A1.  
 XX 12-AUG-1999.  
 XX 04-FEB-1999; 99WO-US002345.  
 XX 04-FEB-1998; 98US-00018584.  
 XX (PROM-) PROMEGA CORP.  
 XX Schumm JW, Bacher JW;  
 XX WPI, 1999-590696/50.  
 XX Isolating DNA containing intermediate tandem repeat sequences, useful in  
 PT DNA profiling.  
 XX PS Claim 30; Page 21; 11pp; English.  
 XX This sequence is a PCR primer for a human DNA marker clone used in the  
 CC method of the invention. The method is for isolating a fragment of DNA  
 CC containing an intermediate tandem repeat (ITR) sequence using  
 CC hybridization selection, and comprises: (a) providing several DNA  
 CC fragments, at least one of which contains an ITR sequence, a region of  
 CC the DNA fragment which contains at least one repeat unit consisting of a  
 CC sequence of five, six or seven bases repeated in tandem at least two  
 CC times; (b) providing a stationary support having at least one  
 CC oligonucleotide associated with it, where the oligonucleotide includes a  
 CC sequence of nucleotides which is complementary to a portion of the ITR  
 CC sequence; and (c) combining the DNA fragments with the support under  
 CC conditions where the DNA fragments including the DNA fragment containing  
 CC the ITR sequence hybridize to the support. The method is particularly  
 CC used to isolate DNA containing pentanucleotide tandem repeat sequences as  
 CC well as to detect target ITR DNA sequences having a low incidence of  
 CC stutter artifacts (no more than 2.4%). The method is useful in DNA  
 CC profiling for linkage analysis, criminal justice, paternity testing and  
 CC other forensic and medical uses. DNA typing is also useful for confirming  
 CC the lineage of horses, dogs and other prize animals. The invention  
 CC overcomes problems related to the use of microsatellite loci in DNA  
 CC profiling. The method can detect polymorphisms with a low incidence of  
 CC stutter artifacts, which has previously been a problem in interpreting  
 CC allelic content of loci. The development of markers based on larger  
 CC repeat units, enables easier separation of the fragments on  
 CC electrophoretic gels. This allows the simultaneous analysis of more loci  
 XX  
 SQ Sequence 23 BP; 8 A; 8 C; 4 G; 3 T; 0 U; 0 Other;  
 XX  
 Query Match 2.0%; Score 19.8; DB 1; Length 23;  
 Best Local Similarity 91.3%; Pred. No. 1.2e+03;  
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 870 ATTACAGGCGTGGAGCCACGCG 892  
 DB 1 ATTACAGGCGTGGAGCCACGCG 23  
 RESULT 580  
 AA227796/C  
 ID AA227796 standard; DNA; 24 BP.  
 XX AA227796;  
 XX 23-DEC-1999 (first entry)  
 DT PCR primer for human DNA marker clone G212.  
 DE

XX Tandem repeat sequence; DNA isolation; intermediate tandem repeat;  
 XX ITR sequence; pentanucleotide tandem repeat; stutter artifact;  
 XX DNA typing; DNA profiling; linkage analysis; criminal justice;  
 XX paternity testing; animal lineage analysis; microsatellite loci;  
 XX polymorphism detection; PCR primer; ss.  
 XX Synthetic.  
 OS Homo sapiens.  
 XX OS Homo sapiens.  
 XX W09940194-A1.  
 XX 12-AUG-1999.  
 XX 04-FEB-1999; 99WO-US002345.  
 XX 04-FEB-1998; 98US-00018584.  
 XX (PROM-) PROMEGA CORP.  
 XX Schumm JW, Bacher JW;  
 XX WPI, 1999-590696/50.  
 XX Isolating DNA containing intermediate tandem repeat sequences, useful in  
 PT DNA profiling.  
 XX PS Claim 30; Page 21; 11pp; English.  
 XX This sequence is a PCR primer for a human DNA marker clone used in the  
 CC method of the invention. The method is for isolating a fragment of DNA  
 CC containing an intermediate tandem repeat (ITR) sequence using  
 CC hybridization selection, and comprises: (a) providing several DNA  
 CC fragments, at least one of which contains an ITR sequence, a region of  
 CC the DNA fragment which contains at least one repeat unit consisting of a  
 CC sequence of five, six or seven bases repeated in tandem at least two  
 CC times; (b) providing a stationary support having at least one  
 CC oligonucleotide associated with it, where the oligonucleotide includes a  
 CC sequence of nucleotides which is complementary to a portion of the ITR  
 CC sequence; and (c) combining the DNA fragments with the support under  
 CC conditions where the DNA fragments including the DNA fragment containing  
 CC the ITR sequence hybridize to the support. The method is particularly  
 CC used to isolate DNA containing pentanucleotide tandem repeat sequences as  
 CC well as to detect target ITR DNA sequences having a low incidence of  
 CC stutter artifacts (no more than 2.4%). The method is useful in DNA  
 CC profiling for linkage analysis, criminal justice, paternity testing and  
 CC other forensic and medical uses. DNA typing is also useful for confirming  
 CC the lineage of horses, dogs and other prize animals. The invention  
 CC overcomes problems related to the use of microsatellite loci in DNA  
 CC profiling. The method can detect polymorphisms with a low incidence of  
 CC stutter artifacts, which has previously been a problem in interpreting  
 CC allelic content of loci. The development of markers based on larger  
 CC repeat units, enables easier separation of the fragments on  
 CC electrophoretic gels. This allows the simultaneous analysis of more loci  
 XX  
 SQ Sequence 24 BP; 5 A; 7 C; 6 G; 6 T; 0 U; 0 Other;  
 XX  
 Query Match 2.0%; Score 19.8; DB 1; Length 24;  
 Best Local Similarity 91.3%; Pred. No. 1.3e+03;  
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 638 TGTCCACGAGCTGAGTGCACT 660  
 DB 23 TATCACCGAGCTGAGTGCAAT 1  
 RESULT 581  
 AAA46454/C  
 ID AAA46454 standard; DNA; 24 BP.  
 XX AAA46454;  
 XX 04-SEP-2000 (first entry)  
 DT

XX Oligonucleotide probe used to detect human cells.  
 DE Transactivator; tetracycline-regulated system; promoter; nervous system;  
 XX tyrosine hydroxylase; neurodegeneration; Parkinson's disease;  
 KM nervous system injury; retinal degeneration; probe; ss.  
 XX Synthetic.  
 OS  
 XX WO200028062-A1.  
 PN  
 XX 18-MAY-2000.  
 PD  
 XX 09-NOV-1999; 99WO-FR002752.  
 XX  
 XX 09-NOV-1998; 99FR-00014080.  
 PR 03-MAR-1999; 99US-0122600P.  
 XX  
 XX (AVERT ) AVENTIS PHARMA SA.  
 PA  
 XX Mallet J, Corti O;  
 PI  
 XX WPI; 2000-387422/33.  
 DR  
 XX  
 PT New nucleic acid for regulating gene expression, particularly expression  
 PT of tyrosine hydroxylase for treatment of Parkinson's disease, includes  
 PT the gene and tetracycline transactivator.  
 XX  
 XX Example; Page 24; 51pp; French.  
 PS  
 XX The specification describes a nucleic acid which comprises a region (R1)  
 XX encoding the transactivator (tTA) of the tetracycline-regulated system,  
 XX controlled by a moderate promoter; and a region (R2) comprising a nucleic  
 XX acid of interest under control of a promoter sensitive to tTA. R1 and R2  
 XX are arranged in the same transcriptional orientation. The nucleic acid is  
 XX used to specifically express the nucleic acid of interest in vivo,  
 XX particularly in the nervous system and especially expression of tyrosine  
 XX hydroxylase for treatment of neurodegeneration (Parkinson's disease),  
 XX nervous system injury and retinal degeneration. More generally, it can be  
 XX used to express a very wide range of therapeutic products, e.g. enzymes,  
 XX blood factors, cytokines, tumour suppressors, antibodies etc., for  
 XX (immuno)therapy of infections, cancer, autoimmune diseases, restenosis,  
 XX genetic diseases etc., also antigens for vaccination or antisense  
 XX sequences and ribozymes. The present sequence represents a probe used to  
 XX identify human cells, in the course of the invention  
 XX  
 XX Sequence 24 BP; 4 A; 7 C; 8 G; 4 T; 0 U; 1 Other;  
 SQ  
 Query Match 2.0%; Score 19.8; DB 1; Length 24;  
 Best Local Similarity 91.3%; Pred. No. 1.3e+03;  
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 661 GGGCAATCTTGGCTCACTGCA 683  
 Db 24 GGGCGATCTCGGCTCACTGCA 2

RESULT 582  
 AAH39521  
 ID AAH39521 standard; DNA; 24 BP.  
 XX  
 AC AAH39521;  
 XX  
 DT 14-AUG-2001 (first entry)  
 XX  
 DE SNP specific upper PCR primer SEQ ID 2317.  
 XX  
 XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
 KM SNP; genotyping; agammaglobulinemia; diabetes insipidus; cancer;  
 KM Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;  
 KM polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
 KM acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
 KM inflammation; forensic investigation; paternity analysis; PCR primer; ss.

XX Homo sapiens.  
 OS  
 XX WO200129262-A2.  
 PN  
 XX 26-APR-2001.  
 PD  
 XX 13-OCT-2000; 2000WO-US028436.  
 PR 15-OCT-1999; 99US-0160096P.  
 XX  
 XX (ORCH-) ORCHID BIOSCIENCES INC.  
 PA  
 XX Picoult-Newburg L, Pohl M;  
 PI  
 XX WPI; 2001-290930/30.  
 DR  
 XX  
 PT New genotyping oligonucleotide, useful for detecting the presence,  
 PT absence or identity of single polynucleotide polymorphism in a nucleic  
 PT acid sample.  
 XX  
 XX Claim 1; Page 61; 83pp; English.  
 PS  
 XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
 XX primer extension (SNPE) primers, and the sequences of regions flanking  
 XX sites of single nucleotide polymorphisms SNPs. The present invention  
 XX includes kits for determining the presence or absence of a SNP, using the  
 XX oligonucleotides of the invention. The PCR primers are used to amplify a  
 XX SNP flanking sequence, the SNPE primer is used as a genotyping primer.  
 XX The oligonucleotides are useful for genotyping a nucleic acid sample by  
 XX performing a single-nucleotide primer extension reaction. The  
 XX oligonucleotides are useful for determining the presence, absence or  
 XX identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
 XX assess by association analysis the genotype of an individual or group of  
 XX individuals, having a pathological phenotypic trait suspected of being  
 XX caused by one or more SNPs. Phenotypic traits include diseases e.g.  
 XX agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular  
 XX dystrophy, familial hypercholesterolaemia, polycystic kidney disease,  
 XX osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
 XX traits also include symptoms of or susceptibility to multifactorial  
 XX diseases of which a component is or may be genetic such as autoimmune  
 XX diseases, including, rheumatoid arthritis, multiple sclerosis,  
 XX inflammation, cancer, nervous system diseases and infection by pathogenic  
 XX microorganism. The method is also useful in forensic investigations and  
 XX paternity analysis. The present sequence represents a PCR primer specific  
 XX for a human SNP containing DNA sequence  
 XX  
 XX Sequence 24 BP; 6 A; 7 C; 3 G; 8 T; 0 U; 0 Other;  
 SQ  
 Query Match 2.0%; Score 19.8; DB 1; Length 24;  
 Best Local Similarity 91.3%; Pred. No. 1.3e+03;  
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 577 ACCACTACACCTGGCTAATTTT 599  
 Db 1 ACCACTACGCGCTGACTAATTTT 23

RESULT 583  
 AAH44468  
 ID AAH44468 standard; DNA; 24 BP.  
 XX  
 AC AAH44468;  
 XX  
 DT 25-OCT-2001 (first entry)  
 XX  
 DE Enolpyruvate phosphate-dependent glycoposphotransferase 9 primer 1.  
 XX  
 XX Human; enolpyruvate phosphate-dependent glycoposphotransferase 9;  
 KM cytosolic; antiinflammatory; haemostatic; immunomodulatory; anti-HIV;  
 KM diagnosis; malignant neoplasm; haemopathy; HIV infection;  
 KM immunological disease; inflammation; PCR primer; ss.

XX	Homo sapiens.
XX	WO200149836-A1.
XX	12-JUL-2001.
XX	25-DEC-2000; 2000WO-CN000649.
XX	29-DEC-1999; 99CN-00127223.
XX	(UYFU-) UNIV FUDAN.
XX	(SHAN-) SHANGHAI BIO DOOR GENE TECHNOLOGY LTD.
XX	Mao Y, Xie Y;
XX	WPI; 2001-432875/46.
XX	Enolpyruvate phosphatase-dependent glycosylphosphotransferase 9 and encoded
XX	polynucleotide, applicable in diagnosis and treatment of malignant
XX	neoplasm, hemopathy, HIV infection, immunological diseases and various
XX	inflammation.
XX	Example 3; Page 18; 35pp; Chinese.
XX	The present invention describes the human enolpyruvate phosphate-
XX	dependent glycosylphosphotransferase 9 protein (1). (1) has cytosolic,
XX	antitumorigenic, haemostatic, immunomodulatory and anti-HIV activities.
XX	(1) and the polynucleotide encoding it are applicable in the diagnosis
XX	and treatment of malignant neoplasm, haemopathy, HIV infection,
XX	immunological diseases and various inflammations. The present sequence
XX	represents a PCR primer for human enolpyruvate phosphate-dependent
XX	glycosylphosphotransferase 9, which is used in an example from the present
XX	invention
XX	Sequence 24 BP; 4 A; 9 C; 6 G; 5 T; 0 U; 0 Other;
XX	Query Match 2.0%; Score 19.8; DB 1; Length 24;
XX	Best Local Similarity 91.3%; Pred. No. 1.3e+03;
XX	Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0.
XX	926 GGAATCTCACTCTGTACCCAGG 948
XX	
XX	2 GGAGTCTCACTCTGTACCCAGG 24
XX	RESULT 584
XX	AA164654/C
XX	ID AA164654 standard; DNA; 24 BP.
XX	AC AA164654;
XX	DT 04-DEC-2001 (first entry)
XX	DE Human RNA helicase 10 PCR primer 2.
XX	Human; RNA helicase 10; cytosolic; virucidal; immunomodulatory;
XX	antitumorigenic; haemostatic; malignant tumour; HIV; infection;
XX	human immunodeficiency virus; immunological disease; PCR primer; ss.
XX	Homo sapiens.
XX	WO200172971-A1.
XX	04-OCT-2001.
XX	26-MAR-2001; 2001WO-CN000435.
XX	27-MAR-2000; 2000CN-00115186.
XX	(SHAN-) SHANGHAI BIOWINDOM GENE DEV INC.
XX	Mao Y, Xie Y;

DR	WPI; 2001-597114/67.
XX	
PT	New human RNA helicase 10 and encoded polynucleotide, applicable in
PT	diagnosis and treatment of malignant neoplasm, haemopathy, human
PT	immunodeficiency virus infection, immunological diseases and
PT	inflammation.
XX	
PS	Example 2; page 17; 39pp; Chinese.
XX	
CC	The invention relates to human RNA helicase 10 with cytosolic,
CC	virucidal, immunomodulatory, anti-inflammatory and haemostatic activity.
CC	The polypeptide and encoded polynucleotide are applicable in diagnosis
CC	and treatment of malignant tumour, haemopathy, HIV infection,
CC	immunological diseases and various inflammations. The present sequence is
CC	that of a human RNA helicase 10 PCR primer, useful to the invention
XX	
SQ	Sequence 24 BP; 7 A; 6 C; 8 G; 3 T; 0 U; 0 Other;
Query Match	2.0%; Score 19.8; DB 1; Length 24;
Best Local Similarity	91.3%; Pred. No. 1.3e+03;
Matches 21; Conservative	0; Mismatches 2; Indels 0; Gaps 0
QY	993 CCGGGGCTCAAGCGATTCCTCG 1015
Db	24 CCTGGTTCAAGCGATTCCTCG 2
RESULT 585	
ABL41338	
ID	ABL41338 standard; DNA; 24 BP.
XX	
AC	ABL41338;
XX	
DT	22-MAY-2002 (first entry)
XX	
DE	Human TFIID subunit p30beta protein 12.54 PCR primer SEQ ID NO 3.
XX	
KW	Human; TFIID subunit p30beta protein 12.54; tumour; inflammation;
KW	protein metabolism dysfunction; immunological diseases; haemopathy; HIV;
XX	infection; PCR; primer; ss.
XX	
OS	Homo sapiens.
XX	
PN	CN126959-A.
XX	
PD	19-DEC-2001.
XX	
PF	05-JUN-2000; 2000CN-00116325.
XX	
PR	05-JUN-2000; 2000CN-00116325.
XX	
PA	(BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX	
PI	Mao Y, Xie Y;
XX	
DR	WPI; 2002-206968/27.
XX	
PT	New polypeptide-human TFIID subunit p 30 beta protein 12.54 and
PT	polynucleotide encoding the polypeptide.
XX	
PS	Example 2; Page 19 (Disclosure); 35pp; Chinese.
XX	
CC	The invention relates to human TFIID subunit p30beta protein 12.54, the
CC	polynucleotide encoding this polypeptide and DNA recombinant processes to
CC	produce the polypeptide. The present invention also discloses the method
CC	of applying the polypeptide in treating various diseases, such as protein
CC	metabolism dysfunction, various tumours, inflammations and immunological
CC	diseases, haemopathy and HIV infection. The present invention also
CC	discloses the antagonist for resisting the polypeptide and its treatment
CC	effect. The present invention also discloses the application of the
CC	polynucleotide for encoding human TFIID subunit p30beta protein 12.54.
CC	The present sequence is that of a PCR primer, useful in examples of the
CC	invention

XX	Sequence	24 BP; 1 A; 8 C; 7 G; 8 T; 0 U; 0 Other;
SO	Query Match	2.0%; Score 19.8; DB 1; Length 24;
	Best Local Similarity	91.3%; Pred. No. 1.3e+03;
	Matches	21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY	930	TTCTGACCTGTTACCCAGCGCTGG 952
DB	2	TTCTCTCTCTGTGGCCAGCGCTGG 24
RESULT 586		
AI166361	standard; DNA; 24 BP.	
ID	AI166361 standard; DNA; 24 BP.	
XX	AI166361;	
AC	23-JAN-2002 (first entry)	
XX	Human phosphatidylinositol-3 kinase 35 CDNA PCR primer #2.	
DE	Human: phosphatidylinositol-3 kinase 35; PTDINS-3 kinase 35; cancer;	
XX	haemopathy; development disorder; HIV infection; immunological disease;	
KW	inflammation; gene therapy; PCR primer; 88.	
KM	Homo sapiens.	
XX	MO2001.75014-A2.	
PN	11-OCT-2001.	
XX	16-MAR-2001; 2001WO-CN000328.	
PF	17-MAR-2000; 2000CN-00114973.	
XX	(BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.	
PA	Mao Y, Xie Y;	
PI	WPI; 2002-025836/03.	
XX	New human phosphatidylinositol-3 (PTDINS3) kinase 35 for diagnosing and	
XX	treating malignant tumor, hemopathy, human immunodeficiency virus	
PT	infection, immunological diseases and various inflammations.	
PS	Example 2; Page 12; 34pp; Chinese.	
XX	The present invention provides the protein and coding sequences of human	
CC	phosphatidylinositol-3 (PTDINS-3) kinase 35. The sequences can be used in	
CC	the treatment of cancer, haemopathy, HIV infection, development	
CC	disorders, immunological diseases and inflammation. The present sequence	
CC	is a PCR primer for the coding sequence of the invention	
XX	Sequence 24 BP; 3 A; 0 C; 1 G; 20 T; 0 U; 0 Other;	
SO	Query Match	2.0%; Score 19.8; DB 1; Length 24;
	Best Local Similarity	91.3%; Pred. No. 1.3e+03;
	Matches	21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY	427	TTTTTATTTTATTTTATTTTAAAG 449
DB	2	TTTTTTTTTTTTTTTTTTTAAAG 24
RESULT 587		
AI1638977	standard; DNA; 24 BP.	
ID	AAD38977 standard; DNA; 24 BP.	
XX	AAD38977;	
AC	23-SEP-2002 (first entry)	
XX		
DT		
XX		

```

DE Human GDD DNA amplifying reverse RT-PCR primer, GDDpr-4r.
XX
XX Human, dipeptidyl peptidase; DPP; neoplasia; type II diabetes; cirrhosis;
XX autoimmunity; human immuno deficiency virus; HIV infection; cytostatic;
XX graft rejection; antidiabetic; antiinflammatory; immunosuppressive;
XX antiviral; enzyme; reverse transcription; RT-PCR; primer; ss.
XX
XX Homo sapiens.
XX
XX WO200234900-A1.
XX
XX 02-MAY-2002.
XX
XX 29-OCT-2001; 2001WO-AU001388.
XX
XX 27-OCT-2000; 2000AU-00001078.
XX
XX (UNSY ) UNIV SYDNEY.
XX
XX Abbott CA, Gorrell MD;
XX
XX WPI; 2002-454646/48.
XX
XX New dipeptidyl peptidase (DPP) peptides, useful for screening inhibitors
XX of DPP catalytic activity, which may be employed to treat e.g. neoplasia,
XX type II diabetes, cirrhosis, autoimmunity, graft rejection and HIV
XX infection.
XX
XX Example; Page 33; 91pp; English.
XX
XX The present invention relates to dipeptidyl peptidase (DPP) proteins and
XX for polymucleotides encoding such proteins. The DPP peptides are useful for
XX screening inhibitors of DPP catalytic activity. The inhibitors are useful
XX for treating neoplasia, type II diabetes, cirrhosis, autoimmunity, graft
XX rejection and HIV (human immuno deficiency virus) infection. The present
XX DNA sequence is a reverse transcription (RT)-PCR primer which is used for
XX amplifying human GDD DNA. This sequence is used in the exemplification of
XX the invention
XX
XX
XX Sequence 24 BP; 2 A; 7 C; 8 G; 7 T; 0 U; 0 Other;
XX
XX
XX Query Match 2.0%; Score 19.8; DB 1; Length 24;
XX Best Local Similarity 91.3%; Pred. No. 1.3e+03;
XX Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0
XX
XX 197 CCATGTTGGTCAGGCTGCTCTCG 219
XX ||||| ||||| |||||
XX Db 2 CCATTTGGCCGAGGCTGCTCTTG 24
XX
XX RESULT 588
XX ABL41577
XX ID ABL41577 standard; DNA; 24 BP.
XX
XX ABL41577;
XX
XX 01-JUL-2002 (first entry)
XX
XX primer #2 relating to human zinc finger protein 27.
XX
XX Zinc finger; zinc finger protein 27; human; cancer; HIV; PCR; primer; ss
XX
XX Homo sapiens.
XX
XX CN1325869-A.
XX
XX 12-DEC-2001.
XX
XX 31-MAY-2000; 2000CN-00116276.
XX
XX 31-MAY-2000; 2000CN-00116276.
XX
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX

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```
XX Mao Y, Xie Y;
XX
XX WPI; 2002-217538/28.
XX
XX Polypeptide-zinc finger protein 27 and polynucleotide for coding it.
XX
XX Example 2; Page 16 (disclosure); 33pp; Chinese.
XX
XX This invention relates to a novel polypeptide-zinc finger protein 27 and
XX the application of the polypeptide in treating diseases such as cancer
XX and HIV infection. The present sequence represents a primer relating to
XX the zinc finger protein 27 encoding sequence
XX
XX Sequence 24 BP; 4 A; 7 C; 5 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 2.0%; Score 19.8; DB 1; Length 24;
XX Best Local Similarity 91.3%; Pred. No. 1.3e+03;
XX Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 752 ACCACGCGCTAGCTATTTTGG 774
XX 1 ACCACGCGCTAGCTATTTTGG 23
XX
XX RESULT 589
XX AB270110
XX ID AB270110 standard; DNA; 24 BP.
XX
XX AC AB270110;
XX
XX 24-APR-2003 (first entry)
XX
XX Human RNA polymerase I-40 kDa subunit 9.68 PCR primer #1.
XX
XX Human, RNA polymerase I-40 kDa subunit 9.68; cancer; cytostatic;
XX HIV infection; anti-HIV; PCR; primer; ss.
XX
XX Homo sapiens.
XX
XX CN1363655-A.
XX
XX 14-AUG-2002.
XX
XX 05-JAN-2001; 2001CN-00105029.
XX
XX 05-JAN-2001; 2001CN-00105029.
XX
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
XX Mao Y, Xie Y;
XX
XX WPI; 2002-742064/81.
XX
XX Polypeptide-human RNA polymerase I-40 kDa subunit 9.68 and polynucleotide
XX for coding it.
XX
XX Example 2; Page 17 (disclosure); 32pp; Chinese.
XX
XX The present invention relates to human RNA polymerase I-40 kDa subunit
XX 9.68 (see ABP59130). The protein can be used for treating diseases such
XX as cancer and HIV infection. The present sequence is a PCR primer, which
XX was used in an example from the invention
XX
XX Sequence 24 BP; 6 A; 8 C; 5 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 2.0%; Score 19.8; DB 1; Length 24;
XX Best Local Similarity 91.3%; Pred. No. 1.3e+03;
XX Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 219 GAATCCCGACCTCAGATGATCC 241
XX 1 GAATCCCGACCTCAGATGATCC 23
XX
```

```
RESULT 590
AD011357
ID AD011357 standard; DNA; 24 BP.
XX
XX AD011357;
XX
XX 06-MAY-2004 (first entry)
XX
XX Human protein phosphatase 2A alpha subunit 22. 66; RT-PCR primer #1.
XX
XX ss; human; protein phosphatase 2A alpha subunit 22. 66; osteoma;
XX leukaemia; RT-PCR; reverse transcriptase; primer.
XX
XX Homo sapiens.
XX
XX CN1355310-A.
XX
XX 26-JUN-2002.
XX
XX 01-DEC-2000; 2000CN-00127647.
XX
XX 01-DEC-2000; 2000CN-00127647.
XX
XX (UYFU-) UNIV FUDAN.
XX
XX Mao Y, Xie Y;
XX
XX WPI; 2003-403873/39.
XX
XX Polypeptide-human protein phosphatase 2A alpha subunit 22.66 and
XX polynucleotide for coding it.
XX
XX Example 2; Page 18; 32pp; Chinese.
XX
XX The invention relates to a new human protein phosphatase 2A alpha subunit
XX 22. 66 polypeptide, the polynucleotide encoding it, and the process for
XX preparing this polypeptide by DNA recombination technique. Also described
XX is the application of the said polypeptide in treating diseases such as
XX osteoma and leukaemia; the antagonist against this polypeptide and its
XX therapeutic action; and the application of the said polynucleotide
XX encoding this novel polypeptide. The present sequence represents a
XX reverse transcriptase (RT)-PCR primer used to isolate cDNA encoding human
XX protein phosphatase 2A alpha subunit 22. 66.
XX
XX Sequence 24 BP; 4 A; 8 C; 5 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 2.0%; Score 19.8; DB 1; Length 24;
XX Best Local Similarity 91.3%; Pred. No. 1.3e+03;
XX Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 997 GGCTCAAGCGATTCTCCTGCTC 1019
XX 2 GGCTCAAGCGATTCTCCTGCTC 24
XX
XX RESULT 591
AD011357
ID AD011357 standard; DNA; 24 BP.
XX
XX AD011357;
XX
XX 15-JUN-2004 (first entry)
XX
XX Single multiplex PCR primer #729.
XX
XX ss; primer; simultaneous amplification;
XX single multiplex polymerase chain reaction; multifactorial disease;
XX genetic alteration; pharmacogenetic reaction; genotyping; polymorphism;
XX gene expression profiling.
XX
XX Synthetic.
XX
```



XX WO200403649-A2.  
 XX 22-APR-2004.  
 XX 07-OCT-2003; 2003WO-US031874.  
 XX 07-OCT-2002; 2002US-0417009P.  
 XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.  
 XX Li H, Li J;  
 XX WPI; 2004-340914/31.  
 XX Designing primers for simultaneous amplification of target DNA fragments  
 PT in a single multiplex polymerase chain reaction, for high throughput  
 PT multiplex DNA sequence amplification, comprises aligning two primers.  
 XX Disclosure; Page 36; 120pp; English.  
 XX The invention relates to a method of designing primers for simultaneous  
 CC amplification of target DNA fragments in a single multiplex polymerase  
 CC chain reaction by aligning a first primer and a second primer. The method  
 CC comprises: (a) aligning a first primer and a second primer; and (b)  
 CC selecting the first primer where the first primer at its 3' end does not  
 CC contain four or more bases that are perfectly matching to the 3' end  
 CC sequence of the first primer or a second primer, the first primer at its  
 CC 3' end does not contain seven or more bases that are perfectly matching  
 CC except one mismatch to the 3' end sequence of the first primer or the  
 CC second primer, the first primer at its 3' end does not contain six or  
 CC more bases that are perfectly matching to a sequence anywhere of the  
 CC first primer or the second primer, and the first primer at its 3' end  
 CC does not contain eleven or more bases that are perfectly matching except  
 CC one mismatch to a sequence anywhere of the first primer or the second  
 CC primer. The method is useful for designing primers for simultaneous  
 CC amplification of target DNA fragments in a single multiplex polymerase  
 CC chain reaction. It is also useful in the identification of multiple genes  
 CC related to multifactorial diseases, the genome-scale detection of genetic  
 CC alterations, the studies in pharmacogenetic reactions, the genotyping  
 CC genetic polymorphisms in a large population, the gene expression  
 CC profiling in various samples and high throughput genotyping technologies.  
 CC This sequence corresponds to an example of a primer of the invention.  
 XX  
 SQ Sequence 24 BP; 5 A; 10 C; 4 G; 5 T; 0 U; 0 Other;  
 Query Match 2.0%; Score 19.8; DB 1; Length 24;  
 Best Local Similarity 91.3%; Pred. No. 1.3e+03;  
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 372 ACCGCTCAGCCTCCCAAGTG 394  
 DB 2 ATCCGCTCAGCCTCCCAAGTG 24  
 RESULT 592  
 AAC61385  
 ID AAC61385 standard; DNA; 21 BP.  
 XX AAC61385;  
 AC  
 XX 19-FEB-2001 (first entry)  
 DT  
 XX PCR primer for androgen-related, prostate-specific gene PCGEM1.  
 DE  
 XX Androgen-regulated gene; prostate specific gene; PCGEM1; prostate cancer;  
 KM prostate cancer gene expression marker 1; prostate related disease;  
 KM benign prostatic hyperplasia; PCR primer; ss.  
 XX Homo sapiens.  
 OS  
 XX WO200058470-A1.  
 PN  
 XX

PD 05-OCT-2000.  
 XX 24-MAR-2000; 2000WO-US007906.  
 XX 26-MAR-1999; 99US-0126469P.  
 XX (SRIK/) SRIKANTAN V.  
 PA (ZOUZ/) ZOU Z.  
 PA (MOUL/) MOUL J W.  
 PA (SRIV/) SRIVASTAVA S.  
 XX  
 PI Srikantan V, Zou Z, Mou J W, Srivastava S;  
 XX WPI; 2000-664926/64.  
 XX Novel androgen-regulated prostate specific gene, prostate cancer gene  
 PT expression marker, useful for detecting, diagnosing, preventing, and  
 PT treating prostate cancer and other prostate related diseases.  
 XX Claim 5; Fig 13; 75pp; English.  
 PS  
 XX The present sequence is a PCR primer for an androgen-regulated, prostate  
 CC specific gene PCGEM1 (prostate cancer gene expression marker 1). The  
 CC PCGEM1 gene is over-expressed in prostate cancer. The PCGEM1  
 CC polynucleotide is useful for detecting prostate cancer in a patient. The  
 CC PCGEM1 promoter may be linked to cytotoxic gene, and be used for  
 CC selectively killing prostate cancer cells. The PCGEM1 polynucleotide is  
 CC also useful as marker of prostate cancer and other prostate related  
 CC diseases, as targets for therapeutic intervention in prostate cancer and  
 CC other prostate related diseases, in detection, diagnosis, prognosis,  
 CC prevention, and treatment of prostate cancer (e.g. prostatic  
 CC interepithelial neoplasia (PIN), adenocarcinomas, nodular hyperplasia,  
 CC and large duct carcinomas) and prostate related diseases (e.g. benign  
 CC prostatic hyperplasia)  
 XX  
 SQ Sequence 21 BP; 5 A; 9 C; 3 G; 4 T; 0 U; 0 Other;  
 Query Match 2.0%; Score 19.4; DB 1; Length 21;  
 Best Local Similarity 95.2%; Pred. No. 1.2e+03;  
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 539 TGCTCAGCCTCCCAAGTAC 559  
 DB 1 TGCTCAGCCTCCCAAGTAC 21  
 RESULT 593  
 AAH38610/C  
 ID AAH38610 standard; DNA; 21 BP.  
 XX AAH38610;  
 AC  
 XX 14-AUG-2001 (first entry)  
 DT  
 XX SNP specific lower PCR primer SEQ ID 1406.  
 DE  
 XX single nucleotide polymorphism; SNP; single nucleotide primer extension;  
 XX SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;  
 KM Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolemia;  
 KM polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
 KM acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
 KM inflammation; forensic investigation; paternity analysis; PCR primer; ss.  
 XX Homo sapiens.  
 OS  
 XX WO200129262-A2.  
 PN  
 XX 26-APR-2001.  
 PD  
 XX 13-OCT-2000; 2000WO-US028436.  
 PF  
 XX 15-OCT-1999; 99US-0160096P.  
 PR  
 XX

PA (ORCH-) ORCHID BIOSCIENCES INC.  
 XX  
 XX Picoult-Newburg L, Pohl M;  
 PI  
 DR WPI; 2001-290930/30.  
 XX  
 XX New genotyping oligonucleotide, useful for detecting the presence,  
 PT absence or identity of single polynucleotide polymorphism in a nucleic  
 PT acid sample.  
 XX  
 PS Claim 1; Page 57; 83pp; English.  
 XX  
 CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
 CC primer extension (SNPE) primers, and the sequences of regions flanking  
 CC sites of single nucleotide polymorphisms SNPs. The present invention  
 CC includes kits for determining the presence or absence of a SNP, using the  
 CC oligonucleotides of the invention. The PCR primers are used to amplify a  
 CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.  
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by  
 CC performing a single-nucleotide primer extension reaction. The  
 CC oligonucleotides are useful for determining the presence, absence or  
 CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
 CC assess by association analysis the genotype of an individual or group of  
 CC individuals, having a pathological phenotypic trait suspected of being  
 CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
 CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular  
 CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,  
 CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
 CC traits also include symptoms of or susceptibility to multifactorial  
 CC disease of which a component is or may be genetic such as autoimmune  
 CC diseases, including, rheumatoid arthritis, multiple sclerosis,  
 CC inflammation, cancer, nervous system diseases and infection by pathogenic  
 CC microorganism. The method is also useful in forensic investigations and  
 CC paternity analysis. The present sequence represents a PCR primer specific  
 CC for a human SNP containing DNA sequence  
 XX  
 SQ Sequence 21 BP; 7 A; 6 C; 5 G; 3 T; 0 U; 0 Other;  
 XX  
 Query Match 2.0%; Score 19.4; DB 1; Length 21;  
 Best Local Similarity 95.2%; Pred. No. 1.2e+03;  
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 696 GGGTTCAGTATTCCTGTC 716  
 DB 21 GGGTTCAGTATTCCTGTC 1  
 RESULT 594  
 AAH38522  
 ID AAH38522 standard; DNA; 21 BP.  
 AC AAH38522;  
 XX  
 DT 14-AUG-2001 (first entry)  
 DE SNP specific lower PCR primer SEQ ID 1318.  
 XX  
 KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
 KW SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;  
 KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;  
 KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
 KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
 KW inflammation; forensic investigation; paternity analysis; PCR primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200129262-A2.  
 XX  
 PD 26-APR-2001.  
 XX  
 PF 13-OCT-2000; 2000WO-US028436.  
 XX  
 PR 15-OCT-1999; 99US-0160096P.

XX  
 PA (ORCH-) ORCHID BIOSCIENCES INC.  
 XX  
 XX Picoult-Newburg L, Pohl M;  
 PI  
 DR WPI; 2001-290930/30.  
 XX  
 XX New genotyping oligonucleotide, useful for detecting the presence,  
 PT absence or identity of single polynucleotide polymorphism in a nucleic  
 PT acid sample.  
 XX  
 PS Claim 1; Page 56; 83pp; English.  
 XX  
 CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
 CC primer extension (SNPE) primers, and the sequences of regions flanking  
 CC sites of single nucleotide polymorphisms SNPs. The present invention  
 CC includes kits for determining the presence or absence of a SNP, using the  
 CC oligonucleotides of the invention. The PCR primers are used to amplify a  
 CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.  
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by  
 CC performing a single-nucleotide primer extension reaction. The  
 CC oligonucleotides are useful for determining the presence, absence or  
 CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
 CC assess by association analysis the genotype of an individual or group of  
 CC individuals, having a pathological phenotypic trait suspected of being  
 CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
 CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular  
 CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,  
 CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
 CC traits also include symptoms of or susceptibility to multifactorial  
 CC disease of which a component is or may be genetic such as autoimmune  
 CC diseases, including, rheumatoid arthritis, multiple sclerosis,  
 CC inflammation, cancer, nervous system diseases and infection by pathogenic  
 CC microorganism. The method is also useful in forensic investigations and  
 CC paternity analysis. The present sequence represents a PCR primer specific  
 CC for a human SNP containing DNA sequence  
 XX  
 SQ Sequence 21 BP; 6 A; 5 C; 6 G; 4 T; 0 U; 0 Other;  
 XX  
 Query Match 2.0%; Score 19.4; DB 1; Length 21;  
 Best Local Similarity 95.2%; Pred. No. 1.2e+03;  
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 388 CAAAGTCTGGGATTACAGGC 408  
 DB 1 CAAAGTCTGGGATTACAGGC 21  
 RESULT 595  
 AAH39585  
 ID AAH39585 standard; DNA; 21 BP.  
 AC AAH39585;  
 XX  
 DT 14-AUG-2001 (first entry)  
 DE SNP specific upper PCR primer SEQ ID 2381.  
 XX  
 KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
 KW SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;  
 KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;  
 KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
 KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
 KW inflammation; forensic investigation; paternity analysis; PCR primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200129262-A2.  
 XX  
 PD 26-APR-2001.  
 XX  
 PF 13-OCT-2000; 2000WO-US028436.  
 XX

PR 15-OCT-1999; 99US-0160096P.  
 XX  
 XX (ORCH-) ORCHID BIOSCIENCES INC.  
 XX  
 XX Picoult-Newburg L, Pohl M;  
 PI WPI; 2001-290930/30.  
 XX  
 XX New genotyping oligonucleotide, useful for detecting the presence,  
 PT absence or identity of single polynucleotide polymorphism in a nucleic  
 PT acid sample.  
 PS Claim 1; Page 62; 83pp; English.  
 XX  
 XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
 CC primer extension (SNPE) primers, and the sequences of regions flanking  
 CC sites of single nucleotide polymorphisms SNPs. The present invention  
 CC includes kits for determining the presence or absence of a SNP, using the  
 CC oligonucleotides of the invention. The PCR primers are used to amplify a  
 CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.  
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by  
 CC performing a single-nucleotide primer extension reaction. The  
 CC oligonucleotides are useful for determining the presence, absence or  
 CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
 CC assess by association analysis the genotype of an individual or group of  
 CC individuals, having a pathological phenotypic trait suspected of being  
 CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
 CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular  
 CC dystrophy, familial hypercholesterolemia, polycystic kidney disease,  
 CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
 CC traits also include symptoms of or susceptibility to multifactorial  
 CC diseases, including a component is or may be genetic such as autoimmune  
 CC diseases, including, rheumatoid arthritis, multiple sclerosis,  
 CC inflammation, cancer, nervous system diseases and infection by pathogenic  
 CC microorganism. The method is also useful in forensic investigations and  
 CC paternity analysis. The present sequence represents a PCR primer specific  
 CC for a human SNP containing DNA sequence  
 XX  
 SQ Sequence 21 BP; 5 A; 9 C; 2 G; 5 T; 0 U; 0 Other;  
 Query Match 2.0%; Score 19.4; DB 1; Length 21;  
 Best Local Similarity 95.2%; Pred. No. 1.2e+03;  
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 967 ATCTCGGCTCAGTCACTC 987  
 Db 1 ATCTCAGCTCAGTCACTC 21  
 RESULT 596  
 AAH8861/c  
 ID AAH8861 standard; DNA; 21 BP.  
 XX  
 AC AAH8861;  
 XX  
 DT 09-SEP-2004 (revised)  
 DT 27-FEB-2002 (first entry)  
 XX  
 DE Human polymorphic oligonucleotide U39064 fragment #1.  
 XX  
 XX Human; single nucleotide polymorphic; SNP; forensic science;  
 KM paternity testing; phenotypic trait; genetic mapping; animal breeding;  
 KM plant breeding; ds.  
 XX  
 OS Homo sapiens.  
 OS Unidentified.  
 XX  
 XX Key Location/Qualifiers  
 FT 11  
 FT variation /\*tag= a  
 FT /standard\_name= "single nucleotide polymorphism"  
 XX  
 PN WO200134840-A2.

XX 17-MAY-2001.  
 PD  
 XX  
 XX 10-NOV-2000; 2000WO-US030766.  
 PF  
 XX  
 XX 10-NOV-1999; 99US-0164596P.  
 PR  
 XX (GLAX) GLAXO GROUP LTD.  
 PA (AFY-) AFFYMETRIX INC.  
 XX  
 PI Au K, Chen J, Patil N, Thomas D;  
 XX  
 XX WPI; 2001-335945/35.  
 DR  
 XX  
 XX New polymorphic sites derived from the human genome are useful to  
 PT determine sites correlating with phenotypic traits, particularly disease,  
 PT and also in forensics and paternity testing.  
 XX  
 PS Claim 33; Page 8; 43pp; English.  
 XX  
 XX The present invention relates to human oligonucleotides comprising a  
 CC single nucleotide polymorphic site (SNP: AAH8797-AAH89219). The present  
 CC sequence is one such oligonucleotide. The oligonucleotides can be used in  
 CC forensics, paternity testing, correlation of polymorphisms with  
 CC phenotypic traits, genetic mapping of phenotypic traits and marker  
 CC assisted breeding of animals and crop plants  
 CC  
 CC Revised record issued on 09-SEP-2004 : Correction to Feature Table Key  
 XX  
 SQ Sequence 21 BP; 4 A; 5 C; 6 G; 6 T; 0 U; 0 Other;  
 Query Match 2.0%; Score 19.4; DB 1; Length 21;  
 Best Local Similarity 95.2%; Pred. No. 1.2e+03;  
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 870 ATTACAGGCTGAGCCACGAC 890  
 Db 21 ATTACAGGCTGAGCCACGAC 1  
 RESULT 597  
 AAH89111  
 ID AAH89111 standard; DNA; 21 BP.  
 XX  
 AC AAH89111;  
 XX  
 DT 09-SEP-2004 (revised)  
 DT 27-FEB-2002 (first entry)  
 XX  
 DE Human polymorphic oligonucleotide U29874 fragment #4.  
 XX  
 XX Human; single nucleotide polymorphic; SNP; forensic science;  
 KM paternity testing; phenotypic trait; genetic mapping; animal breeding;  
 KM plant breeding; ds.  
 XX  
 OS Homo sapiens.  
 OS Unidentified.  
 XX  
 XX Key Location/Qualifiers  
 FT 11  
 FT variation /\*tag= a  
 FT /standard\_name= "single nucleotide polymorphism"  
 XX  
 PN WO200134840-A2.  
 PD  
 XX 17-MAY-2001.  
 XX  
 XX 10-NOV-2000; 2000WO-US030766.  
 PF  
 XX  
 XX 10-NOV-1999; 99US-0164596P.  
 PR  
 XX (GLAX) GLAXO GROUP LTD.  
 PA (AFY-) AFFYMETRIX INC.  
 XX  
 PI (AFY-) AFFYMETRIX INC.  
 XX  
 PN WO200134840-A2.

XX Au K, Chen J, Pacil N, Thomas D;  
PI  
XX  
DR WPI; 2001-335945/35.  
XX  
XX New polymorphic sites derived from the human genome are useful to  
PT determine sites correlating with phenotypic traits, particularly disease,  
PR and also in forensic and paternity testing.  
XX  
PS Claim 85; Page 14; 43pp; English.  
XX  
XX The present invention relates to human oligonucleotides comprising a  
CC single nucleotide polymorphic site (SNP: AAH8797-AAH89219). The present  
CC sequence is one such oligonucleotide. The oligonucleotides can be used in  
CC forensics, paternity testing, correlation of polymorphisms with  
CC phenotypic traits, genetic mapping of phenotypic traits and marker  
CC assisted breeding of animals and crop plants  
CC  
CC Revised record issued on 09-SEP-2004 : Correction to Feature Table Key  
XX  
SQ Sequence 21 BP; 1 A; 10 C; 5 G; 5 T; 0 U; 0 Other;  
  
Query Match 2.0%; Score 19.4; DB 1; Length 21;  
Best Local Similarity 95.2%; Pred. No. 1.2e+03;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 836 TGATCTGCGCTGCGCTC 856  
Db 1 TGATCTGCGCTGCGCTC 21  
  
RESULT 598  
AAF74150  
ID AAF74150 standard; DNA; 21 BP.  
XX  
XX AAF74150;  
AC  
XX  
DT 30-APR-2001 (first entry)  
XX  
XX  
DE Primer #84.  
XX  
XX Solute carrier family 6 neurotransmitter transporter; seotonin 4; SLC6A4;  
KW genotyping; allele specific oligonucleotide; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200109161-A1.  
PN  
XX  
PD 08-FEB-2001.  
XX  
XX 31-JUL-2000; 2000WO-US020638.  
PF  
XX  
XX 29-JUL-1999; 99US-0146290P.  
PR  
XX  
XX (GENA-) GENAISSANCE PHARM INC.  
PA  
XX  
PI Denton RR, Duda A, Nandabalan K, Sanchis A, Stephens JC;  
XX  
XX WPI; 2001-123317/13.  
DR  
XX  
XX New isolated polynucleotide comprising a polymorphic variant for the  
PT solute carrier family 6 neurotransmitter transporter, seotonin member 4  
PT gene for identifying drugs for treating disorders related to expression  
PT of the protein.  
XX  
XX Example 1; Page 39; 152pp; English.  
PS  
XX  
XX The present invention relates to a polymorphic variant of a reference  
CC sequence for the solute carrier family 6 neurotransmitter transporter,  
CC seotonin member 4 (SLC6A4) gene or a fragment of it or a sequence  
CC complementary to the first sequence. The invention is used in producing a  
CC recombinant organism that can be used to express SLC6A4 for protein  
CC structure analysis and binding studies. A composition comprising a

CC genotyping oligonucleotide is used to detect a polymorphism in the SLC6A4  
CC gene  
XX  
XX  
SQ Sequence 21 BP; 5 A; 3 C; 8 G; 5 T; 0 U; 0 Other;  
  
Query Match 2.0%; Score 19.4; DB 1; Length 21;  
Best Local Similarity 95.2%; Pred. No. 1.2e+03;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 391 AGTCTGGGATTACAGCGCTG 411  
Db 1 AATGCTGGGATTACAGCGCTG 21  
  
RESULT 599  
ABO93614/C  
ID ABO93614 standard; DNA; 21 BP.  
XX  
XX ABO93614;  
AC  
XX  
XX 16-OCT-2002 (first entry)  
DT  
XX  
XX Human DISC1/DISC2 PCR primer disc20 r2.  
DE  
XX  
XX Human; Disrupted in Schizophrenia 1; DISC1; neuroleptic; gene therapy;  
KW neuropsychiatric disorder; schizoaffective disorder; bipolar disorder;  
KW unipolar affective disorder; adolescent conduct disorder; schizophrenia;  
KW PCR; primer; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200258637-A2.  
PN  
XX  
XX 01-AUG-2002.  
PD  
XX  
XX 23-JAN-2002; 2002WO-US002186.  
PF  
XX  
XX 24-JAN-2001; 2001US-00770107.  
PR  
XX  
XX (MILL-) MILLINIUM PHARM INC.  
PA  
XX  
PI Meyer JM, Barrington-Martin R, Parker A, Barnes GT;  
XX  
XX WPI; 2002-590791/63.  
DR  
XX  
XX New human Disrupted-In-Schizophrenia (DISC) 1 and DISC2 genes containing  
PT single nucleotide polymorphisms, useful for preventing or treating  
PT neuropsychiatric disorders e.g. schizophrenia.  
XX  
XX  
PS Claim 17; Fig 4; 169pp; English.  
XX  
XX The invention relates to a novel Disrupted-In-Schizophrenia (DISC) 1  
CC allelic variant polynucleotide. The polypeptides of the invention have  
CC neuroleptic activity. The polynucleotides may have a use in gene therapy.  
CC DISC1 or DISC2 nucleic acid molecules are useful for diagnosing or  
CC treating a subject having a disease or disorder associated with specific  
CC DISC1 or DISC2 alleles and/or aberrant DISC1 expression or activity e.g.  
CC neuropsychiatric disorder such as schizoaffective, bipolar, unipolar  
CC affective or adolescent conduct disorder or schizophrenia. Similarly, the  
CC compound that inhibits DISC1 protein activity may be used in the method  
CC for treating such neuropsychiatric disorders. The sequences shown in  
CC ABO93575-ABO93658 represent the PCR primers used in the invention to  
CC amplify the sequences of DISC2 and DISC2  
XX  
SQ Sequence 21 BP; 4 A; 3 C; 10 G; 4 T; 0 U; 0 Other;  
  
Query Match 2.0%; Score 19.4; DB 1; Length 21;  
Best Local Similarity 95.2%; Pred. No. 1.2e+03;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 535 CTCCTGCTGAGCTCCCAAG 555  
Db 21 CTCCTGCTGAGCTCCCAAG 1

RESULT 600  
ABS98164  
ID ABS98164 standard; DNA; 21 BP.  
XX  
XX ABS98164;  
XX  
XX 23-DEC-2002 (first entry)  
XX  
XX Human multidrug resistance gene polymorphic sequence #66.  
XX  
XX Human; ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;  
XX cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;  
XX adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR112;  
XX aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;  
XX cyclooxgenase 2; COX2; diazepam binding inhibitor; DBI; haematological;  
XX epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;  
XX glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;  
XX HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;  
XX NADPH quinone oxidoreductase 2; NQO2; sulforantransferase thermolabile; STM;  
XX UGT2B7; UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;  
XX UGT2B7; UDP-glucuronosyl transferase; UGT2B15; uridine kinase receptor; UPA;  
XX multidrug resistance 1; lactotransferrin; orphan nuclear receptor;  
XX multidrug resistance associated protein 3; cancer; prostate;  
XX acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;  
XX altered drug metabolism; cardiovascular function; colorectal tumour;  
XX central nervous system; pulmonary; immunological; SNP;  
XX single nucleotide polymorphism.  
XX  
XX Homo sapiens.  
XX  
XX MO200257410-A2.  
XX  
XX 25-UTL-2002.  
XX  
XX 28-NOV-2001; 2001WO-US044838.  
XX  
XX 28-NOV-2000; 2000US-00724389.  
XX  
XX (DNAS-) DNA SCI LAB INC.  
XX  
XX Guida M, Hall J;  
XX  
XX WPI; 2002-698522/75.  
XX  
XX Isolated nucleic acid molecules having polymorphisms in known human genes  
XX e.g. cytochrome P450 and cathepsin S useful as genetic linkage markers  
XX for locating, identifying and characterizing the genes responsible for  
XX disorder-related traits.  
XX  
XX Example 22; Page 144; 714pp; English.  
XX  
XX This invention relates to the sequence of an isolated nucleic acid  
XX molecule comprising at least one base variation from that of a known  
XX human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),  
XX cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADRB1),  
XX aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator  
XX (ARNT), cathepsin S (CTSS), cyclooxgenase 2 (COX2), diazepam binding  
XX inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating  
XX protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl  
XX transferase (HNMT), (kallikrein 2) KLK2, nicotinamide -N-methyl  
XX transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),  
XX sulforantransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4  
XX (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl  
XX transferase (UGT2B15), uridine kinase receptor (UPA), multidrug resistance 1  
XX (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3  
XX (MRP3), orphan nuclear receptor (NR112), or acetylcholine muscarinic  
XX receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.  
XX The polymorphisms in the human genes cited in the invention are useful as  
XX genetic linkage markers for locating and characterizing the genes that  
XX are responsible for specific traits within the genome and eventually  
XX identifying the genes responsible for a variety of disorder-related

traits as a result of their e.g., overexpression, constitutive  
XX expression, mutation or underexpression, which may be used in diagnosing  
XX and/or treating the disorders. The nucleic acid molecules comprising the  
XX polymorphic sequences contained in CYP4501A1, CYP4501A2, CYP4502E1,  
XX ARNT, EPHX2, GST12, NNMT, NQO2, NR112, STM, UGT2B4, UGT2B7, UGT2B15, AHR,  
XX MDR1 and/or MDR3 are useful for screening individuals for altered drug  
XX metabolism. The polymorphic sequences contained in CYP4501A1, CYP4501A2,  
XX AHR, MDR1 and/or MDR3 may also be used to screen individuals for  
XX susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are  
XX used to screen for altered cardiovascular function. In COX2 for altered  
XX susceptibility to colorectal tumours, in DBI or CHMR1 for altered central  
XX nervous system function, in FLAP and HNMT for altered pulmonary,  
XX immunological or haematological function, in KLK2 for altered serine  
XX protease activity in the prostate, in LTF for altered immunological or  
XX haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and  
XX peripheral nervous system function. The present sequence represents a  
XX polymorphic DNA sequence of the invention  
XX  
XX Sequence 21 BP; 5 A; 5 C; 7 G; 4 T; 0 U; 0 Other;  
XX  
XX Query Match 2.0%; Score 19.4; DB 1; Length 21;  
XX Best Local Similarity 95.2%; Pred. No. 1.2e+03;  
XX Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX QY 868 GGATTACAGCGCTGAGCCACC 888  
XX |||||||  
XX DB 1 GGATTACAGGTGTGAGCCACC 21  
XX  
XX RESULT 601  
XX ADC42593  
XX ID ADC42593 standard; DNA; 21 BP.  
XX  
XX ADC42593;  
XX  
XX 18-DEC-2003 (first entry)  
XX  
XX Human FANCD2 PCR primer hFANCD2\_exon7\_F.  
XX  
XX cancer; Fanconi Anaemia; FA; BRCA; cytostatic; microarray;  
XX chemosensitising; ss; PCR; primer.  
XX  
XX Synthetic.  
XX  
XX MO2003039327-A2.  
XX  
XX 15-MAY-2003.  
XX  
XX 06-JUN-2002; 2002WO-US018153.  
XX  
XX 02-NOV-2001; 2001US-00998027.  
XX  
XX 02-NOV-2001; 2001WO-US045561.  
XX  
XX (DAND ) DANA FARBER CANCER INST.  
XX (UYOR-) UNIV OREGON HEALTH SCI.  
XX  
XX D'andrea AD, Taniguchi T, Timmers C, Grompe M, Fox EA;  
XX WPI; 2003-441436/41.  
XX  
XX Diagnosing or determining cancer or increased risk of cancer in a  
XX patient, by testing Fanconi Anemia/BRCA pathway gene or protein for a  
XX cancer-associated defect, that indicates cancer or increased risk of  
XX cancer.  
XX  
XX Example 14; Page 101; 160pp; English.  
XX  
XX The invention relates to a novel method of diagnosing or determining if a  
XX patient has cancer or is at increased risk of cancer, involving testing a  
XX Fanconi Anaemia (FA)/BRCA pathway gene or protein for the presence of a  
XX cancer-associated defect, where the presence of one or more cancer-  
XX associated defects is indicative of cancer or an increased risk of cancer  
XX in the patient. The method of the invention has cytostatic activity. The

CC method is useful for determining if a patient has cancer, or is at  
CC increased risk of developing cancer, e.g. breast, ovarian or prostate  
CC cancer. A microarray of the invention is useful for determining if a  
CC patient has cancer, or is at increased risk of developing cancer, by  
CC hybridizing a nucleic acid sample to the nucleic acid sequences from the  
CC array, and detecting the presence of mutations in PA/BRCA pathway genes  
CC in the nucleic acid sample from the patient, where detecting the presence  
CC of mutations is indicative of a patient who has cancer, or is at  
CC increased risk of developing cancer. A method of the invention is useful  
CC for screening a chemosensitizing agent, and the agent obtained is useful  
CC for treating a patient having a cancer. The present sequence is used in  
CC the exemplification of the invention.

CC Sequence 21 BP; 5 A; 7 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 2.0%; Score 19.4; DB 1; Length 21;  
Best Local Similarity 95.2%; Pred. No. 1.2e+03;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 966 AATCTCGCTCACTGCAACCT 986  
DB 1 AATCTCGCTCACTGCAACCT 21

RESULT 602

ADE14130/C  
ID ADE14130 standard; DNA; 21 BP.

XX ADE14130;

DT 29-JAN-2004 (first entry)

DE Optineurin promoter motif, repeat element or regulatory region #239.

XX Human; optineurin; de; ophthalmological; single nucleotide polymorphism;  
KM SNP; glaucoma; progressive ocular hypertensive disorder;

XX glaucoma related disorder; motif; repeat element; regulatory region.

XX Homo sapiens.

OS US2003190617-A1.

XX 09-OCT-2003.

PD 06-MAR-2002; 2002US-00091281.

PF 06-MAR-2002; 2002US-00091281.

PR (SIEE/) SI E.

PA (RAYM/) RAYMOND V.

PA (MORI/) MORISSETTE J.

PI Raymond V, Morissette J, Si E;

XX WPI; 2003-864168/80.

DR New nucleic acid sequences of the optineurin gene are useful to detect  
XX polymorphisms particularly single nucleotide polymorphisms in the  
PT optineurin promoter to diagnose, prognose and treat glaucoma and related  
PT disorders.

PS Claim 11; SEQ ID NO 241; 159pp; English.

CC The invention relates to an isolated nucleic acid (N1) comprising at  
CC least 20 but not more than 1500 consecutive nucleotides of the optineurin  
CC promoter appearing as ADE13890. Also included are the optineurin promoter  
CC operably linked to a heterologous nucleic acid, a nucleic acid capable of  
CC detecting a single nucleotide polymorphism (SNP) in the optineurin  
CC promoter, a host cell comprising the promoter operably linked to a  
CC heterologous sequence, diagnosing or prognosing glaucoma in a sample  
CC obtained from a cell or bodily fluid (comprising detecting a polymorphism  
CC in a promoter region of the optineurin gene, associated with a glaucoma  
CC phenotype), detecting a SNP sequence variation in a sample containing

CC DNA, detecting the presence of an optineurin promoter sequence variation  
CC in a sample containing DNA, determining the presence or increased  
CC susceptibility to glaucoma or to a progressive ocular hypertensive  
CC disorder resulting in loss of visual field in a patient (or the severity  
CC or progression of glaucoma in a patient, comprising providing  
CC amplification reaction primers that direct amplification of a selected  
CC nucleic acid region containing the variation within the optineurin  
CC promoter and amplifying the DNA) and detecting a polymorphism (comprising  
CC obtaining a sample containing human genomic DNA, providing a nucleic acid  
CC capable of detecting a SNP located within an optineurin promoter, and  
CC detecting the polymorphism). The invention is used to diagnose and  
CC prognose glaucoma and also to treat glaucoma related disorders. The  
CC present sequence is an optineurin promoter motif, repeat element or  
CC putative regulatory region.

CC Sequence 21 BP; 5 A; 7 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 19.4; DB 1; Length 21;  
Best Local Similarity 95.2%; Pred. No. 1.2e+03;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 849 TCGGCTCCCAAGTCTGGG 869  
DB 21 TCGGCTCCCAAGTCTGGG 1

RESULT 603

ADH59619  
ID ADH59619 standard; DNA; 21 BP.

XX ADH59619;

DT 25-MAR-2004 (first entry)

DE Non-nucleotide probe of the invention #23.

XX non-nucleotide probe; Bacterial Artificial Chromosome clone; BAC; ss;  
KM probe.

XX Synthetic.

OS WO2003027328-A2.

XX 03-APR-2003.

PD 24-SEP-2002; 2002WO-US030573.

PF 24-SEP-2001; 2001US-0324499P.

PR (BOST-) BOSTON PROBS INC.

PA (DAKO-) DAKOCYTOMATION DENMARK AS.

PI Kirszen NV, Hyldig-Nielsen UJ, Williams BF;

XX WPI; 2003-421160/39.

DR Non-nucleotide probe for suppressing binding of detectable nucleic acid  
XX probes to undesired sequences, has aggregate nucleobase sequence  
PT homologous to randomly distributed repeat sequence of genomic nucleic  
PT acid.

PS Claim 10; SEQ ID NO 25; 103pp; English.

CC The present sequence represents a non-nucleotide probe. The probe is  
CC useful for suppressing the binding of one or more detectable nucleic acid  
CC probes, that are greater than 100 base pairs and that have been derived  
CC from genomic nucleic acid, to one or more undesired sequences in an assay  
CC for determining target genomic nucleic acid of a sample. The method  
CC comprises contacting the sample with the mixture of probes (preferably  
CC comprising 5-50 probes), contacting the sample with the one or more  
CC detectable nucleic acid probes, and determining the target genomic  
CC nucleic acid of the sample by determining the hybridization of the one or  
CC more detectable nucleic acid probes to the target genomic nucleic acid of





XX Kirsens NV, Hyldig-Nielsen JU, Williams BF;  
 PI WPI; 2003-421160/39.  
 XX  
 DR  
 XX  
 XX Non-nucleotide probe for suppressing binding of detectable nucleic acid  
 PT probes to undesired sequences, has aggregate nucleobase sequence  
 PT homologous to randomly distributed repeat sequence of genomic nucleic  
 PT acid.  
 XX  
 PS Claim 10; SEQ ID NO 6; 103bp; English.  
 XX  
 XX The present sequence represents a non-nucleotide probe. The probe is  
 CC useful for suppressing the binding of one or more detectable nucleic acid  
 CC probes, that are greater than 100 base pairs and that have been derived  
 CC from genomic nucleic acid, to one or more undesired sequences in an assay  
 CC for determining target genomic nucleic acid of a sample. The method  
 CC comprises contacting the sample with the mixture of probes (preferably  
 CC comprising 5-50 probes), contacting the sample with the one or more  
 CC detectable nucleic acid probes, and determining the target genomic  
 CC nucleic acid of the sample by determining the hybridization of the one or  
 CC more detectable nucleic acid probes to the target genomic nucleic acid of  
 CC the sample. The genomic nucleic acid is contained in a fixed tissue or a  
 CC cell, and the sample is metaphase spreads, interphase nucleic or nucleic  
 CC found in paraffin embedded tissue material or frozen tissue sections. The  
 CC probe is also useful in comparing a sample of genomic nucleic acid with  
 CC that of a control sample using a genomic nucleic acid reference array.  
 CC The method comprises treating a sample of genomic nucleic acid and  
 CC control genomic nucleic acid, which are differentially labelled, the  
 CC array or both the sample and control genomic nucleic acid and the array  
 CC with the mixture of the probe under suitable hybridization conditions,  
 CC contacting the array with treated mixture of sample and control genomic  
 CC nucleic acid under suitable hybridization conditions, and comparing the  
 CC intensities of the signals from the differential labels of the array to  
 CC that caused by hybridization of the probes to genomic nucleic acid, thus  
 CC determining one or more variations in copy numbers of sequences in the  
 CC sample as compared with the relative copy numbers of substantially  
 CC identical sequences in the control. The hybridization of the genomic  
 CC array is determined using an intercalating dye or a detectable antibody,  
 CC or its fragment, that is specific for a nucleic acid/nucleic acid hybrid.  
 CC The sample of genomic nucleic acid to be tested and the reference of  
 CC nucleic acid are labelled with detectable moiety such that hybridization  
 CC of the genomic array is determined by determining the presence, absence,  
 CC amount or location of the detectable label on the one or more genomic  
 CC arrays. The genomic array comprises nucleic acid that is prepared from  
 CC Bacterial Artificial Chromosome (BAC) clones. The present sequence  
 CC represents a non-nucleotide probe of the invention.  
 XX  
 SQ Sequence 21 BP; 3 A; 8 G; 4 T; 0 U; 0 Other;  
 XX  
 Query Match 2.0%; Score 19.4; DB 1; Length 21;  
 Best Local Similarity 95.2%; Pred. No. 1.2e+03;  
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 205 GTCAGGCTGTCTCGAATCC 225  
 | |||||  
 Db 1 GCCAGGCTGTCTCGAATCC 21  
 |||||  
 RESULT 606  
 ADH59617/c  
 ID ADH59617 standard; DNA; 21 BP.  
 XX  
 AC ADH59617;  
 XX  
 DT 25-MAR-2004 (first entry)  
 XX  
 DE Non-nucleotide probe of the invention #21.  
 XX  
 KW non-nucleotide probe; Bacterial Artificial Chromosome clone; BAC; ss;  
 XX probe.  
 XX  
 OS Synthetic.

XX  
 PN WO2003027328-A2.  
 XX  
 XX 03-APR-2003.  
 PD  
 XX  
 XX 24-SEP-2002; 2002WO-US030573.  
 PF  
 XX 24-SEP-2001; 2001US-0324499P.  
 PR  
 XX  
 XX (BOST-) BOSTON PROBES INC.  
 PA (DAKO-) DAKOCYTOMATION DENMARK AS.  
 PA  
 PI Kirsens NV, Hyldig-Nielsen JU, Williams BF;  
 XX WPI; 2003-421160/39.  
 DR  
 XX  
 XX Non-nucleotide probe for suppressing binding of detectable nucleic acid  
 PT probes to undesired sequences, has aggregate nucleobase sequence  
 PT homologous to randomly distributed repeat sequence of genomic nucleic  
 PT acid.  
 XX  
 PS Claim 10; SEQ ID NO 23; 103bp; English.  
 XX  
 XX The present sequence represents a non-nucleotide probe. The probe is  
 CC useful for suppressing the binding of one or more detectable nucleic acid  
 CC probes, that are greater than 100 base pairs and that have been derived  
 CC from genomic nucleic acid, to one or more undesired sequences in an assay  
 CC for determining target genomic nucleic acid of a sample. The method  
 CC comprises contacting the sample with the mixture of probes (preferably  
 CC comprising 5-50 probes), contacting the sample with the one or more  
 CC detectable nucleic acid probes, and determining the target genomic  
 CC nucleic acid of the sample by determining the hybridization of the one or  
 CC more detectable nucleic acid probes to the target genomic nucleic acid of  
 CC the sample. The genomic nucleic acid is contained in a fixed tissue or a  
 CC cell, and the sample is metaphase spreads, interphase nucleic or nucleic  
 CC found in paraffin embedded tissue material or frozen tissue sections. The  
 CC probe is also useful in comparing a sample of genomic nucleic acid with  
 CC that of a control sample using a genomic nucleic acid reference array.  
 CC The method comprises treating a sample of genomic nucleic acid and  
 CC control genomic nucleic acid, which are differentially labelled, the  
 CC array or both the sample and control genomic nucleic acid and the array  
 CC with the mixture of the probe under suitable hybridization conditions,  
 CC contacting the array with treated mixture of sample and control genomic  
 CC nucleic acid under suitable hybridization conditions, and comparing the  
 CC intensities of the signals from the differential labels of the array to  
 CC that caused by hybridization of the probes to genomic nucleic acid, thus  
 CC determining one or more variations in copy numbers of sequences in the  
 CC sample as compared with the relative copy numbers of substantially  
 CC identical sequences in the control. The hybridization of the genomic  
 CC array is determined using an intercalating dye or a detectable antibody,  
 CC or its fragment, that is specific for a nucleic acid/nucleic acid hybrid.  
 CC The sample of genomic nucleic acid to be tested and the reference of  
 CC nucleic acid are labelled with detectable moiety such that hybridization  
 CC of the genomic array is determined by determining the presence, absence,  
 CC amount or location of the detectable label on the one or more genomic  
 CC arrays. The genomic array comprises nucleic acid that is prepared from  
 CC Bacterial Artificial Chromosome (BAC) clones. The present sequence  
 CC represents a non-nucleotide probe of the invention.  
 XX  
 SQ Sequence 21 BP; 5 A; 5 C; 8 G; 3 T; 0 U; 0 Other;  
 XX  
 Query Match 2.0%; Score 19.4; DB 1; Length 21;  
 Best Local Similarity 95.2%; Pred. No. 1.2e+03;  
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 990 CCTCCGGGCTCAAGCGATTC 1010  
 | |||||  
 Db 21 CCTCCGGGCTCAAGCGATTC 1  
 |||||  
 RESULT 607  
 ADH59605  
 ID ADH59605 standard; DNA; 21 BP.



XX AC ADH59605;  
 XX DT 25-MAR-2004 (first entry)  
 XX DE Non-nucleotide probe of the invention #9.  
 XX KM non-nucleotide probe; Bacterial Artificial Chromosome clone; BAC; ss;  
 XX KM probe.  
 XX OS Synthetic.  
 XX PN WO2003027328-A2.  
 XX PD 03-APR-2003.  
 XX PF 24-SEP-2002; 2002WO-US030573.  
 XX PR 24-SEP-2001; 2001US-0324499P.  
 XX PA (BOST-) BOSTON PROBES INC.  
 XX PA (DAKO-) DAKOCYTOMATION DENMARK AS.  
 XX PI Kirtsen NV, Hyldig-Nielsen JU, Williams BF;  
 XX PI WPI; 2003-421160/39.  
 XX PT Non-nucleotide probe for suppressing binding of detectable nucleic acid  
 PT probes to undesired sequences, has aggregate nucleobase sequence  
 PT homologous to randomly distributed repeat sequence of genomic nucleic  
 PT acid.  
 XX SS Claim 10; SEQ ID NO 11; 103bp; English.  
 XX CC The present sequence represents a non-nucleotide probe. The probe is  
 CC useful for suppressing the binding of one or more detectable nucleic acid  
 CC probes, that are greater than 100 base pairs and that have been derived  
 CC from genomic nucleic acid, to one or more undesired sequences in an assay  
 CC for determining target genomic nucleic acid of a sample. The method  
 CC comprises contacting the sample with the mixture of probes (preferably  
 CC comprising 5-50 probes), contacting the sample with the one or more  
 CC detectable nucleic acid probes, and determining the target genomic  
 CC nucleic acid of the sample by determining the hybridization of the one or  
 CC more detectable nucleic acid probes to the target genomic nucleic acid of  
 CC the sample. The genomic nucleic acid is contained in a fixed tissue or a  
 CC cell, and the sample is metaphase spreads, interphase nucleic or nucleic  
 CC found in paraffin embedded tissue material or frozen tissue sections. The  
 CC probe is also useful in comparing a sample of genomic nucleic acid with  
 CC that of a control sample using a genomic nucleic acid reference array.  
 CC The method comprises treating a sample of genomic nucleic acid and  
 CC control genomic nucleic acid, which are differentially labelled, the  
 CC array or both the sample and control genomic nucleic acid and the array  
 CC with the mixture of the probe under suitable hybridization conditions,  
 CC contacting the array with treated mixture of sample and control genomic  
 CC nucleic acid under suitable hybridization conditions, and comparing the  
 CC intensities of the signals from the differential labels of the array to  
 CC that caused by hybridization of the probes to genomic nucleic acid, thus  
 CC determining one or more variations in copy numbers of sequences in the  
 CC sample as compared with the control. The hybridization of the genomic  
 CC identical sequences in the control. The hybridization of the genomic  
 CC array is determined using an intercalating dye or a detectable antibody,  
 CC or its fragment, that is specific for a nucleic acid/nucleic acid hybrid.  
 CC The sample of genomic nucleic acid to be tested and the reference of  
 CC nucleic acid are labelled with detectable moiety such that hybridization  
 CC of the genomic array is determined by determining the presence, absence,  
 CC amount or location of the detectable label on the one or more genomic  
 CC arrays. The genomic array comprises nucleic acid that is prepared from  
 CC Bacterial Artificial Chromosome (BAC) clones. The present sequence  
 CC represents a non-nucleotide probe of the invention.  
 XX SQ Sequence 21 BP; 3 A; 8 C; 5 G; 5 T; 0 U; 0 Other;  
 Query Match 2.0%; Score 19.4; DB 1; Length 21;

Best Local Similarity 95.2%; Pred. No. 1.2e+03;  
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 990 CCTCCCGGGCTCAAGGATTC 1010  
 Db 1 CCTCCCGGGCTCAAGGATTC 21  
 RESULT 608  
 ID ACAS4779  
 ACAS4779 standard; DNA; 21 BP.  
 ACAS4779;  
 05-JUN-2003 (first entry)  
 DE Human NF-kappaB associated polynucleotide PCR primer #36.  
 XX KM Human; nuclear factor-kappaB; NF-kappaB; immune disorder; cancer;  
 KM inflammatory disorder; apoptosis; hepatic disorder; Hodgkin's lymphoma;  
 KM haematopoietic tumour; hyper-igm syndrome; viral infection; asthma;  
 KM hypohidrotic ectodermal dysplasia; human immunodeficiency virus; HIV;  
 KM X-linked anhidrotic ectodermal dysplasia; al incontinentia pigmenti;  
 KM influenza; rheumatoid arthritis; inflammatory bowel disease; colitis;  
 KM atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;  
 KM experimental allergic encephalomyelitis; autoimmune disorder; wound;  
 KM hyper immune activity; acute phase response; hypercongenital condition;  
 KM birth defect; necrotic lesion; organ transplant rejection; pancreas;  
 KM signal transduction; hyperproliferative disorder; diabetes mellitus;  
 KM vitamin B12 malabsorption; neurological disorder; Huntington's chorea;  
 KM Turner's syndrome; bacterial infection; cardiovascular disorder;  
 KM infertility; psoriasis; haemolytic anaemia; antiinflammatory; anti-HIV;  
 KM cytostatic; hepatotropic; vitruclide; antineumatic; antiahrtritic;  
 KM antiasthmatic; immunosuppressive; vulnery; antibacterial;  
 KM neuroprotective; immunosuppressive; vulnery; antibacterial;  
 KM antinfertility; antinaemic; antipsoriatic; cerebroprotective; cardiac;  
 KM antiatherosclerotic; PCR; primer; ss.  
 XX OS Homo sapiens.  
 XX PN WO200286076-A2.  
 XX PD 31-OCT-2002.  
 XX PF 19-APR-2002; 2002WO-US012636.  
 XX PR 19-APR-2001; 2001US-0284962P.  
 XX PR 26-APR-2001; 2001US-0286645P.  
 XX PR 09-JUN-2002; 2002US-0346986P.  
 XX PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 XX PI Carman J, Feder J, Nadler S;  
 XX DT WPI; 2003-093119/08.  
 XX PT Novel NF-kappaB-associated polypeptides and polynucleotides useful for  
 PT diagnosing, treating and preventing cancer, hepatic disorders, aberrant  
 PT apoptosis, viral infections, autoimmune disorders, asthma and stroke.  
 XX PS Example 3; Page 341; 608bp; English.  
 XX CC The present invention relates to the isolation of human nuclear factor-  
 CC kappaB (NF-kappaB) associated polypeptides and polynucleotides. The NF-  
 CC kappaB associated polypeptide and polynucleotide sequences are useful for  
 CC preventing, treating or ameliorating various disorders including immune  
 CC disorders, inflammatory disorders, cancer, disorders relating to  
 CC aberrant apoptosis, hepatic disorders, Hodgkin's lymphomas,  
 CC haematopoietic tumours, hyper-igm syndromes, hypohidrotic ectodermal  
 CC dysplasia, X-linked anhidrotic ectodermal dysplasia, immunodeficiency, al  
 CC incontinentia pigmenti, viral infections (e.g. those caused by human  
 CC immunodeficiency virus (HIV), human T-cell lymphotropic virus (HTLV),  
 CC hepatitis B, hepatitis C, Epstein Barr virus (EBV), influenza),

CC rheumatoid arthritis, inflammatory bowel disease, colitis, asthma,  
CC atherosclerosis, cachexia, euthyroid sick syndrome, stroke, experimental  
CC allergic encephalomyelitis (EAE), autoimmune disorders, disorders related  
CC to hyper immune activity, disorders related to aberrant acute phase  
CC responses, hypercongenital conditions, birth defects, necrotic lesions,  
CC wounds, organ transplant rejection, disorders related to aberrant signal  
CC transduction, hyperproliferative disorders, diseases of the pancreas  
CC (e.g. diabetes mellitus, vitamin B12 malabsorption), neurological  
CC disorders (e.g. Huntington's chorea), Turner's syndrome, bacterial  
CC infections, cardiovascular disorders, infertility, psoriasis and  
CC haemolytic anaemia. The present sequence represents a PCR primer used in  
CC the examples of the present invention

CC  
XX  
SQ Sequence 21 BP; 4 A; 2 C; 9 G; 6 T; 0 U; 0 Other;

Query Match 2.0%; Score 19.4; DB 1; Length 21;  
Best Local Similarity 95.2%; Pred. No. 1.2e+03;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 476 TGAAGTGCAGTGTGTGATCA 496  
DB 1 TCGAGTGCAGTGTGTGATCA 21

RESULT 609

AD123732  
ID AD123732 standard; DNA; 21 BP.

AC AD123732;

DT 06-MAY-2004 (first entry)

DE Human LPDLR PCR primer #12.

XX lipase; LPDL; LPDLR; lipase deficiency; atherosclerosis;  
XX fatty liver disease; dyslipidaemia; hypercholesterolaemia;  
XX hypertriglyceridaemia; mixed dyslipidaemia; lipid deficient state;  
XX lipoprotein deficient state; human; ss; PCR; primer.  
XX  
OS Homo sapiens.

PN WO2003055995-A2.

PD 10-JUL-2003.

PF 23-DEC-2002; 2002WO-CA001998.

PR 21-DEC-2001; 2001US-0341786P.

PR 10-JAN-2002; 2002US-0346603P.

PA (WENX/) WEN X.

PA (STEW/) STEWART A. K.

PA (TSUI/) TSUI L.

PA (HEGE/) HEGELE R. A.

PI Wen X, Stewart AK, Tsui L, Hegele RA;

PT WPI; 2003-569444/53.

PT Novel isolated LPDL or LPDLR lipase polypeptides, useful for identifying

PT substances that bind to the protein and which are useful for treating

PT diseases associated with lipase function e.g. atherosclerosis and

PT hypercholesterolemia.

PS Disclosure; SEQ ID NO 68; 172pp; English.

XX The invention relates to an isolated mammalian (e.g., human or mouse)

XX lipase polypeptide (polyp), e.g., LPDL (I) or LPDLR polyp (II). (I) or

XX (II) is useful for identifying substances which can bind with LPDL or

XX LPDLR polyp, and for identifying a compound that affects the binding of

XX LPDL or LPDLR polyp and an LPDL or LPDLR binding polyp. (I) or (II) or

XX their nucleic acid is useful for identifying a compound that affects LPDL

CC is useful for detecting or monitoring a condition associated with  
CC increased or decreased LPDL or LPDLR expression or activity in an animal,  
CC where the condition is lipase deficiency, atherosclerosis, fatty liver  
CC disease and dyslipidaemia, such as hypercholesterolemia,  
CC hypertriglyceridaemia, mixed (combined) dyslipidaemia, lipid or lipoprotein  
CC deficient states, and/or any other tissue or plasma disorders of lipid or  
CC lipoprotein metabolism. The nucleic acid is useful for diagnosing the  
CC presence of or a predisposition for a disorder in a subject which  
CC involves detecting a germline alteration in the nucleic acid in the  
CC subject. An inhibitor is useful for modulating triglyceride activity by  
CC inhibiting expression or activity of (I) or (II). The nucleic acid is  
CC useful as a probe or primer. The present sequence is used in the  
CC exemplification of the invention.

CC  
XX  
SQ Sequence 21 BP; 5 A; 3 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 19.4; DB 1; Length 21;  
Best Local Similarity 95.2%; Pred. No. 1.2e+03;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 863 TGTGTGATTACAGCGGTGAG 883  
DB 1 TGTGTGATTACAGCGGTGAG 21

RESULT 610

AD012329  
ID AD012329 standard; DNA; 21 BP.

AC AD012329;

DT 15-JUL-2004 (first entry)

DE Single multiplex PCR primer #1701.

XX ss; primer; simultaneous amplification;  
XX single multiplex polymerase chain reaction; multifactorial disease;  
XX genetic alteration; pharmacogenetic reaction; genotyping; polymorphism;  
XX gene expression profiling.  
XX  
OS Synthetic.

PN WO2004033649-A2.

PD 22-APR-2004.

PF 07-OCT-2003; 2003WO-US031874.

PR 07-OCT-2002; 2002US-0417009P.

PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.

PI Li H, Li J;

PT WPI; 2004-340914/31.

PT Designing primers for simultaneous amplification of target DNA fragments  
PT in a single multiplex polymerase chain reaction, for high throughput  
PT multiplex DNA sequence amplification, comprises aligning two primers.

PS Disclosure; Page 41; 120pp; English.

XX The invention relates to a method of designing primers for simultaneous

XX amplification of target DNA fragments in a single multiplex polymerase

XX chain reaction by aligning a first primer and a second primer. The method

XX comprises: (a) aligning a first primer and a second primer; and (b)

XX selecting the first primer where the first primer at its 3' end does not

XX contain four or more bases that are perfectly matching to the 3' end

XX sequence of the first primer or a second primer, the first primer at its

XX 3' end does not contain seven or more bases that are perfectly matching

XX except one mismatch to the 3' end sequence of the first primer or the

XX second primer, the first primer at its 3' end does not contain six or

XX more bases that are perfectly matching to a sequence anywhere of the

CC first primer or the second primer, and the first primer at its 3' end  
CC does not contain eleven or more bases that are perfectly matching except  
CC one mismatch to a sequence anywhere of the first primer or the second  
CC primer. The method is useful for designing primers for simultaneous  
CC amplification of target DNA fragments in a single multiplex polymerase  
CC chain reaction. It is also useful in the identification of multiple genes  
CC related to multifactorial diseases, the genome-scale detection of genetic  
CC alterations, the studies in pharmacogenetic reactions, the genotyping  
CC genetic polymorphisms in a large population, the gene expression  
CC profiling in various samples and high throughput genotyping technologies.  
CC This sequence corresponds to an example of a primer of the invention.  
XX  
XX  
SQ Sequence 21 BP; 4 A; 8 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 19.4; DB 1; Length 21;  
Best Local Similarity 95.2%; Pred. No. 1.2e+03;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 209 GGCTGCTCGAAGCTCCGAC 229  
1 GGCTGCTCGAAGCTCCGAC 21

RESULT 611  
AA225156  
ID AA225156 standard; DNA; 22 BP.  
XX  
XX AA225156;  
XX  
XX 13-DEC-1999 (first entry)  
XX  
XX Human short interspersed repetitive element PCR primer #14.  
DE

KM Human; short interspersed repetitive element; SINE; PCR; primer;  
KW Oncochynchus; restriction primer; short interspersed repeated sequence;  
KM eukaryote; restricted polymerase chain reaction fingerprinting;  
XX identification; DNA specimen; discrimination; ss.  
XX

OS Synthetic.  
OS Homo sapiens.  
XX

PN JP2913035-B1.  
XX

PD 28-JUN-1999.  
XX

PF 10-JUL-1998; 98BP-00195692.  
XX

PR 10-JUL-1998; 98BP-00195692.  
XX

PA (NORQ) NORINSUISANSHO SUISANCHO YOSHOKU KENKYUSHOCHO.  
XX

DR WPI; 1999-583348/50.  
XX

PT Restriction primer for distinguishing individuals with short interspersed  
XX repeated sequence of eukaryotes by restricted polymerase chain reaction  
XX fingerprinting.  
XX

PS Claim 6; Page 3; 17pp; Japanese.  
XX

CC The present invention describes a restriction primer for eukaryotic short  
CC interspersed repeated sequences (SINE), which has one or more additional  
CC bases that are a mismatch to, or are unrelated to, the 3'-terminal end of  
CC the SINE. The annealing temperature of the primer to the DNA sequence is  
CC kept higher than the fusion temperature of the primer during polymerase  
CC chain reaction (PCR). The PCR fragments obtained are subjected to  
CC electrophoresis to obtain a fingerprint. By comparing the polymorphs from  
CC the electrophoresis band pattern, eukaryotic individuals are  
CC distinguished. The primer is used for amplifying a eukaryotic  
CC deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by  
CC polymerase chain reaction (PCR) fingerprinting. In particular it may be  
CC used individual identification of humans for medical and legal  
CC applications and ecological studies. DNA specimens in traces  
CC (approximately 10 ng in mass) can be used for individual discrimination

CC of eukaryotes using the primer in a polymerase chain reaction (PCR).  
CC AA225143 to AA225191 represent specifically claimed examples of primers  
CC from the present invention  
XX

SQ Sequence 22 BP; 7 A; 5 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 19.4; DB 1; Length 22;  
Best Local Similarity 95.2%; Pred. No. 1.3e+03;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 869 GATTACAGGCGTAGCCACCA 889  
1 GATTACAGGCGTAGCCACCA 21

RESULT 612  
AA225168  
ID AA225168 standard; DNA; 22 BP.  
XX

AC AA225168;  
XX

DT 13-DEC-1999 (first entry)  
XX

DE Human short interspersed repetitive element PCR primer #26.  
XX

KM Human; short interspersed repetitive element; SINE; PCR; primer;  
KW Oncochynchus; restriction primer; short interspersed repeated sequence;  
KM eukaryote; restricted polymerase chain reaction fingerprinting;  
XX identification; DNA specimen; discrimination; ss.  
XX

OS Synthetic.  
OS Homo sapiens.  
XX

PN JP2913035-B1.  
XX

PD 28-JUN-1999.  
XX

PF 10-JUL-1998; 98BP-00195692.  
XX

PR 10-JUL-1998; 98BP-00195692.  
XX

PA (NORQ) NORINSUISANSHO SUISANCHO YOSHOKU KENKYUSHOCHO.  
XX

DR WPI; 1999-583348/50.  
XX

PT Restriction primer for distinguishing individuals with short interspersed  
XX repeated sequence of eukaryotes by restricted polymerase chain reaction  
XX fingerprinting.  
XX

PS Claim 6; Page 4; 17pp; Japanese.  
XX

CC The present invention describes a restriction primer for eukaryotic short  
CC interspersed repeated sequences (SINE), which has one or more additional  
CC bases that are a mismatch to, or are unrelated to, the 3'-terminal end of  
CC the SINE. The annealing temperature of the primer to the DNA sequence is  
CC kept higher than the fusion temperature of the primer during polymerase  
CC chain reaction (PCR). The PCR fragments obtained are subjected to  
CC electrophoresis to obtain a fingerprint. By comparing the polymorphs from  
CC the electrophoresis band pattern, eukaryotic individuals are  
CC distinguished. The primer is used for amplifying a eukaryotic  
CC deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by  
CC polymerase chain reaction (PCR) fingerprinting. In particular it may be  
CC used individual identification of humans for medical and legal  
CC applications and ecological studies. DNA specimens in traces  
CC (approximately 10 ng in mass) can be used for individual discrimination  
CC of eukaryotes using the primer in a polymerase chain reaction (PCR).  
CC AA225143 to AA225191 represent specifically claimed examples of primers  
CC from the present invention  
XX

SQ Sequence 22 BP; 6 A; 5 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 19.4; DB 1; Length 22;  
Best Local Similarity 95.2%; Pred. No. 1.3e+03;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 869 GATTACAGCGGTGAGCCACCA 889  
 |||||  
 DB 1 GATTACAGCGGTGAGCCACCA 21

RESULT 613  
 AAZ25162  
 ID AAZ25162 standard; DNA; 22 BP.

XX AC AAZ25162;  
 XX XX  
 DT 13-DEC-1999 (first entry)

DE Human short interspersed repetitive element PCR primer #20.

XX KM Human; short interspersed repetitive element; SINE; PCR; primer;  
 KM Oncohychnus; restriction primer; short interspersed repeated sequence;  
 KM eukaryote; restricted polymerase chain reaction fingerprinting;  
 KM identification; DNA specimen; discrimination; ss.

XX OS Synthetic.  
 OS Homo sapiens.

XX PN JP2913035-B1.

XX PD 28-JUN-1999.

XX PF 10-JUL-1998; 98UP-00195692.

XX PR 10-JUL-1998; 98UP-00195692.

XX PA (NORO ) NORINSUISANSO SUIANCHO YOSHOKU KENKYUSHOCHO.

XX DR WPI; 1999-583348/50.

XX PT Restriction primer for distinguishing individuals with short interspersed  
 PT repeated sequence of eukaryotes by restricted polymerase chain reaction  
 PT fingerprinting.

XX PS Claim 6; Page 3; 17pp; Japanese.

XX CC The present invention describes a restriction primer for eukaryotic short  
 CC interspersed repeated sequences (SINEs), which has one or more additional  
 CC bases that are a mismatch to, or are unrelated to, the 3'-terminal end of  
 CC the SINE. The annealing temperature of the primer to the DNA sequence is  
 CC kept higher than the fusion temperature of the primer during polymerase  
 CC chain reaction (PCR). The PCR fragments obtained are subjected to  
 CC electrophoresis to obtain a fingerprint. By comparing the polymorphs from  
 CC the electrophoresis band pattern, eukaryotic individuals are  
 CC distinguished. The primer is used for amplifying a eukaryotic  
 CC deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by  
 CC polymerase chain reaction (PCR) fingerprinting. In particular it may be  
 CC used for individual identification of humans for medical and legal  
 CC applications and ecological studies. DNA specimens in traces  
 CC (approximately 10 ng in mass) can be used for individual discrimination  
 CC of eukaryotes using the primer in a polymerase chain reaction (PCR).  
 CC AAZ25143 to AAZ25191 represent specifically claimed examples of primers  
 CC from the present invention

XX SQ Sequence 22 BP; 6 A; 5 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 19.4; DB 1; Length 22;

Best Local Similarity 95.2%; Pred. No. 1.3e+03;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 869 GATTACAGCGGTGAGCCACCA 889  
 |||||  
 DB 1 GATTACAGCGGTGAGCCACCA 21

RESULT 614

AAZ25161  
 ID AAZ25161 standard; DNA; 22 BP.

XX AC AAZ25161;  
 XX XX  
 DT 13-DEC-1999 (first entry)

DE Human short interspersed repetitive element PCR primer #19.

XX KM Human; short interspersed repetitive element; SINE; PCR; primer;  
 KM Oncohychnus; restriction primer; short interspersed repeated sequence;  
 KM eukaryote; restricted polymerase chain reaction fingerprinting;  
 KM identification; DNA specimen; discrimination; ss.

XX OS Synthetic.  
 OS Homo sapiens.

XX PN JP2913035-B1.

XX PD 28-JUN-1999.

XX PF 10-JUL-1998; 98UP-00195692.

XX PR 10-JUL-1998; 98UP-00195692.

XX PA (NORO ) NORINSUISANSO SUIANCHO YOSHOKU KENKYUSHOCHO.

XX DR WPI; 1999-583348/50.

XX PT Restriction primer for distinguishing individuals with short interspersed  
 PT repeated sequence of eukaryotes by restricted polymerase chain reaction  
 PT fingerprinting.

XX PS Claim 6; Page 3; 17pp; Japanese.

XX CC The present invention describes a restriction primer for eukaryotic short  
 CC interspersed repeated sequences (SINEs), which has one or more additional  
 CC bases that are a mismatch to, or are unrelated to, the 3'-terminal end of  
 CC the SINE. The annealing temperature of the primer to the DNA sequence is  
 CC kept higher than the fusion temperature of the primer during polymerase  
 CC chain reaction (PCR). The PCR fragments obtained are subjected to  
 CC electrophoresis to obtain a fingerprint. By comparing the polymorphs from  
 CC the electrophoresis band pattern, eukaryotic individuals are  
 CC distinguished. The primer is used for amplifying a eukaryotic  
 CC deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by  
 CC polymerase chain reaction (PCR) fingerprinting. In particular it may be  
 CC used for individual identification of humans for medical and legal  
 CC applications and ecological studies. DNA specimens in traces  
 CC (approximately 10 ng in mass) can be used for individual discrimination  
 CC of eukaryotes using the primer in a polymerase chain reaction (PCR).  
 CC AAZ25143 to AAZ25191 represent specifically claimed examples of primers  
 CC from the present invention

XX SQ Sequence 22 BP; 7 A; 5 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 19.4; DB 1; Length 22;

Best Local Similarity 95.2%; Pred. No. 1.3e+03;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 869 GATTACAGCGGTGAGCCACCA 889  
 |||||  
 DB 1 GATTACAGCGGTGAGCCACCA 21

RESULT 615

AAZ25167  
 ID AAZ25167 standard; DNA; 22 BP.

XX AC AAZ25167;  
 XX XX  
 DT 13-DEC-1999 (first entry)

DE Human short interspersed repetitive element PCR primer #25.

XX Human; short interspersed repetitive element; SINE; PCR; primer;  
 KW Oncohychnus; restriction primer; short interspersed repeated sequence;  
 KW eukaryote; restricted polymerase chain reaction fingerprinting;  
 KW identification; DNA specimen; discrimination; ss.

OS Synthetic.  
 OS Homo sapiens.

XX JP2913035-B1.

XX 28-JUN-1999.

XX 10-JUL-1998; 98JP-00195692.

XX 10-JUL-1998; 98JP-00195692.

XX (NORQ ) NORINSUISANSHO SUISANCHO YOSHOKU KENKYUSHOCHO.

XX WPI; 1999-583348/50.

PT Restriction primer for distinguishing individuals with short interspersed  
 PT repeated sequence of eukaryotes by restricted polymerase chain reaction  
 PT fingerprinting.

PS Claim 6; Page 4; 17pp; Japanese.

XX The present invention describes a restriction primer for eukaryotic short  
 CC interspersed repeated sequences (SINE), which has one or more additional  
 CC bases that are a mismatch to, or are unrelated to, the 3'-terminal end of  
 CC the SINE. The annealing temperature of the primer to the DNA sequence is  
 CC kept higher than the fusion temperature of the primer during polymerase  
 CC chain reaction (PCR). The PCR fragments obtained are subjected to  
 CC electrophoresis to obtain a fingerprint. By comparing the polymorphs from  
 CC the electrophoresis band pattern, eukaryotic individuals are  
 CC distinguished. The primer is used for amplifying a eukaryotic  
 CC deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by  
 CC polymerase chain reaction (PCR) fingerprinting. In particular it may be  
 CC used for individual identification of humans for medical and legal  
 CC applications and ecological studies. DNA specimens in traces  
 CC (approximately 10 ng in mass) can be used for individual discrimination  
 CC of eukaryotes using the primer in a polymerase chain reaction (PCR).  
 CC AA25143 to AA25191 represent specifically claimed examples of primers  
 CC from the present invention

SO Sequence 22 BP; 7 A; 5 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 19.4; DB 1; Length 22;

Best Local Similarity 95.2%; Pred. No. 1.3e+03;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 869 GATTACAGCGGTGAGCCACCA 889

DB 1 GATTACAGCGGTGAGCCACTA 21

RESULT 616

AA25155 ID AA25155 standard; DNA; 22 BP.

XX AA25155;

XX 13-DEC-1999 (first entry)

XX Human short interspersed repetitive element PCR primer #13.

XX Human; short interspersed repetitive element; SINE; PCR; primer;  
 KW Oncohychnus; restriction primer; short interspersed repeated sequence;  
 KW eukaryote; restricted polymerase chain reaction fingerprinting;  
 KW identification; DNA specimen; discrimination; ss.

XX Synthetic.  
 OS Homo sapiens.

XX JP2913035-B1.

XX 28-JUN-1999.

XX 10-JUL-1998; 98JP-00195692.

XX 10-JUL-1998; 98JP-00195692.

XX (NORQ ) NORINSUISANSHO SUISANCHO YOSHOKU KENKYUSHOCHO.

XX WPI; 1999-583348/50.

PT Restriction primer for distinguishing individuals with short interspersed  
 PT repeated sequence of eukaryotes by restricted polymerase chain reaction  
 PT fingerprinting.

PS Claim 6; Page 3; 17pp; Japanese.

XX The present invention describes a restriction primer for eukaryotic short  
 CC interspersed repeated sequences (SINE), which has one or more additional  
 CC bases that are a mismatch to, or are unrelated to, the 3'-terminal end of  
 CC the SINE. The annealing temperature of the primer to the DNA sequence is  
 CC kept higher than the fusion temperature of the primer during polymerase  
 CC chain reaction (PCR). The PCR fragments obtained are subjected to  
 CC electrophoresis to obtain a fingerprint. By comparing the polymorphs from  
 CC the electrophoresis band pattern, eukaryotic individuals are  
 CC distinguished. The primer is used for amplifying a eukaryotic  
 CC deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by  
 CC polymerase chain reaction (PCR) fingerprinting. In particular it may be  
 CC used for individual identification of humans for medical and legal  
 CC applications and ecological studies. DNA specimens in traces  
 CC (approximately 10 ng in mass) can be used for individual discrimination  
 CC of eukaryotes using the primer in a polymerase chain reaction (PCR).  
 CC AA25143 to AA25191 represent specifically claimed examples of primers  
 CC from the present invention

SO Sequence 22 BP; 8 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 19.4; DB 1; Length 22;

Best Local Similarity 95.2%; Pred. No. 1.3e+03;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 869 GATTACAGCGGTGAGCCACCA 889

DB 1 GATTACAGCGGTGAGCCACCA 21

RESULT 617

AA511629 ID AA511629 standard; DNA; 22 BP.

XX AA511629;

XX 24-OCT-2001 (first entry)

XX Human CYP2B6 allele sequencing primer seqCYP2B6-7F for exon 7.

XX CYP2B6; cytosolic; gene therapy; genotyping; cancer; metabolism; ss;  
 KW human; cancer susceptibility; environmental carcinogen;  
 KW sequencing primer.

XX Homo sapiens.

XX WO200159152-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-EP001456.

XX 09-FEB-2000; 2000BP-00102701.

XX (EPID-) EPIDAKROS BIOTECHNOLOGIE AG.

XX Zanger UM, Lang T;  
PI WPI, 2001-502719/55.  
XX  
XX  
XX New polynucleotide(s) of the polymorphic human CYP2B6 gene for the  
PT detection and treatment of disorders i.e. cancer.  
PS Claim 36; Page 45; 83pp; English.  
XX  
XX The sequence represents a sequencing primer used to sequence an exon of  
CC the human CYP2B6 gene. It is used for specific detection and genotyping  
CC of CYP2B6 alleles in humans, determination of which is useful for the  
CC optimization of therapies utilizing CYP2B6 substrates. Oligonucleotide  
CC sequences are useful in detection of the individual predisposition to  
CC several common cancers caused by environmental carcinogens, and diseases  
CC treated with drugs that are targets of the CYP2B6 gene product, whose  
CC metabolism is therefore dependent on CYP2B6. Cancer or susceptibility to  
CC cancer can be diagnosed by detecting the presence of a molecular variant  
CC of CYP2B6. From variants of the alleles, modulators of the activity can  
CC be developed for use in treatment and prevention of CYP2B6-related  
CC disorders  
XX  
SQ Sequence 22 BP; 7 A; 6 C; 5 G; 4 T; 0 U; 0 Other;  
Query Match 2.0%; Score 19.4; DB 1; Length 22;  
Best Local Similarity 95.2%; Pred. No. 1.3e+03;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 869 GATTACAGCGCTGAGCCACCA 889  
DB 1 GATTACAGCGCATGAGCCACCA 21  
RESULT 618  
ID AAF93028/C  
XX AAF93028 standard; DNA; 22 BP.  
XX  
XX AAF93028;  
XX  
XX 17-MAY-2001 (first entry)  
XX  
XX Polymorphic sequence for ABC1 polymorphic site #38.  
XX  
XX High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ds.  
XX  
XX Homo sapiens.  
XX  
XX WO200115676-A2.  
XX  
XX 08-MAR-2001.  
XX  
XX 01-SEP-2000; 2000WO-1B001492.  
XX  
XX 01-SEP-1999; 99US-0151977P.  
XX 15-MAR-2000; 2000US-00526193.  
XX 23-JUN-2000; 2000US-0213958P.  
XX  
XX (UYBR-) UNIV BRITISH COLUMBIA.  
XX (XENO-) XENON GENETICS INC.  
XX  
XX Hayden MR, Brooks-Wilson AR, Pimstone SN, Clee SM;  
PI WPI; 2001-244356/25.  
XX  
XX  
XX Treating a lower than normal high density lipoprotein-cholesterol (HDL-C)  
PT level, a higher than normal triglyceride level, or a cardiovascular  
PT disease, by administering a compound that modulates LXR- or RXR-mediated  
PT transcriptional activity.  
XX  
XX Disclosure; Fig 4; 317pp; English.  
XX  
XX The present invention relates to a method for treating a patient

CC diagnosed as having a lower than normal high density lipoprotein-  
CC cholesterol (HDL-C) level, a higher than normal triglyceride level, or a  
CC cardiovascular disease, involving administering a compound that modulates  
CC LXR- or RXR-mediated transcriptional activity or ABC1 expression or  
CC activity. The LXR gene product may be used in an assay to identify  
CC compounds useful for the treatment of a disease or condition selected a  
CC lower than normal HDL cholesterol level, a higher than normal  
CC triglyceride level, and a cardiovascular disease  
XX  
SQ Sequence 22 BP; 6 A; 2 C; 10 G; 3 T; 0 U; 1 Other;  
Query Match 2.0%; Score 19.4; DB 1; Length 22;  
Best Local Similarity 90.9%; Pred. No. 1.3e+03;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 533 TCCTCTGCGCTGAGCTCCCA 554  
DB 22 TCCTCTGCTTACCTCCCA 1  
RESULT 619  
ID ADC24360  
XX ADC24360 standard; DNA; 22 BP.  
XX  
XX ADC24360;  
XX  
XX 18-DEC-2003 (first entry)  
XX  
XX PCR primer for amplifying the BRCA1 gene #SEQ ID 50.  
XX  
XX DNA amplification; copy number; polymerase chain reaction; PCR; primer;  
XX ss.  
XX  
XX Synthetic.  
XX  
XX JP2002345466-A.  
XX  
XX 03-DEC-2002.  
XX  
XX 08-MAY-2001; 2001JP-00137858.  
XX  
XX 08-MAY-2001; 2001JP-00137858.  
XX  
XX  
XX (TAKA-) TAKARA BIO KK.  
XX (KOKU-) KOKURITSU GAN CENT SOCHO.  
XX (YAK-) IYAKUHIN FUKUSAYO HIGAI KYUSAI KENKYU SH.  
XX  
XX WPI; 2003-460878/44.  
XX  
XX  
XX Amplification of DNA maintaining genes and copy number of the sequence on  
PT a genome, and their ratios in the resultant DNA fragment.  
XX  
XX Example 3; SEQ ID NO 50; 33pp; Japanese.  
XX  
XX The invention relates to a method for the amplification of DNA that  
CC maintains genes and copy number of the sequence. This method is useful  
CC for easy and operable amplification of DNA. The method was carried out by  
CC fragmentation genomic DNA, preparation of blunt end of the fragmented  
CC DNA, ligation of an adapter to the blunted DNA, PCR of the ligated DNA in  
CC 2 steps, and confirmation of the amplified APC gene. The current sequence  
CC represents a PCR primer used in an example from the invention.  
XX  
SQ Sequence 22 BP; 7 A; 4 C; 7 G; 4 T; 0 U; 0 Other;  
Query Match 2.0%; Score 19.4; DB 1; Length 22;  
Best Local Similarity 95.2%; Pred. No. 1.3e+03;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 387 CCAAGTGTGCGATTACAG 407  
DB 1 CCAAGTGTGCGATTACAG 21

```
RESULT 620
AAQ73576
ID AAQ73576 standard; DNA; 24 BP.
XX
AC AAQ73576;
XX
DT 25-MAR-2003 (revised)
DT 25-JUN-1995 (first entry)
XX
DE Enhancer element er-6 conserved basepair sequence.
XX
XX Enhancer element; carcinoma; tumor; cancer; SLP1 gene;
KW secretory leukoprotease-inhibitor gene; cytokeratin gene-8; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT misc_difference 14 /*tag= a
FT /*label= purine
FT misc_difference 16 /*tag= b
FT /*label= pyrimidine
FT misc_difference 22 /*tag= c
FT /*label= purine
XX
PN WO9421118-A1.
XX
PD 29-SEP-1994.
XX
PF 24-MAR-1994; 94WO-US003197.
XX
PR 24-MAR-1993; 93US-00035435.
XX
PA (UABR-) UAB RES FOUND.
XX
PI Garver RI, Sorscher EJ;
XX
DR WPI; 1994-316537/39.
XX
PT DNA construct for treating human carcinoma - includes a cancer-
PT therapeutic gene under the control of a promoter and a gp. of enhancer
PT sequences.
XX
PS Claim 1; Fig 6; 54pp; English.
XX
CC This enhancer element is part of a DNA construct used for treating human
CC carcinoma which contains a cancer therapeutic protein under the control
CC of a promoter and 3 enhancer sequences in a specific 5'-3' order. This
CC enhancer element is derived from the flanking region of the human
CC epithelial cell cytokeratin-8 gene. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 24 BP; 3 A; 8 C; 6 G; 4 T; 0 U; 3 Other;
XX
QY
DB 1 CCTCAGCCTCCTGAGTAGTGGA 739
1 CCTCAGCCTCCTGAGTAGTGGA 24

Query Match 2.0%; Score 19.4; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
XX
DE Enhancer element er-6 conserved basepair sequence.
XX
XX Enhancer element; carcinoma; tumor; cancer; SLP1 gene;
KW secretory leukoprotease-inhibitor gene; cytokeratin gene-8; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT misc_difference 14 /*tag= a
FT /*label= purine
FT misc_difference 16 /*tag= b
FT /*label= pyrimidine
FT misc_difference 22 /*tag= c
FT /*label= purine
XX
PN WO9421118-A1.
XX
PD 29-SEP-1994.
XX
PF 24-MAR-1994; 94WO-US003197.
XX
PR 24-MAR-1993; 93US-00035435.
XX
PA (UABR-) UAB RES FOUND.
XX
PI Garver RI, Sorscher EJ;
XX
DR WPI; 1994-316537/39.
XX
PT DNA construct for treating human carcinoma - includes a cancer-
PT therapeutic gene under the control of a promoter and a gp. of enhancer
PT sequences.
XX
PS Claim 1; Fig 6; 54pp; English.
XX
CC This enhancer element is part of a DNA construct used for treating human
CC carcinoma which contains a cancer therapeutic protein under the control
CC of a promoter and 3 enhancer sequences in a specific 5'-3' order. This
CC enhancer element is derived from the flanking region of the human
CC epithelial cell secretory leukoprotease-inhibitor gene. (Updated on 25-
CC MAR-2003 to correct PN field.)
XX
SQ Sequence 24 BP; 3 A; 8 C; 6 G; 4 T; 0 U; 3 Other;
XX
QY
DB 1 CCTCAGCCTCCTGAGTAGTGGA 739
1 CCTCAGCCTCCTGAGTAGTGGA 24

RESULT 622
AAT63214
ID AAT63214 standard; DNA; 20 BP.
XX
AC AAT63214;
XX
DT 17-JUN-1997 (first entry)
XX
DE Primer Alu 5' used in Inter-Alu PCR for PAC isolation.
XX
KW S182 gene; familial Alzheimer's disease; diagnosis; transgenic animal;
KW polymerase chain reaction; PCR; primer; artificial chromosome; PAC; ss.
XX
OS Synthetic.
XX
PN WO9703999-A1.
```

```
XX 06-FEB-1997.
PD
XX
PF 26-JUN-1996; 96WO-US011065.
XX
XX 18-JUL-1995; 95US-0001500P.
PR 02-AUG-1995; 95US-0001800P.
XX
PA (UNITW ) UNIV WASHINGTON SCHOOL MED.
XX (USF-) UNIV SOUTH FLORIDA.
XX
PI Goate AM, Hardy JA;
XX
DR WPI; 1997-132571/12.
XX
PT New mutance of the S182 gene associated with familial Alzheimer's disease
PT - and related protein and transgenic animals, useful as models for
PT screening and assessing potential drugs.
XX
XX Example 2; Page 11; 26pp; English.
XX
CC Inter-Alu PCR was performed on YACs 905C2 and 763B11. Unpurified YAC DNA
CC was amplified with generate primers Alu 5' (AAT63214) and Alu 3'
CC (AAT63215). Genetic linkage strategies have placed a gene causing early
CC onset Alzheimer's disease (AD) on the long arm of chromosome 14 between
CC D14S289 and D14S61. The gene, S182 (see also AAT63207), was localised to
CC a 100 kb region between D14S77 and D14S668E (see also AAT63216-22). A
CC number of novel mutations in the S182 gene have been identified in
CC families multiply affected by early onset AD
XX
SQ Sequence 20 BP; 5 A; 4 C; 6 G; 3 T; 0 U; 2 Other;
XX
Query Match 1.9%; Score 19.2; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.2e+03;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 868 GGATTACAGCGCTGAGCCAC 887
Db 1 GGATTACAGCGCTGAGCCAC 20
XX
RESULT 623
AAA55956
ID AAA55956 standard; DNA; 24 BP.
XX
AC AAA55956;
XX
XX 26-JUL-2000 (first entry)
XX
DE Human genomic SNP allele specific oligonucleotide SEQ ID NO:13.
XX
XX Human; single nucleotide polymorphism; SNP; genotyping; DNA analysis;
XX allele specific oligonucleotide; ASO; reduced complexity genome; RCG;
XX genomic classification; identification; DNA fingerprinting;
XX tumour characterisation; hybridisation; ss.
XX
OS Homo sapiens.
XX
XX WO200018960-A2.
XX
XX 06-APR-2000.
XX
XX 24-SEP-1999; 99WO-US022283.
XX
XX 25-SEP-1998; 98US-0101757P.
XX
XX (MASI ) MASSACHUSETTS INST TECHNOLOGY.
XX
XX Landers JE, Jordan B, Houseman DE, Charest A;
XX
XX WPI; 2000-293181/25.
XX
PT Detection of single nucleotide polymorphisms in genomes by preparation
```

```
PT and analysis of reduced complexity genomes, useful for genotyping,
PT fingerprinting and determining allele frequency of SNPs.
XX
XX Disclosure; Page 53; 11pp; English.
XX
XX A method has been developed for detecting the presence or absence of a
XX single nucleotide polymorphism (SNP) allele in a genomic sample. The
XX method comprises preparing a reduced complexity genome (RCG) from the
XX genomic sample and analysing the RCG for the presence or absence of a SNP
XX allele. The method can be used to characterise a tumour, to generate a
XX genomic pattern for an individual genome or to generate a genomic
XX classification code for a genome. The method can be used to assess
XX whether a subject is at risk for developing a disease or to identify a
XX set of SNP alleles associated with a disease. The method can also be used
XX to perform linkage analysis. AAA5944 to AAA5947 represent sequences
XX used in the exemplification of the present invention. AAA5948 to
XX AAA5652 represent nucleotide sequences containing SNPs
XX
SQ Sequence 24 BP; 6 A; 8 C; 6 G; 4 T; 0 U; 0 Other;
XX
Query Match 1.9%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 870 ATTACAGCGCTGAGCCACCGCC 893
Db 1 ATTACAGCGCTGAGCCACCGCC 24
XX
RESULT 624
AAA27180/C
ID AAA27180 standard; DNA; 24 BP.
XX
XX AAA27180;
XX
XX 11-SEP-2000 (first entry)
XX
XX Forward primer P2 for target sequence human P2 gene.
XX
XX P2; CXSC chemokine; Chromosome 5q31; gene therapy; asthma; PCR primer;
XX allergic rhinitis; urticaria; anaphylactic shock; hives; hay fever; human;
XX ss.
XX
XX Homo sapiens.
XX
XX WO200029621-A2.
XX
XX 25-MAY-2000.
XX
XX 12-NOV-1999; 99WO-US026931.
XX
XX 16-NOV-1998; 98US-00193320.
XX
XX (GENE-) GENELABS TECHNOLOGIES INC.
XX
XX Dolganov G, Novikov A;
XX
XX WPI; 2000-387825/33.
XX
XX Measuring target polynucleotide sequences in biological samples by
XX contracting sequence-selective primer pairs, forming conjugates with
XX adaptor molecules, polymerizing target-identifier dimers and quantifying
XX them.
XX
XX Disclosure; Page 99; 103pp; English.
XX
XX A novel method for simultaneously determining the level of a number of
XX target polynucleotides in a sample has been disclosed. The method
XX involves forming double stranded copies of the target sequence in direct
XX proportion to the target levels in the original sample. The target
XX sequence is copied using primer pairs designed to flank a defined region
XX in the target sequence. The double stranded copies are then cleaved and
XX reacted with either first or second adaptor sequences. The first and
```



second conjugate mixtures are then allowed to form dimers with each other through the target sequences. The adaptor sequences are then removed to leave target sequence dimers. These dimers are then polymerised to form dimer multimers. The relative abundances of target identifiers in the multimer allow expression levels to be determined. This method is useful for developing polynucleotide abundance level profiles for cells and tissues under various conditions, stages of development and disease states, particularly where the target polynucleotide is present at low levels. The method may also be used in the discovery and evaluation of candidate therapeutic agents and their effective dosage levels. In addition to the method described above, the invention also includes the polynucleotide and polypeptide of P2. P2 is thought to be a member of a novel chemokine family, denoted CX5C and may be associated with immune function. Compositions of the P2 polypeptide may be useful in the treatment of asthma, allergic rhinitis (hay fever), urticaria (hives), anaphylactic shock and conditions involving immune system hypersensitivity. The P2 polynucleotide to treat conditions using gene therapy. The human P2 gene has been localised to chromosome 5, within the cytokine gene cluster at 5q31. The present sequence is the forward primer P2 for target sequence human P2 gene

Sequence 24 BP; 4 A; 3 C; 12 G; 5 T; 0 U; 0 Other;

Query Match 1.9%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 1.4e+03;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 676 CACTGCACTCTGCTCCGGGT 699  
DB 24 CACTGCACTCTGCTCCGGGT 1

RESULT 625  
AAH45660/C  
ID AAH45660 standard; DNA; 24 BP.

AAH45660;

24-SEP-2001 (first entry)

PCR primer specific for human protease regulatory protein 9 cDNA.

Protease regulatory protein 9; malignant tumour; haemopathy; cytostatic;  
HIV infection; immunological disease; inflammation; haemostatic;

viinucleide; immunomodulatory; PCR primer; ss.

Homo sapiens.

WO200149731-A1.

12-JUL-2001.

25-DEC-2000; 2000MO-CN000652.

29-DEC-1999; 99CN-00127227.

(YTFU-) UNIV FUDAN  
(SHAN-) SHANGHAI BIO DOOR GENE TECHNOLOGY LTD.

Mao Y, Yie Y;

WPI; 2001-441850/47.

Human protease regulatory protein 9 and encoded polynucleotide, used in diagnosis and treatment of malignant tumours, hemopathy, human immunodeficiency virus infection, immunological diseases and inflammation.

Example 3; Page 17; 35pp; Chinese.

This invention relates to human protease regulatory protein 9, and the cDNA encoding it. The invention includes a vector containing the cDNA, a host cell transformed with the vector, and an antibody directed against

the protein. The protein and polynucleotide sequences can be used in the diagnosis and treatment of malignant tumours, haemopathy, human immunodeficiency virus (HIV) infection, immunological diseases, and various inflammatory conditions. Use of the protein or polynucleotide or their agonists/antagonists causes cytostatic, haemostatic, viinucleide or immunomodulatory activity. The present sequence represents a PCR primer specific for cDNA encoding human protease regulatory protein 9

Sequence 24 BP; 5 A; 2 C; 12 G; 5 T; 0 U; 0 Other;

Query Match 1.9%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 1.4e+03;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 968 TCTCGGCTCACTGCACTCTGCC 991  
DB 24 TCTCGGCTCACTGCACTCTGCC 1

RESULT 626  
AAH46154/C  
ID AAH46154 standard; DNA; 24 BP.

AAH46154;

12-SEP-2001 (first entry)

Cysteine protease 10 RT-PCR primer, SEQ ID NO:3.

Cysteine protease 10; human; recombinant production; malignant tumour;

cancer; blood disease; HIV infection; human immunodeficiency virus;

immune disorder; inflammatory condition; cytostatic; anti-HIV;

antiinflammatory; immunomodulator; reverse transcription-PCR;

RT-PCR primer; ss.

Homo sapiens.

WO200146442-A1.

28-JUN-2001.

18-DEC-2000; 2000MO-CN000608.

22-DEC-1999; 99CN-00125682.

(BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.

Mao Y, Xie Y;

WPI; 2001-418079/44.

Cysteine protease 10 and encoded polynucleotide, applicable in diagnosis and treatment of malignant tumor, hemopathy, HIV infection, immunological diseases and various inflammation.

Example 3; Page 12; 35pp; Chinese.

This sequence represents cDNA encoding cysteine protease 10. The protein has a molecular weight of 10 kD, and has homology with a cysteine protease given in AAB73748 over a 51 amino acid stretch. The invention relates to cysteine protease 10 (AAB73746), nucleic acids encoding it (AAH46153), and a method for the recombinant production of cysteine protease 10. The present invention additionally discloses an agonist of cysteine protease 10 for therapeutic use, and an antibody which specifically binds to cysteine protease 10. Cysteine protease 10, and nucleotides which encode it may be used for treating a variety of

diseases, such as malignant tumours, blood diseases, HIV (human immunodeficiency virus) infection, immune disorders and inflammatory conditions. The protein may also be used to screen for modulators of its activity or for peptide fingerprinting identification. The polynucleotide can be used as a primer for nucleic acid amplification reactions or as a probe for hybridisation reactions, or in producing gene chips or microarrays. Sequences AAH46154-AAH46155 represent reverse transcription-

CC PCR (RT-PCR) primers used in an exemplification of the invention to  
CC isolate human cysteine protease 10 cDNA  
XX  
SQ Sequence 24 BP; 7 A; 5 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 1.9%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 1.4e+03;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 536 TCCTGCTCAGCCTCCAGTAGC 559  
DB 24 TCTTGTCTCAGCCTCCAGTAGC 1

RESULT 627

AAH75665  
ID AAH75665 standard; DNA; 24 BP.

XX AAH75665;

DT 08-NOV-2001 (first entry)

XX Human Pax protein 9 PCR primer 2.

XX Human; Pax protein 9; cytosolic; virucide; immunomodulatory;  
KW antiinflammatory; haemostatic; anti-HIV; paired box domain; neoplasm;  
KW human immunodeficiency virus; HIV; infection; immunological disease;  
KW developmental disorder; growth developmental disturbance;  
KW Waardenburger's syndrome; gene therapy; PCR primer; ss.

XX Homo sapiens.

XX WO200165584-A1.

XX 13-SEP-2001.

XX 26-FEB-2001; 2001WO-CN000198.

XX 07-MAR-2000; 2000CN-0011895.

XX (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.

XX Mao Y, Xie Y;

XX WPI; 2001-565571/63.

PT New human Pax protein 9 for diagnosing and treating developmental  
PT disorders, malignant neoplasm, hemopathy, human immunodeficiency virus  
PT infection, immunological diseases and various inflammations.

XX Example 2; Page 11; 35pp; Chinese.

CC The invention relates to the human Pax protein 9 with cytosolic,  
CC virucide, immunomodulatory, antiinflammatory, haemostatic and anti-HIV  
CC activity. The polypeptide and encoded polynucleotide, with paired box  
CC domain, are applicable in diagnosis and treatment of malignant neoplasm,  
CC haemopathy, human immunodeficiency virus (HIV) infection, immunological  
CC diseases, various inflammations, developmental disorders, growth  
CC developmental disturbance and Waardenburger's syndrome. The  
CC polynucleotide is useful for gene therapy. The present sequence is that  
CC of a human Pax protein 9 PCR primer, useful to the invention  
XX  
SQ Sequence 24 BP; 3 A; 0 C; 5 G; 16 T; 0 U; 0 Other;

Query Match 1.9%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 1.4e+03;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 170 TTTTCTTCTAGTACGATGAGTT 193  
DB 1 TTTTCTTCTTCTAGTACGAGTT 24

RESULT 628  
AAF92846  
ID AAF92846 standard; DNA; 24 BP.

XX AAF92846;

DT 17-MAY-2001 (first entry)

XX Human ABC1 transcription factor binding site #9.

XX High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ds.

XX Homo sapiens.

XX WO200115676-A2.

XX 08-MAR-2001.

XX 01-SEP-2000; 2000WO-IB001492.

XX 01-SEP-1999; 99US-0151977P.

XX 15-MAR-2000; 2000US-00526193.

XX 23-JUN-2000; 2000US-0213958P.

XX (UTBR-) UNIV BRITISH COLUMBIA.

XX (XENO-) XENON GENETICS INC.

XX Hayden MR, Brooks-Wilson AR, Pimstone SN, Clee SM;

XX WPI; 2001-244356/25.

XX Treating a lower than normal high density lipoprotein-cholesterol (HDL-C)

XX level, a higher than normal triglyceride level, or a cardiovascular

XX disease, by administering a compound that modulates LXR- or RXR-mediated

XX transcriptional activity.

XX Disclosure; Fig 3; 317pp; English.

XX The present invention relates to a method for treating a patient  
XX diagnosed as having a lower than normal high density lipoprotein-  
XX cholesterol (HDL-C) level, a higher than normal triglyceride level, or a  
XX cardiovascular disease, involving administering a compound that modulates  
XX LXR- or RXR-mediated transcriptional activity or ABC1 expression or  
XX activity. The LXR gene product may be used in an assay to identify  
XX compounds useful for the treatment of a disease or condition selected a  
XX lower than normal HDL cholesterol level, a higher than normal  
XX triglyceride level, and a cardiovascular disease

XX Sequence 24 BP; 4 A; 6 C; 6 G; 8 T; 0 U; 0 Other;

Query Match 1.9%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 1.4e+03;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 208 AGGCTGTTCTGCACTCCGACT 231  
DB 1 AGGTTGTTTCACTCTGACT 24

RESULT 629

AAH48397  
ID AAH48397 standard; DNA; 24 BP.

XX AAH48397;

DT 15-SEP-2001 (first entry)

XX Fumarase 9 PCR primer 1.

XX Fumarase 9; cytosolic; antiviral; immunomodulatory; antiinflammatory;  
KW carciant; cancer; haemopathy; human immunodeficiency virus; HIV;  
KW infection; immunological disease; inflammatory disease; PCR primer; ss.

OS Unidentified.  
 XX  
 XX WO200148176-A1.  
 XX  
 PD 05-JUL-2001.  
 XX  
 PF 18-DEC-2000; 2000WO-CN000612.  
 XX  
 PR 24-DEC-1999; 99CN-00125763.  
 XX  
 PA (BIOW-) BIOWINDOW GENE DEV LTD SHANGHAI.  
 XX  
 PI Mao Y, Xie Y;  
 XX  
 DR WPI; 2001-418271/44.  
 XX  
 PT Fumarase 9 polynucleotide and polypeptide, useful in diagnosis and  
 PT treatment of malignant neoplasm, hemopathy, HIV infection, immunological  
 XX diseases and various inflammatory diseases.  
 XX  
 PS Example 3; Page 11; 34pp; Chinese.  
 XX  
 CC The invention relates to an isolated polypeptide of Fumarase 9 comprising  
 CC the 80 amino acid sequence defined in the specification, or its fragment,  
 CC analogue or derivative. The polypeptide and the polynucleotide encoding  
 CC it are useful in the diagnosis and treatment of malignant neoplasms,  
 CC haemopathy, HIV infection, immunological diseases and various  
 CC inflammatory diseases. The present sequence is a primer used to isolate a  
 CC polynucleotide encoding the polypeptide of the invention  
 XX  
 SQ Sequence 24 BP; 12 A; 7 C; 2 G; 3 T; 0 U; 0 Other;  
 XX  
 Query Match 1.9%; Score 19.2; DB 1; Length 24;  
 Best Local Similarity 87.5%; Pred. No. 1.4e+03;  
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 XX  
 QY 607 TTTTAAATTTTGGACAGAGTC 630  
 DB 24 TTTTGGTTTTTTCAGACGAGTC 1  
 XX  
 RESULT 630  
 AAF27674  
 ID AAF27674 standard; DNA; 24 BP.  
 XX  
 AC AAF27674;  
 XX  
 DT 02-APR-2001 (first entry)  
 XX  
 DE Primer #7.  
 XX  
 KW IL-1; interleukin; inflammation; infection; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200100880-A2.  
 XX  
 PD 04-JAN-2001.  
 XX  
 PF 30-JUN-2000; 2000WO-US018318.  
 XX  
 PR 30-JUN-1999; 99US-00345217.  
 XX  
 PA (INTE-) INTERLEUKIN GENETICS INC.  
 XX  
 PI Duff GW, Cox A, Camp NJ, Di Giovine FS;  
 XX  
 DR WPI; 2001-102903/11.  
 XX  
 PT Determining whether a subject has or is predisposed to disease associated  
 PT with IL-1 polymorphism involves determining presence of marker or allele  
 PT comprising IL-1 inflammatory haplotype.  
 XX

PS Claim 5; Page 48; 84pp; English.  
 XX  
 XX The present invention relates to a new method for determining whether a  
 CC subject has or is predisposed to developing a disease or condition that  
 CC is associated with an IL (interleukin)-1 inflammatory haplotype,  
 CC comprising detecting at least one allele of the haplotype, where the  
 CC presence of the allele indicates that the subject is predisposed to the  
 CC development or has the disease or condition. The method is useful for  
 CC determining whether a subject has or is predisposed to inflammatory  
 CC disease, a degenerative disease, an immunological disorder, an infectious  
 CC disease, trauma induced disease, or cancer. The above conditions  
 CC associated with an IL-1 inflammatory haplotype can be treated or  
 CC prevented by administering a therapeutic that compensates for a causative  
 CC mutation that is in linkage disequilibrium with at least one IL-1  
 CC polymorphism  
 XX  
 SQ Sequence 24 BP; 5 A; 7 C; 10 G; 2 T; 0 U; 0 Other;  
 XX  
 Query Match 1.9%; Score 19.2; DB 1; Length 24;  
 Best Local Similarity 87.5%; Pred. No. 1.4e+03;  
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 XX  
 QY 868 GGATTACAGCGCGTACACACAG 891  
 DB 1 GGGATTACAGCGCGTACACACAG 24  
 XX  
 RESULT 631  
 AAH40034/c  
 ID AAH40034 standard; DNA; 24 BP.  
 XX  
 AC AAH40034;  
 XX  
 DT 14-AUG-2001 (first entry)  
 XX  
 DE SNP specific lower PCR primer SEQ ID 2830.  
 XX  
 KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
 KW SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;  
 KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolemia;  
 KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
 KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
 KW inflammation; forensic investigation; paternity analysis; PCR primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200129262-A2.  
 XX  
 PD 26-APR-2001.  
 XX  
 PF 13-OCT-2000; 2000WO-US028436.  
 XX  
 PR 15-OCT-1999; 99US-0160096P.  
 XX  
 PA (ORCH-) ORCHID BIOSCIENCES INC.  
 XX  
 PI Picoult-Newburg L, Pohl M;  
 XX  
 DR WPI; 2001-290930/30.  
 XX  
 PT New genotyping oligonucleotide, useful for detecting the presence,  
 PT absence or identity of single polynucleotide polymorphism in a nucleic  
 PT acid sample.  
 XX  
 PS Claim 1; Page 64; 83pp; English.  
 XX  
 CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
 CC primer extension (SNPE) primers, and the sequences of regions flanking  
 CC sites of single nucleotide polymorphisms SNPs. The present invention  
 CC includes kits for determining the presence or absence of a SNP, using the  
 CC oligonucleotides of the invention. The PCR primers are used to amplify a  
 CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.  
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by

CC performing a single-nucleotide primer extension reaction. The  
CC oligonucleotides are useful for determining the presence, absence or  
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
CC assess by association analysis the genotype of an individual or group of  
CC individuals, having a pathological phenotypic trait suspected of being  
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
CC agammaglobulinaemia, diabetes insipidus, Leech-Nyhan syndrome, muscular  
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,  
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
CC traits also include symptoms of or susceptibility to multifactorial  
CC disease of which a component is or may be genetic such as autoimmune  
CC diseases, including, rheumatoid arthritis, multiple sclerosis,  
CC inflammation, cancer, nervous system diseases and infection by pathogenic  
CC microorganism. The method is also useful in forensic investigations and  
CC paternity analysis. The present sequence represents a PCR primer specific  
CC for a human SNP containing DNA sequence

XX Sequence 24 BP; 6 A; 6 C; 5 G; 7 T; 0 U; 0 Other;

CC The oligonucleotides are useful for genotyping a nucleic acid sample by  
CC performing a single-nucleotide primer extension reaction. The  
CC oligonucleotides are useful for determining the presence, absence or  
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
CC assess by association analysis the genotype of an individual or group of  
CC individuals, having a pathological phenotypic trait suspected of being  
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular  
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,  
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
CC traits also include symptoms of or susceptibility to multifactorial  
CC disease of which a component is or may be genetic, such as autoimmune  
CC diseases, including rheumatoid arthritis, multiple sclerosis,  
CC inflammation, cancer, nervous system diseases and infection by pathogenic  
CC microorganism. The method is also useful in forensic investigations and  
CC paternity analysis. The present sequence represents a PCR primer specific  
CC for a human SNP containing DNA sequence  
XX  
XX Sequence 24 BP; 4 A; 8 C; 3 G; 9 T 0 U; 0 Other;

CC locate the positions of the SNPs. PTGS2 proteins and polynucleotide  
CC sequences are used to express variant PTGS2 proteins, for structural  
CC analysis or drug-binding studies and also in gene therapy (either  
CC expressing PTGS2 or inhibitory RNA). Antibodies raised against PTGS2 are  
CC useful for diagnosis, prognosis and therapy and analysis of the new, and  
CC known, polymorphisms and used to determine between a particular trait, e.g. a  
CC especially for determining association between PTGS2 haplotype and genotype.  
CC clinical response to drugs that target PTGS2 but also disease  
CC susceptibility, severity or stage. Anti-PTGS2 antibodies are particularly  
CC used for developing diagnostic tests and treatments for immune-related  
CC disorders such as arthritis and inflammation. The polymorphisms may also  
CC be used to study expression and biological function of PTGS2. Transgenic  
CC animals that express PTGS2 are used to study expression of PTGS2  
CC isogenes, for in vivo drug screening and testing, and for assessing  
CC effects of therapeutic agents  
CC  
SQ Sequence 24 BP; 7 A; 4 C; 9 G; 4 T; 0 U; 0 Other;  
  
Query Match 1.9%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 1.4e+03;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
OY 710 CTCTGCCCCAGCTCTGTAGTAG 733  
DB 24 CTCTGCTCACTGCTCTGTAGTAG 1  
  
RESULT 634  
AA164727/C  
ID AA164727 standard; DNA; 24 BP.  
XX  
AC AA164727;  
XX  
DT 07-DEC-2001 (first entry)  
DE Human line 1-12 PCR primer 1.  
XX  
DE Human line 1-12 PCR primer 1.  
XX  
KM Human; line 1-12; cytostatic; virucidal; immunomodulatory;  
KM antiinflammatory; haemostatic; malignant tumour; HIV; infection;  
KM human immunodeficiency virus; immunological disease; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200173068-A1.  
XX  
PD 04-OCT-2001.  
XX  
PF 26-MAR-2001; 2001WO-CN000495.  
XX  
PR 27-MAR-2000; 2000CN-00115143.  
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.  
XX  
PI Mao Y, Xie Y;  
XX  
DR WPI; 2001-597126/67.  
PT Line 1-12 and encoded polynucleotide, used in diagnosis and treatment of  
PT malignant tumors, hemopathy, human immunodeficiency virus infection,  
PT immunological diseases and inflammation.  
XX  
PS Example 3; Page 16; 33pp; Chinese.  
XX  
CC The invention relates to human line 1-12 with cytostatic, virucidal,  
CC immunomodulatory, antiinflammatory and haemostatic activity. The protein  
CC and encoding polynucleotide are used in diagnosis and treatment of  
CC malignant tumour, haemopathy, human immunodeficiency virus (HIV)  
CC infection, immunological diseases and various inflammations. The present  
CC sequence is that of a human line 1-12 PCR primer, useful to the invention  
XX  
SQ Sequence 24 BP; 5 A; 4 C; 10 G; 5 T; 0 U; 0 Other;  
  
Query Match 1.9%; Score 19.2; DB 1; Length 24;

Best Local Similarity 87.5%; Pred. No. 1.4e+03;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
OY 976 CACTGCAACTCTGCTCTGAGGAC 999  
DB 24 CACTGCAACTCTGCTCTGAGAC 1  
  
RESULT 635  
AB083629  
ID AB083629 standard; DNA; 24 BP.  
XX  
AC AB083629;  
XX  
DT 26-JAN-2003 (first entry)  
DE Human mPer3-10.01 PCR primer 1 SEQ ID NO:3.  
XX  
DE Human; mPer3-10.01; vegetative nervous dysfunction; psychic disease;  
KM endocrinopathy; growth development disturbance disease; tumour;  
KM PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN CN1345805-A.  
XX  
PD 24-APR-2002.  
XX  
PF 26-SEP-2000; 2000CN-00125425.  
XX  
PR 26-SEP-2000; 2000CN-00125425.  
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.  
XX  
PI Mao Y, Xie Y;  
XX  
DR WPI; 2002-539321/58.  
PT Novel polypeptide-human mPer 3-10.01 and polynucleotide for encoding the  
PT polypeptide.  
XX  
PS Example 2; Page 17 (Disclosure); 33pp; Chinese.  
XX  
CC The present invention describes human mPer3-10.01 (1). Also described is  
CC a method for producing (1) using DNA recombination technology. (1) can be  
CC used in the treatment of several diseases, such as vegetative nervous  
CC dysfunction, psychic disease, endocrinopathy, growth development  
CC disturbance disease and tumours. The present sequence represents a PCR  
CC primer for (1), which is used in an example from the present invention  
XX  
SQ Sequence 24 BP; 4 A; 8 C; 6 G; 6 T; 0 U; 0 Other;  
  
Query Match 1.9%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 1.4e+03;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
OY 930 TCTCACTGTGTACCGAGCTGGA 953  
DB 1 TCTCACTGTGTCCGCAAGCTGGA 24  
  
RESULT 636  
ABV76754  
ID ABV76754 standard; DNA; 24 BP.  
XX  
AC ABV76754;  
XX  
DT 28-MAR-2003 (first entry)  
DE Human sailor transposase 9.35 RT-PCR primer, SEQ ID NO:3.  
XX  
DE Human; sailor transposase 9.35; recombinant production; gene therapy;  
KM cancer; tumour; HIV infection; human immunodeficiency virus; cytostatic;

KM reverse transcription-PCR; RT-PCR; primer; ss.  
XX Homo sapiens.  
OS CN1360027-A.  
XX  
XX 24-JUL-2002.  
PD  
XX 20-DEC-2000; 2000CN-00135114.  
PF  
XX 20-DEC-2000; 2000CN-00135114.  
PR  
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
PA  
XX Mao Y, Xie Y;  
XX  
XX WPI; 2002-733552/80.  
DR  
XX polypeptide-human sailor transposase 9.35 and polynucleotide for coding  
PT it.  
PS Example 2; Page 17 (Disclosure); 32pp; Chinese.  
XX  
XX The invention relates to human sailor transposase 9.35 (ABP58531) and  
CC nucleic acids encoding it (ABV76753). The protein has a molecular weight  
CC of 9.35 kD. The invention also relates to a method for the recombinant  
CC production of the protein, an antagonist of the protein, and the use of  
CC the protein, gene and antagonist in therapeutic applications. Sailor  
CC transposase 9.35 can be used in the treatment of a variety of diseases  
CC such as cancer and HIV (human immunodeficiency virus) infection.  
CC Sequences ABV76754-ABV76755 represent reverse transcription-PCR (RT-PCR)  
CC primers used in an exemplification of the invention to isolate human  
CC sailor transposase 9.35 cDNA  
XX  
SQ Sequence 24 BP; 6 A; 9 C; 6 G; 3 T; 0 U; 0 Other;  
Query Match 1.9%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 1.4e+03;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 868 GGATTACGAGCGCTGAGCCGACCG 891  
DB 1 GGATTACGAGCGCTGAGCCGACCG 24  
RESULT 637  
AB084159  
ID AB084159 standard; DNA; 24 BP.  
XX  
XX AB084159;  
AC  
XX  
XX 19-FEB-2003 (first entry)  
DT  
XX  
XX Human transcription regulatory factor 16.06 PCR primer SEQ ID NO:4.  
DE  
XX  
XX Human; transcription regulatory factor 16.06; tumour; PCR primer; ss;  
KW embryonic development malformation; protein metabolic disorder disease.  
XX  
XX Homo sapiens.  
OS  
XX  
XX CN1352077-A.  
PN  
XX 05-JUN-2002.  
PD  
XX 02-NOV-2000; 2000CN-00127179.  
PF  
XX 02-NOV-2000; 2000CN-00127179.  
PR  
XX 02-NOV-2000; 2000CN-00127179.  
PA  
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
PI  
XX Mao Y, Xie Y;  
XX  
XX WPI; 2002-637132/69.

XX  
XX New polypeptide-human transcription regulatory factor 16.06 and  
PT polynucleotide for encoding the polypeptide, embryonic development  
PT malformation, tumour, and protein metabolic disorder disease.  
XX  
XX  
XX Example 2; Page 18 (Disclosure); 34pp; Chinese.  
PS  
XX  
XX The present invention describes human transcription regulatory factor  
CC 16.06 (I). Also described is a DNA recombination process used to produce  
CC (I). (I) can be used for treating various diseases, such as embryonic  
CC development malformation, tumours and protein metabolic disorder disease.  
CC The present sequence represents a PCR primer for (I), which is used in an  
CC example from the present invention  
XX  
SQ Sequence 24 BP; 4 A; 8 C; 6 G; 6 T; 0 U; 0 Other;  
Query Match 1.9%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 1.4e+03;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 924 ATGGATCTCACTCTGTACCCAG 947  
DB 1 ATGGATCTCACTCTGTACCCAG 24  
RESULT 638  
ABV72841  
ID ABV72841 standard; DNA; 24 BP.  
XX  
XX ABV72841;  
AC  
XX  
XX 30-DEC-2002 (first entry)  
DT  
XX  
XX Human alpha 2,3-sialyltransferase 9.90 PCR primer 1.  
DE  
XX  
XX Human; alpha 2,3-sialyltransferase 9.90; immunological defect; tumour;  
KW inflammation; PCR; primer; ss.  
XX  
XX  
XX Homo sapiens.  
OS  
XX  
XX CN1352272-A.  
PN  
XX 05-JUN-2002.  
PD  
XX  
XX 10-NOV-2000; 2000CN-00127416.  
PF  
XX  
XX 10-NOV-2000; 2000CN-00127416.  
PR  
XX  
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
PA  
XX  
XX Mao Y, Xie Y;  
XX  
XX WPI; 2002-628720/68.  
DR  
XX  
XX New polypeptide-human alpha 2,3-sialyltransferase 9.90 for treating  
PT immunological defect, various tumours and various inflammations.  
PT  
XX  
XX Example 2; Page 19 (Disclosure); 33pp; Chinese.  
PS  
XX  
XX The invention relates to the novel human alpha 2,3-sialyltransferase  
CC 9.90, and the polynucleotide encoding it. The polypeptide is useful for  
CC treating various diseases, such as an immunological defect, various  
CC tumours and various inflammations. The invention also discloses the  
CC antagonist resisting the polypeptide and its treatment effect. The  
CC present sequence represents a PCR primer used to amplify the human  
CC alpha 2,3-sialyltransferase 9.90 gene of the invention  
XX  
SQ Sequence 24 BP; 4 A; 7 C; 5 G; 8 T; 0 U; 0 Other;  
Query Match 1.9%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 1.4e+03;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 636 GGGTCACTATTTCTCTGCCCC 719  
DB 1 GAGTTCAGTGATTCCTGCTC 24

## RESULT 639

ABZ20663  
ID ABZ20663 standard; DNA; 24 BP.

ABZ20663;

03-MAR-2003 (first entry)

Human G protein subunit 9-02 coding sequence PCR primer #2.

Human; G protein subunit 9.02; cancer; constipation; diarrhoea; cough;  
cardiac asthma; colic; psychic disease; PCR; primer;  
morphine analgesic acute poisoning; ss.

Homo sapiens.

CN1345751-A.

24-APR-2002.

26-SEP-2000; 2000CN-00125456.

26-SEP-2000; 2000CN-00125456.

(SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.

Mao Y, Xie Y;

WPI; 2002-675773/73.

Novel polypeptide-human G protein subunit 9.01.

Example 2; Page 19(Disclosure); 34pp; Chinese.

The present invention provides the protein and coding sequences of human  
G protein subunit 9.02. The sequences can be used in the treatment of  
cancers, coughs, cardiac asthma, diarrhoea, constipation, colic, psychic  
disease and morphine analgesic acute poisoning. The present sequence is  
a PCR primer used to isolate the coding sequence of the invention

Sequence 24 BP; 4 A; 8 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 1.9%; Score 19.2; DB 1; Length 24;

Best Local Similarity 87.5%; Pred. No. 1.4e+03;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 924 ATGGAATTCACCTCTGTTACCCAG 947

DB 1 ACGGAGCTCAGCTCTGTGCCAG 24

## RESULT 640

ABX14631/C

ID ABX14631 standard; DNA; 24 BP.

ABX14631;

04-MAR-2003 (first entry)

Guanosine triphosphatase activator protein 10.12 RT-PCR primer #1.

ss; guanosine triphosphatase activator protein 10.12; PCR; primer;  
malignant tumour; inflammation; immunological disease; haemopathy;  
human immunodeficiency virus infection; HIV; RT-PCR;  
reverse transcriptase PCR.

Unidentified.

PN CN1352022-A.

PD 05-JUN-2002.

10-NOV-2000; 2000CN-00127330.

10-NOV-2000; 2000CN-00127330.

(BODE-) BODE GENE DEV CO LTD SHANGHAI.

Mao Y, Xie Y;

WPI; 2002-714410/78.

New polypeptide-guanosine triphosphatase activator protein 10.12 and  
polynucleotide for encoding such polypeptide.

Example 2; Page 17 (disclosure); 33pp; Chinese.

The present invention discloses a new kind of polypeptide, guanosine  
triphosphatase activator protein 10.12, polynucleotides encoding this  
polypeptide and DNA recombination process to produce the polypeptide. The  
present invention also discloses applying the polypeptide in treating  
various diseases, such as malignant tumours, inflammations, immunological  
diseases, haemopathy and human immunodeficiency virus (HIV) infection.  
The present invention also discloses the antagonist resisting the  
polypeptide and its treatment effect. The present invention also  
discloses the application of the polynucleotides for encoding guanosine  
triphosphatase activator protein 10.12. The present sequence is a reverse  
transcriptase (RT)-PCR primer used to isolate nucleic acids encoding  
guanosine triphosphatase activator protein 10.12

Sequence 24 BP; 5 A; 5 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 1.9%; Score 19.2; DB 1; Length 24;

Best Local Similarity 87.5%; Pred. No. 1.4e+03;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 203 TGGTCAGGCTGCTCTGAACTCCC 226

DB 24 TGCCGAGCTGCTCTCAACTCCC 1

## RESULT 641

ABV76761/C

ID ABV76761 standard; DNA; 24 BP.

ABV76761;

07-MAR-2003 (first entry)

Ras GTP enzyme-activating protein 20.68 RT-PCR primer, SEQ ID NO:3.

Ras GTP enzyme-activating protein 20.68; cancer suppressor protein-20.68;  
recombinant production; gene therapy; cancer; tumour; HIV infection;  
human immunodeficiency virus; cytostatic; reverse transcription-PCR;  
RT-PCR; primer; ss.

Unidentified.

CN1363596-A.

14-AUG-2002.

05-JAN-2001; 2001CN-00105082.

05-JAN-2001; 2001CN-00105082.

(BODE-) BODE GENE DEV CO LTD SHANGHAI.

Mao Y, Xie Y;

WPI; 2002-742044/81.

XX Polypeptide-cancer suppressor protein-20.68 and polynucleotide for coding  
PT it.  
XX  
XX Example 2; Page 17 (Disclosure); 33pp; Chinese.  
XX  
XX The invention relates to Ras GTP enzyme-activating protein 20.68  
CC (ABV9633) and nucleic acids encoding it (ABV76760). The protein has a  
CC molecular weight of 20.68 kD and is also referred to as cancer suppressor  
CC protein-20.68. The invention also relates to a method for the recombinant  
CC production of the protein, an antagonist of the protein, and the use of  
CC the protein, gene and antagonist in therapeutic applications. Ras GTP  
CC enzyme-activating protein 20.68 can be used in the treatment of a variety  
CC of diseases such as cancer and HIV (human immunodeficiency virus)  
CC infection. Sequences ABV76761-ABV76762 represent reverse transcription-  
CC PCR (RT-PCR) primers used in an exemplification of the invention to  
CC isolate Ras GTP enzyme-activating protein 20.68 cDNA  
XX  
SQ Sequence 24 BP; 7 A; 3 C; 11 G; 3 T; 0 U; 0 Other;  
  
Query Match 1.9%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 1.4e+03;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1004 GCGATTCTCTGCTCAGCCTCC 1027  
DB 24 GTGATTCTCTCTCAGCCTCC 1  
  
RESULT 642  
ABV9633  
ID ABV9633 standard; DNA; 24 BP.  
XX  
XX ABV9633;  
XX  
DT 03-FEB-2003 (first entry)  
XX  
XX Human natriuretic peptide receptor 11.66 PCR primer SEQ ID NO 4.  
DE  
XX Human; natriuretic peptide receptor 11.66; receptor; tumour; haemopathy;  
KM HIV; human immunodeficiency virus; infection; immunological disease;  
KM inflammation; PCR; primer; ss.  
XX  
XX Homo sapiens.  
OS  
XX CN1352083-A.  
PN  
XX 05-JUN-2002.  
PD  
XX 02-NOV-2000; 2000CN-00127189.  
PF  
XX 02-NOV-2000; 2000CN-00127189.  
PR  
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
PA  
XX Mao Y, Xie Y;  
PI  
XX WPI; 2002-644453/70.  
DR  
XX  
XX New polypeptide-human natriuretic peptide 11.66 and polynucleotide for  
PT encoding the polypeptide, useful for treating malignant tumors,  
PT hemopathy, HIV infection, immunological diseases and various  
PT inflammations.  
XX  
XX Example 2; Page 16 (Disclosure); 31pp; Chinese.  
PS  
XX The invention relates to human natriuretic peptide receptor 11.66. The  
CC polypeptide is useful for treating various diseases, such as malignant  
CC tumours, haemopathy, HIV infection, immunological diseases and various  
CC inflammations. The present sequence is that of a human natriuretic  
CC peptide receptor 11.66 PCR primer useful in examples of the invention  
XX  
SQ Sequence 24 BP; 3 A; 7 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 1.9%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 1.4e+03;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 924 ATGGAATCTCACTGTTTACCAG 947  
DB 1 ATGGAATCTCACTGTTTACCAG 24  
  
RESULT 643  
AAS20139  
ID AAS20139 standard; DNA; 24 BP.  
XX  
XX AAS20139;  
XX  
DT 09-APR-2002 (first entry)  
XX  
XX Human phytochrome 12 RT-PCR primer #1.  
DE  
XX Human; ss; phytochrome 12; malignant tumour; haemopathy;  
KM human immunodeficiency virus infection; HIV; immunological disease;  
KM inflammation; RT-PCR; primer.  
XX  
XX Homo sapiens.  
OS  
XX WO200192316-A1.  
PN  
XX 06-DEC-2001.  
PD  
XX 21-MAY-2001; 2001WO-CN000834.  
PF  
XX 24-MAY-2000; 2000CN-00115823.  
PR  
XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.  
PA  
XX Mao Y, Xie Y;  
PI  
XX WPI; 2002-083184/11.  
DR  
XX  
XX phytochrome 12 and encoding polynucleotide, used in diagnosis and  
PT treatment of malignant tumors, hemopathy, human immunodeficiency virus  
PT infection, immunological diseases and inflammation.  
XX  
XX Example 2; Page 17; 36pp; Chinese.  
PS  
XX The invention relates to an isolated polypeptide of phytochrome 12, the  
CC cDNA encoding it, and its fragment, analogue or derivative. Also included  
CC are vectors expressing protein, a host cell comprising the vector, the  
CC isolation of modulators of the protein and an anti-phytochrome 12  
CC antibody. The protein and nucleic acid are used in diagnosis and  
CC treatment of a malignant tumour, haemopathy, human immunodeficiency virus  
CC (HIV) infection, immunological diseases and various inflammations. The  
CC present sequence is an RT-PCR (reverse transcriptase PCR) primer used to  
CC isolate the cDNA encoding the phytochrome 12  
XX  
SQ Sequence 24 BP; 4 A; 8 C; 5 G; 7 T; 0 U; 0 Other;  
  
Query Match 1.9%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 1.4e+03;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1001 CAAGGATTCTCTGCTCAGCCT 1024  
DB 1 CAAGGATTCTCTGCTCAGCCT 24  
  
RESULT 644  
ABI9962  
ID ABI9962 standard; DNA; 24 BP.  
XX  
XX ABI9962;  
XX



DT 31-MAY-2002 (first entry)  
 XX Human phosphatidic acid phosphatase 2-12 RT-PCR primer, SEQ ID NO:4.  
 DE  
 XX  
 XX Human; phosphatidic acid phosphatase 2-12; recombinant production;  
 KM cancer; HIV infection; human immunodeficiency virus; gene therapy;  
 KM cytosolic; anti-HIV; reverse transcription-PCR; RT-PCR; primer; ss.  
 XX Homo sapiens.  
 XX  
 XX CN1325990-A.  
 XX  
 XX  
 XX 12-DEC-2001.  
 XX  
 XX  
 XX 31-MAY-2000; 2000CN-00116248.  
 XX  
 XX 31-MAY-2000; 2000CN-00116248.  
 XX  
 XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
 XX  
 XX Mao Y, Xie Y;  
 XX  
 XX WPI; 2002-196710/26.  
 XX  
 XX New polypeptide-human phosphatidic acid phosphatase 2-12 for treating  
 PT diseases such as cancer and human immunodeficiency virus infection.  
 XX  
 XX Example 2; Page 17 (disclosure); 34pp; Chinese.  
 XX  
 XX The invention relates to human phosphatidic acid phosphatase 2-12  
 CC (AAM49149) and to nucleic acids encoding it (AB199960). The protein has a  
 CC molecular weight of 12 kD. The invention also relates to a method for the  
 CC recombinant production of the protein, an antagonist of the protein, and  
 CC the use of the protein, gene and antagonist in therapeutic applications.  
 CC Phosphatidic acid phosphatase 2-12 can be used in the treatment of a  
 CC variety of diseases such as cancer and HIV (human immunodeficiency virus)  
 CC infection. Sequences AB199961-AB199962 represent reverse transcription-  
 CC PCR (RT-PCR) primers used in an exemplification of the invention to  
 CC isolate human phosphatidic acid phosphatase 2-12 cDNA  
 XX  
 XX Sequence 24 BP; 6 A; 3 C; 6 G; 9 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.9%; Score 19.2; DB 1; Length 24;  
 Best Local Similarity 87.5%; Pred. No. 1.4e+03;  
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 OY 310 TTTGTGTGAGAAACAGGCTTCAC 333  
 DB 1 TTTTGTAGTACAGACAGGCTTCAC 24  
 RESULT 645  
 AAI72742  
 ID AAI72742 standard; DNA; 24 BP.  
 XX  
 XX AAI72742;  
 AC  
 XX 03-JUL-2002 (first entry)  
 DT  
 XX Human cytokine receptor 15 PCR primer #1.  
 DE  
 XX  
 XX Gene; human cytokine receptor 15; malignant tumour; haemopathy;  
 KM human immunodeficiency virus; HIV; inflammation; gene therapy; PCR;  
 KM primer; ss.  
 XX  
 XX Homo sapiens.  
 XX OS  
 XX WO200183536-A1.  
 XX  
 XX 08-NOV-2001.  
 PD  
 XX 23-APR-2001; 2001WO-CN000577.  
 XX

PR 27-APR-2000; 2000CN-00115491.  
 XX  
 XX (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.  
 XX  
 XX Mao Y, Xie Y;  
 XX  
 XX WPI; 2002-026253/03.  
 XX  
 XX  
 XX Cytokine receptor 15 and encoded polynucleotide, applicable in diagnosis  
 PT and treatment of developmental disorders, cancer, hemopathy, HIV  
 PT infection, immunological diseases and various inflammations.  
 XX  
 XX Example 3; Page 12; 38pp; Chinese.  
 XX  
 XX The present invention relates to human cytokine receptor 15 (see  
 CC AAB47984). Human cytokine receptor 15, and the DNA encoding it, are used  
 CC in diagnosis and treatment of malignant tumour, haemopathy, human  
 CC immunodeficiency virus (HIV) infection, immunological diseases and  
 CC various inflammations. This sequence is a PCR primer which was used in an  
 CC example from the invention  
 XX  
 XX Sequence 24 BP; 7 A; 2 C; 7 G; 8 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.9%; Score 19.2; DB 1; Length 24;  
 Best Local Similarity 87.5%; Pred. No. 1.4e+03;  
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 OY 179 AGTAGATGATGAGTTTCATGT 202  
 DB 1 AGTAGATGATGAGTTTCATGT 24  
 RESULT 646  
 AAL43822  
 ID AAL43822 standard; DNA; 24 BP.  
 XX  
 XX AAL43822;  
 AC  
 XX 19-SEP-2002 (first entry)  
 DT  
 XX Human oncogene protein 11-66 PCR primer 1.  
 DE  
 XX Human; ss; gene therapy; oncogene protein 11.66; malignant tumour;  
 KM haemopathy; development disorder; HIV; immunological disease;  
 KM inflammation; PCR; primer.  
 XX  
 XX Homo sapiens.  
 XX OS  
 XX CN1333235-A.  
 XX  
 XX 30-JAN-2002.  
 PD  
 XX 07-JUL-2000; 2000CN-00119427.  
 XX  
 XX 07-JUL-2000; 2000CN-00119427.  
 XX  
 XX (SHAN-) SHANGHAI BIODOR GENE DEV CO LTD.  
 XX  
 XX Mao Y, Xie Y;  
 XX  
 XX WPI; 2002-305565/35.  
 XX  
 XX Novel polypeptide-oncoprotein 11.66 and polynucleotide for encoding said  
 PT polypeptide.  
 XX  
 XX Example 2; Page 18 (disclosure); 33pp; Chinese.  
 XX  
 XX The invention comprises the amino acid and coding sequence of the human  
 CC oncogene protein 11.66. The oncogene protein 11.66 DNA and protein  
 CC sequences are useful for treating malignant tumour, haemopathy,  
 CC development disturbance, HIV infection, immunological disease and various  
 CC inflammations. The present DNA sequence represents a human oncogene  
 CC protein 11.66 PCR primer

```
XX SQ Sequence 24 BP; 4 A; 4 C; 8 G; 8 T; 0 U; 0 Other;
Query Match 1.9%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 181 TAGAGATGAGGTTCTCCATGTTG 204
   |||||
   |||||
Db 1 TCGAGATGAGGTTTCACCGTGTG 24

RESULT 647
ABSL40967
ID ABL40967 standard; DNA; 24 BP.
XX AC ABS55854;
XX AC ABS55854;
XX DT 23-DEC-2002 (first entry)
XX DE Human SOX3 protein 13.31 cDNA RT-PCR primer #1.
XX KW Human; SOX3 protein 13.31; primer; ss; malignant tumour; haemopathy;
XX KW HIV infection; human immunodeficiency virus; immunological disease;
XX KW inflammation; RT-PCR; reverse transcriptase.
XX OS Homo sapiens.
XX PN CN1352146-A.
XX PD 05-JUN-2002.
XX PF 10-NOV-2000; 2000CN-00127333.
XX PR 10-NOV-2000; 2000CN-00127333.
XX PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX PI Mao Y, Xie Y;
XX DR WPI; 2002-708125/77.
XX PT New polypeptide-human SOX3 protein 13.31.
XX PS Example 2; Page 16 (Disclosure); 32pp; Chinese.
XX CC The invention relates to the human SOX3 protein 13.31 and the
XX CC polynucleotide encoding it. The polypeptide is used in treating various
XX CC diseases, such as malignant tumours, haemopathy, HIV infection,
XX CC immunological diseases and various inflammations. This sequence
XX CC represents a reverse transcriptase PCR (RT-PCR) primer used in isolation
XX CC of cDNA encoding the human SOX3 protein 13.31
XX SQ Sequence 24 BP; 8 A; 6 C; 6 G; 4 T; 0 U; 0 Other;
Query Match 1.9%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 868 GGATTACAGCGGTGACCCACG 891
   |||||
   |||||
Db 1 GGATTACAGCATGACCCACATG 24

RESULT 648
ABSL40967
ID ABL40967 standard; DNA; 24 BP.
XX AC ABL40967;
XX AC ABL40967;
XX DT 03-JUL-2002 (first entry)
XX DE Polypeptide-hexokinase protein cDNA isolating primer 2.
```

```
XX KW Polypeptide-hexokinase protein; cytosolic; haemostatic; virucide;
XX KW immunomodulatory; antiinflammatory; RT-PCR; primer; ss.
XX OS Synthetic.
XX PN WO200220795-A1.
XX PD 14-MAR-2002.
XX PF 02-JUL-2001; 2001WO-CN001115.
XX PR 07-JUL-2000; 2000CN-00117013.
XX PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX PI Mao Y, Xie Y;
XX DR WPI; 2002-258030/30.
XX DE Polypeptide-hexokinase protein and encoding polynucleotide, used in
XX PT diagnosis and treatment of malignant tumors, hemopathy, human
XX PT immunodeficiency virus infection, immunological diseases and
XX PT inflammation.
XX PS Example 2; Page 11; 35pp; Chinese.
XX CC The invention relates to a novel polypeptide-hexokinase protein. The
XX CC protein can be expressed by standard recombinant methodology. The novel
XX CC polypeptide and encoding polynucleotides are used in diagnosis and
XX CC treatment of malignant tumour; haemopathy, human immunodeficiency virus
XX CC (HIV) infection, immunological diseases and various inflammations. The
XX CC present sequence represents the polypeptide-hexokinase protein cDNA
XX CC isolating RT-PCR primer
XX SQ Sequence 24 BP; 3 A; 2 C; 9 G; 10 T; 0 U; 0 Other;
Query Match 1.9%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 174 TTTTACAGATGAGGTTCTC 197
   |||||
   |||||
Db 1 TTTTACAGATGAGGTTCTC 24

RESULT 649
ABSL7191
ID ABS7191 standard; DNA; 24 BP.
XX AC ABS7191;
XX AC ABS7191;
XX DT 30-JAN-2003 (first entry)
XX DE Amylase 9.35 specific RT-PCR primer, #2.
XX KW Amylase 9.35; RT-PCR; ss; tumour; haemopathy; antagonist; HIV;
XX KW human immunodeficiency virus; immunological disease; inflammation;
XX KW reverse transcription; primer.
XX OS Unidentified.
XX PN CN1345971-A.
XX PD 24-APR-2002.
XX PF 29-SEP-2000; 2000CN-00125588.
XX PR 29-SEP-2000; 2000CN-00125588.
XX PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX PI Mao Y, Xie Y;
```

XX WPI; 2002-539369/58.  
DR  
XX New polypeptide-amylose 9.35 for treating malignant tumor, hemopathy,  
PT human immunodeficiency virus infection, immunological disease and various  
PT inflammations.  
XX  
XX Example 2; Page 15 (disclosure); 31pp; Chinese.  
XX  
XX The present invention discloses a novel amylose 9.35, polynucleotide  
CC coding for the polypeptide and method for producing this polypeptide by  
CC using DNA recombination technology. The invention also discloses the  
CC method for curing several diseases, such as malignant tumor, haemopathy,  
CC human immunodeficiency virus (HIV) infection, immunological diseases and  
CC various inflammations by using the polypeptide. The invention also  
CC discloses an antagonist for resisting said polypeptide and its  
CC therapeutic action and also discloses the application of the  
CC polynucleotide for coding this novel amylose 9.35. The sequence presented  
CC is the reverse transcription (RT)-PCR primer, #2, which was used to  
CC isolate amylose 9.35 cDNA  
XX  
SQ Sequence 24 BP; 4 A; 8 C; 6 G; 6 T; 0 U; 0 Other;  
  
Query Match 1.9%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 1.4e+03;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 924 ATGGATCTCATCTCTTACCCAG 947  
DB 1 ATGGAGTCTCATCTCTGTACCCGG 24  
  
RESULT 650  
AB081233/C  
ID AB081233 standard; DNA; 24 BP.  
XX  
XX AB081233;  
AC  
XX  
DT 05-DEC-2002 (first entry)  
XX  
DE Human 14273 probe.  
XX  
XX Human; 14273; metabolic disorder; obesity; diabetes; anorexia; cachexia;  
KM anorectic; antidiabetic; anabolic; transgenic animal; gene therapy;  
KM probe; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
PN WO200267868-A2.  
XX  
PD 06-SEP-2002.  
XX  
XX 26-FEB-2002; 2002WO-US006131.  
PF  
XX 26-FEB-2001; 2001US-0271655P.  
PR  
XX (MILL-) MILENNIUM PHARM INC.  
PA  
XX  
XX Gimeno R, Tsai F;  
PI  
XX  
XX WPI; 2002-698629/75.  
DR  
XX  
XX Identifying a nucleic acid associated with a metabolic disorder, useful  
PT for diagnosing metabolic disorders, e.g. obesity, comprises contacting  
PT the sample with a probe comprising at least 25 contiguous nucleotides of  
PT the 14273 gene.  
XX  
XX Example 1; Page 61; 95pp; English.  
PS  
XX The present sequence is a probe, created by PCR, for human 14273 (see  
CC AB081226), a nucleic acid associated with metabolic disorders. The probe  
CC was used to examine the expression profile of human 14273 in different  
CC tissues. It was found that 14273 molecules are expressed at high levels.

CC in adipose tissue, e.g. white adipose tissue and brown adipose tissue, as  
CC well as in pancreatic islets. They are upregulated during exposure to  
CC cold (i.e. under conditions that affect brown or white adipocyte  
CC metabolism) and downregulated in genetic models of obesity. The present  
CC invention provides 14273 nucleic acids, polypeptides and antibodies  
CC useful for the diagnosis and treatment of metabolic disorders including  
CC obesity, anorexia, cachexia and diabetes. Also provided are methods for  
CC identifying a subject having a metabolic disorder, for identifying a  
CC compound capable of modulating metabolic activity, methods for modulating  
CC metabolic activity or adipocyte activity (hyperplastic growth,  
CC hypertrophic growth or lipogenesis), methods for modulating lipogenesis  
CC or lipolysis in a subject, and a method for regulating endogenous glucose  
CC levels  
XX  
SQ Sequence 24 BP; 5 A; 6 C; 8 G; 5 T; 0 U; 0 Other;  
  
Query Match 1.9%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 1.4e+03;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 956 GCAATGGCCAAATCTGCGTCACT 979  
DB 24 GCAATGGCAGATCTGCGTCACT 1  
  
RESULT 651  
ABK50651/C  
ID ABK50651 standard; DNA; 24 BP.  
XX  
XX ABK50651;  
AC  
XX  
DT 30-JUL-2002 (first entry)  
XX  
DE Human Parkinson's syndrome associated protein 11.11, RT-PCR primer #1.  
XX  
XX Human; Parkinson's syndrome associated protein 11.11; cancer;  
KM human immunodeficiency virus; HIV infection; reverse transcriptase-PCR;  
KM RT-PCR; primer; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
PN CN1331232-A.  
XX  
PD 16-JAN-2002.  
XX  
XX 30-JUN-2000; 2000CN-00116961.  
PF  
XX 30-JUN-2000; 2000CN-00116961.  
PR  
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
XX  
XX  
XX MAO Y, XIE Y;  
PI  
XX  
XX WPI; 2002-292874/34.  
DR  
XX  
XX New polypeptide-human Parkinsons syndrome associated protein 11.11 for  
PT treating diseases such as cancer and human immunodeficiency virus  
PT infection.  
XX  
XX Example 2; Page 17 (disclosure); 34pp; Chinese.  
PS  
XX  
XX The present invention relates to the isolation of human Parkinson's  
CC syndrome associated protein 11.11, and the polynucleotide encoding it.  
CC Also described is a process for preparing the polypeptide by DNA  
CC recombination and the application of the polypeptide and polynucleotide  
CC in treating various diseases such as cancer and human immunodeficiency  
CC virus (HIV) infection. Antagonist against the polypeptide can also be  
CC used in treating such diseases. The present sequence for reverse  
CC transcriptase (RT)-PCR primer #1 is used with RT-PCR primer #2 (ABK50652)  
CC for isolating cDNA encoding human Parkinson's syndrome associated protein  
CC 11.11  
XX  
SQ Sequence 24 BP; 8 A; 6 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 1.9%; Score 19.2; DB 1; Length 24;  
 Best Local Similarity 87.5%; Pred. No. 1.4e+03;  
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 925 TGGATCTCACTCTGTACCCGAG 948  
 |||||  
 DB 24 TGGAGTCTCACTCTTTGCCGAG 1

## RESULT 652

AB04729/c  
 ID ABA04729 standard; DNA; 24 BP.

AC ABA04729;

DT 01-MAR-2002 (first entry)

DE Human ubiquitin-binding enzyme 9 PCR primer #1.

XX Human; cytostatic; haemostatic; virocid; immunomodulatory; PCR primer;

KW antiinflammatory; gene therapy; ubiquitin-binding enzyme 9; tumour;

KW haemopathy; HIV infection; immunological disease; inflammation; ss.

OS Homo sapiens.

PN WO200188142-A1.

PD 22-NOV-2001.

PF 08-MAY-2001; 2001WO-CN000731.

PR 09-MAY-2000; 2000CN-00115634.

XX (SHAN-) SHANGHAI BOWINDOW GENE DEV INC.

PI Mao Y, Xie Y;

DR WPI; 2002-055699/07.

PT Human ubiquitin-binding enzyme 9A and encoding polynucleotide, used in  
 PT diagnosis and treatment of malignant tumors, hemopathy, human  
 PT immunodeficiency virus infection, immunological diseases and  
 PT inflammation.

PS Example 2; Page 18; 35pp; Chinese.

CC The present invention relates to human ubiquitin-binding enzyme 9 (see  
 CC AAM47737). The enzyme and its coding sequence are useful in the diagnosis  
 CC and treatment of malignant tumors, haemopathy, HIV infection,  
 CC immunological diseases and various inflammations. The present sequence is  
 CC a PCR primer, which was used in an example from the present invention

SQ Sequence 24 BP; 3 A; 9 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 1.9%; Score 19.2; DB 1; Length 24;  
 Best Local Similarity 87.5%; Pred. No. 1.4e+03;

Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 874 CAGGCGTGAGCCACACGCCCGGC 897  
 |||||  
 DB 24 CAGGCGTGAGCCACCTGTGCCGCGC 1

## RESULT 653

AB077823  
 ID AB077823 standard; DNA; 24 BP.

AC AB077823;

DT 20-DEC-2002 (first entry)

DE Human protein phosphatase 13.64 RT-PCR primer, SEQ ID NO.3.

XX Human; protein phosphatase 13.64; recombinant production; gene therapy;  
 KW female genital development disorder; abnormal female sex characteristic;  
 KW female genital tract tumour; oestrogen-related metabolic abnormality;  
 KW cytostatic; gynaecological; reverse transcription-PCR; RT-PCR; primer;  
 KW ss.

OS Homo sapiens.

PN CN1352290-A.

PD 05-JUN-2002.

PF 10-NOV-2000; 2000CN-00127328.

PR 10-NOV-2000; 2000CN-00127328.

PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.

PI Mao Y, Xie Y;

DR WPI; 2002-667814/72.

PT New human protein phosphatase 13.64 polypeptide for treating female  
 PT genital organ maldevelopment, female sex characteristics abnormality,  
 PT female genital system tumor and estrogenic relative metabolic  
 PT abnormality.

PS Example 2; Page 16 (Disclosure); 32pp; Chinese.

CC The invention relates to human protein phosphatase 13.64 (ABB93687) and  
 CC nucleic acids encoding it (AB077822). The protein has a molecular weight  
 CC of 13.64 kD. The invention also relates to a method for the recombinant  
 CC production of the protein, an antagonist of the protein, and the use of  
 CC the protein, gene and antagonist in therapeutic applications. Protein  
 CC phosphatase 13.64 can be used in the treatment of a variety of diseases  
 CC such as disorders of female genital development, abnormal female sex  
 CC characteristics, tumours of the female genital tract and oestrogen-  
 CC related metabolic abnormalities. Sequences AB077823-AB077824 represent  
 CC reverse transcription-PCR (RT-PCR) primers used in an exemplification of  
 CC the invention to isolate human protein phosphatase 13.64 cDNA

SQ Sequence 24 BP; 4 A; 3 C; 9 G; 8 T; 0 U; 0 Other;

Query Match 1.9%; Score 19.2; DB 1; Length 24;  
 Best Local Similarity 87.5%; Pred. No. 1.4e+03;  
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 180 GTAGAGATGAGATTTCATGTT 203  
 |||||  
 DB 1 GTAGAGATGAGGTTTCAACCGTGT 24

## RESULT 654

ADE14009  
 ID ADE14009 standard; DNA; 24 BP.

AC ADE14009;

DT 29-JAN-2004 (first entry)

DE Optineurin promoter motif, repeat element or regulatory region #118.

KW Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;

KW SNF; glaucoma; progressive ocular hypertensive disorder;

KW glaucoma related disorder; motif; repeat element; regulatory region.

OS Homo sapiens.

PN US2003190617-A1.

PD 09-OCT-2003.

```
PF 06-MAR-2002; 2002US-00091281.
XX
XX 06-MAR-2002; 2002US-00091281.
XX
XX (SIEE/) SI E.
XX (RAYM/) RAYMOND V.
XX (MORI/) MORISSETTE J.
XX
XX Raymond V, Morissette J, Si E;
XX
XX WPI; 2003-864168/80.
XX
XX New nucleic acid sequences of the optineurin gene are useful to detect
XX polymorphisms particularly single nucleotide polymorphisms in the
XX optineurin promoter to diagnose, prognose and treat glaucoma and related
XX disorders.
XX
XX Claim 11; SEQ ID NO 120; 159pp; English.
XX
XX The invention relates to an isolated nucleic acid (N1) comprising at
XX least 20 but not more than 1500 consecutive nucleotides of the optineurin
XX promoter appearing as AD313890. Also included are the optineurin promoter
XX operably linked to a heterologous nucleic acid, a nucleic acid capable of
XX detecting a single nucleotide polymorphism (SNP) in the optineurin
XX promoter, a host cell comprising the promoter operably linked to a
XX heterologous sequence, diagnosing or prognosing glaucoma in a sample
XX obtained from a cell or bodily fluid (comprising detecting a polymorphism
XX in a promoter region of the optineurin gene, associated with a glaucoma
XX phenotype), detecting a SNP sequence variation in a sample containing
XX DNA, detecting the presence of an optineurin promoter sequence variation
XX in a sample containing DNA, determining the presence or increased
XX susceptibility to glaucoma or to a progressive ocular hypertensive
XX disorder resulting in loss of visual field in a patient (or the severity
XX or progression of glaucoma in a patient, comprising providing
XX amplification reaction primers that direct amplification of a selected
XX nucleic acid region containing the variation within the optineurin
XX promoter and amplifying the DNA) and detecting a polymorphism (comprising
XX obtaining a sample containing human genomic DNA, providing a nucleic acid
XX capable of detecting a SNP located within an optineurin promoter, and
XX detecting the polymorphism). The invention is used to diagnose and
XX prognose glaucoma and also to treat glaucoma related disorders. The
XX present sequence is an optineurin promoter motif, repeat element or
XX putative regulatory region.
XX
XX Sequence 24 BP; 7 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 1.9%; Score 19.2; DB 1; Length 24;
XX Best Local Similarity 87.5%; Pred. No. 1.4e+03;
XX Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1020 AGCCTCCAGACGCTGGATTAC 1043
XX ||||| ||||| ||||| |||||
XX 1 AGCCTCTCAGTACTGAGATTAC 24
XX
XX RESULT 655
XX AAT94763
XX ID AAT94763 standard; DNA; 19 BP.
XX
XX AAT94763;
XX
XX 25-MAR-2003 (revised)
XX 18-FEB-1998 (first entry)
XX
XX Human progesterone receptor gene primer.
XX
XX Human; progesterone receptor; breast cancer; ovarian cancer; mutant;
XX antibody; mutation; primer; ss.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX US5683985-A.
XX
XX
```

```
XX
XX 04-NOV-1997.
XX
XX 03-DEC-1996; 96US-00759873.
XX
XX 12-APR-1996; 96US-00629939.
XX
XX (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
XX Kieback DG;
XX
XX WPI; 1997-548981/50.
XX
XX Diagnosis of increased risk for breast or ovarian cancer - by immunoassay
XX for mutant progesterone receptor protein.
XX
XX Disclosure; Col 7; 26pp; English.
XX
XX The present sequence represents a primer used in the detection of an Alu
XX insertion sequence in intron G in the human progesterone receptor gene.
XX The present invention has developed a novel method for diagnosing an
XX increased risk for breast or ovarian cancer. The method involves assaying
XX a sample containing human progesterone receptor protein (hPR) with an
XX antibody that distinguishes wild-type hPR from a mutant hPR having a Val-
XX to-Leu substitution at amino acid 660, where the presence of such a
XX mutant indicates an increased risk for breast or ovarian cancer.
XX Detection of the G-to-T point mutation gives an odds ratio for ovarian
XX cancer of 3.1 (sensitivity 46%, specificity 78%) and an odds ratio for
XX breast cancer of 2.0 (sensitivity 36%, specificity 78%). (Updated on 25-
XX MAR-2003 to correct PF field.)
XX
XX Sequence 19 BP; 6 A; 2 C; 7 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 1.9%; Score 19; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+03;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 389 AAGTCTGGATTACAGG 407
XX ||||| ||||| ||||| |||||
XX 1 AAGTCTGGATTACAGG 19
XX
XX RESULT 656
XX AAT84754
XX ID AAT84754 standard; DNA; 19 BP.
XX
XX AAT84754;
XX
XX 04-NOV-1997 (first entry)
XX
XX FISH primer for human progesterone receptor intron G.
XX
XX Breast; ovarian; cancer; diagnosis; risk; predisposition; human;
XX detection; point mutation; progesterone; receptor; FISH; primer;
XX Alu insertion; intron G; fluorescent in situ hybridisation; ss.
XX
XX Synthetic.
XX
XX US5645995-A.
XX
XX 08-JUL-1997.
XX
XX 12-APR-1996; 96US-00629939.
XX
XX 12-APR-1996; 96US-00629939.
XX
XX (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
XX Kieback DG;
XX
XX WPI; 1997-362926/33.
XX
XX Diagnosis of increased risk of breast or ovarian cancer - by detecting
XX
```

PT point mutation in codon 660 of exon 4 of human progesterone receptor  
PR gene.  
XX  
XX  
PS Claim 18; Col 19-20; 26pp; English.  
CC Increased risk of breast or ovarian cancer can be diagnosed by detecting  
CC a G to T point mutation at the 1st nucleotide of codon 660 in exon 4 of  
CC the human progesterone receptor (PR) gene, i.e. nucleotide 2153 of  
CC AAT84747. The odds ratio is 3.1 (sensitivity 46%, specificity 78%) for  
CC ovarian cancer, and 2.0 (sensitivity 36%, specificity 78%) for breast  
CC cancer. The method may also include detecting a C to T point mutation at  
CC the 3rd nucleotide of codon 770 in exon 5 of the human PR gene, i.e.  
CC nucleotide 2485 of AAT84747, and/or an Alu insertion in codon 897 of  
CC intron G, i.e. AAT84749 inserted between nucleotides 120 and 121 of  
CC AAT84748. The mutation in exon 4 can be detected by digesting a test  
CC nucleic acid with BstI, and detecting the loss of a BstI restriction  
CC site. The mutation in exon 5 can be detected by digesting a test nucleic  
CC acid with NlaIII and detecting the addition of a NlaIII restriction site.  
CC The mutation in intron G can be detected by digesting a test nucleic acid  
CC with TaqI and detecting a 1.9 kb DNA fragment, by PCR using the primers  
CC AAT84750-53, by FISH using AAT84754 or by Southern blotting using a probe  
CC comprising the Alu insertion AAT84749  
XX  
SQ Sequence 19 BP; 6 A; 2 C; 7 G; 4 T; 0 U; 0 Other;  
Query Match 1.9%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 389 AAAGTCTGGGATTACAGG 407  
DB 1 AAAGTCTGGGATTACAGG 19  
|||||  
RESULT 657  
AAH38421  
ID AAH38421 standard; DNA; 19 BP.  
XX  
XX AAH38421;  
AC  
XX  
DT 14-AUG-2001 (first entry)  
XX  
XX SNP specific upper PCR primer SEQ ID 1217.  
DE  
XX  
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;  
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;  
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
KW inflammation; forensic investigation; paternity analysis; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200129262-A2.  
XX  
PD 26-APR-2001.  
XX  
PF 13-OCT-2000; 2000WO-US028436.  
XX  
PR 15-OCT-1999; 99US-0160096P.  
XX  
PA (ORCH-) ORCHID BIOSCIENCES INC.  
XX  
PI Picoult-Newburg L, Pohl M;  
XX  
PI Picoult-Newburg L, Pohl M;  
DR WPI; 2001-290930/30.  
XX  
XX New genotyping oligonucleotide, useful for detecting the presence,  
PT absence or identity of single polynucleotide polymorphism in a nucleic  
PT acid sample.  
XX  
XX Claim 1; Page 56; 83pp; English.  
XX

CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
CC primer extension (SNPE) primers, and the sequences of regions flanking  
CC sites of single nucleotide polymorphisms SNPs. The present invention  
CC includes kits for determining the presence or absence of a SNP, using the  
CC oligonucleotides of the invention. The PCR primers are used to amplify a  
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.  
CC The oligonucleotides are useful for genotyping a nucleic acid sample by  
CC performing a single-nucleotide primer extension reaction. The  
CC oligonucleotides are useful for determining the presence, absence or  
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
CC assess by association analysis the genotype of an individual or group of  
CC individuals, having a pathological phenotypic trait suspected of being  
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular  
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,  
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
CC traits also include symptoms of or susceptibility to multifactorial  
CC disease of which a component is or may be genetic, such as autoimmune  
CC diseases, including, rheumatoid arthritis, multiple sclerosis,  
CC inflammation, cancer, nervous system diseases and infection by pathogenic  
CC microorganism. The method is also useful in forensic investigations and  
CC paternity analysis. The present sequence represents a PCR primer specific  
CC for a human SNP containing DNA sequence  
XX  
SQ Sequence 19 BP; 3 A; 9 C; 2 G; 5 T; 0 U; 0 Other;  
Query Match 1.9%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 675 TCACGTCAACCTCTGCTC 693  
DB 1 TCACGTCAACCTCTGCTC 19  
|||||  
RESULT 658  
AAH38469  
ID AAH38469 standard; DNA; 19 BP.  
XX  
XX AAH38469;  
AC  
XX  
DT 14-AUG-2001 (first entry)  
XX  
XX SNP specific upper PCR primer SEQ ID 1265.  
DE  
XX  
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;  
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;  
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
KW inflammation; forensic investigation; paternity analysis; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200129262-A2.  
XX  
PD 26-APR-2001.  
XX  
PF 13-OCT-2000; 2000WO-US028436.  
XX  
PR 15-OCT-1999; 99US-0160096P.  
XX  
PA (ORCH-) ORCHID BIOSCIENCES INC.  
XX  
PI Picoult-Newburg L, Pohl M;  
XX  
PI Picoult-Newburg L, Pohl M;  
DR WPI; 2001-290930/30.  
XX  
XX New genotyping oligonucleotide, useful for detecting the presence,  
PT absence or identity of single polynucleotide polymorphism in a nucleic  
PT acid sample.  
XX  
XX Claim 1; Page 56; 83pp; English.  
XX

XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
CC primer extension (SNPE) primers, and the sequences of regions flanking  
CC sites of single nucleotide polymorphisms SNPs. The present invention  
CC includes kits for determining the presence or absence of a SNP, using the  
CC oligonucleotides of the invention. The PCR primers are used to amplify a  
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.  
CC The oligonucleotides are useful for genotyping a nucleic acid sample by  
CC performing a single-nucleotide primer extension reaction. The  
CC oligonucleotides are useful for determining the presence, absence or  
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
CC assess by association analysis the genotype of an individual or group of  
CC individuals, having a pathological phenotypic trait suspected of being  
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular  
CC dystrophy, familial hypercholesterolemia, polycystic kidney disease,  
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
CC traits also include symptoms of or susceptibility to multifactorial  
CC disease of which a component is or may be genetic such as autoimmune  
CC diseases, including, rheumatoid arthritis, multiple sclerosis,  
CC inflammation, cancer, nervous system diseases and infection by pathogenic  
CC microorganism. The method is also useful in forensic investigations and  
CC paternity analysis. The present sequence represents a PCR primer specific  
CC for a human SNP containing DNA sequence  
SQ Sequence 19 BP; 5 A; 6 C; 5 G; 3 T; 0 U; 0 Other;  
Query Match 1.9%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03; Indels 0; Gaps 0;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 870 ATTACAGGCGTGGAGCCACC 888  
DB 1 ATTACAGGCGTGGAGCCACC 19  
RESULT 659  
AAF29784  
ID AAF29784 standard; DNA; 19 BP.  
XX AAF29784;  
XX 09-APR-2001 (first entry)  
XX  
XX Presenilin-1 gene promoter PCR primer Prom1F.  
XX DE  
XX Human; PSEN1; Alzheimer's disease; polymorphism; diagnosis;  
XX KM Presenilin-1; chromosome 14; PCR primer; ss.  
XX OS Homo sapiens.  
XX OS  
XX PN W0200079000-A1.  
XX PD 28-DEC-2000.  
XX PF 22-JUN-2000; 2000WO-EP005942.  
XX PR 22-JUN-1999; 99EP-00201991.  
XX PA (VIAA-) VIAAMS INTERNUNIVERSITAIR INST BIOTECHNOG.  
XX PI Theunis J, Cruts M, Van Broeckhoven C;  
XX WPI; 2001-071402/08.  
XX DR  
XX PT Determining whether a human subject has or is at risk of developing (early  
XX -onset) Alzheimer's disease comprises detecting the presence/absence of a  
XX genetic lesion in the presenilin-1 gene.  
XX PS Example 1; Page 45; 56pp; English.  
XX CC The present invention describes a method for determining the presence of  
CC or susceptibility to Alzheimer's disease in humans, involving detecting a

CC genetic lesion in the presenilin-1 (PSEN1) gene, found on chromosome 14.  
CC The genetic lesion is a polymorphism in the promoter or upstream  
CC regulatory region of the gene. The invention also describes transgenic  
CC animals which can be used to identify compounds useful in treating  
CC Alzheimer's disease  
XX  
SQ Sequence 19 BP; 4 A; 8 C; 3 G; 4 T; 0 U; 0 Other;  
Query Match 1.9%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 539 TGCCCTCAGCCTCCCAAGTA 557  
DB 1 TGCCCTCAGCCTCCCAAGTA 19  
RESULT 660  
ABL44474/C  
ID ABL44474 standard; DNA; 19 BP.  
XX ABL44474;  
XX 11-APR-2002 (first entry)  
XX  
XX Human chromosome 1p36-35 PCR primer SEQ ID NO:1518.  
XX DE  
XX Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;  
XX KM PCR primer; ss.  
XX OS Homo sapiens.  
XX PN JP2001321190-A.  
XX PD 20-NOV-2001.  
XX PF 12-MAR-2001; 2001JP-00068285.  
XX PR 10-MAR-2000; 2000JP-00066716.  
XX PA (RIKA ) RIKAGAKU KENKYUSHO.  
XX PA (GENO-) GENOTEX YG.  
XX DR WPI; 2002-144136/19.  
XX PT Arraying genome clones.  
XX PS Claim 4; Page 34; 528pp; Japanese.  
XX  
XX The present invention describes a method of arraying genome clones. The  
XX method comprises: (a) clones of the genomic libraries contained in  
XX multiwell plates numbered for discrimination are mixed in each of the  
XX multiwell plates; (b) a primer designed based on the chromosome marker  
XX sequence is added to the mixture to carry out an amplification reaction;  
XX (c) a signal corresponding to the marker is detected from the resultant  
XX amplified product to specify the discrimination Nos. of the multiwell  
XX plates containing the clones having said marker sequence; (d) the order  
XX of the markers is changed so that the same discrimination Nos. succeeded to  
XX the maximum in the specified discrimination Nos. to array the multiwell  
XX plates; (e) the clones in the multiwell plates of the specified  
XX discrimination Nos. are mixed respectively in each wells of longitudinal  
XX and lateral directions; (f) the mixed clones are cultured and the  
XX resultant cultures are amplified by using the above primer; (g) signals  
XX are detected from the amplified products; (h) the clones in the multiwell  
XX plates are specified from the detected result; and (i) the clones are  
XX reconstituted as the positions on the chromosome and arrayed. The  
XX microarray is useful for gene analysis. ABL42957 to ABL45322 represent  
XX PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634  
XX represent PCR primers for human chromosome 21q22.1, which are  
XX specifically claimed for use in the present invention  
SQ Sequence 19 BP; 5 A; 5 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 1.9%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 384 CTCGCCAAGTCTGGGATT 402  
DB 19 CTCGCCAAGTCTGGGATT 1

## RESULT 661

ADL25033  
ID ADL25033 standard; DNA, 19 BP.

ADL25033;  
AC

20-MAY-2004 (first entry)  
DT

Intestinal epithelium/peyer's patch M cell-associated PCR primer #178.  
DE

Intestinal epithelium cell development; peyer's patch M cell development;  
inflammatory bowel disease; glutenenteropathy; infectious disease;  
autoimmune disease; haemolytic anaemia; rheumatoid arthritis; dermatitis;  
grave's disease; multiple sclerosis; allergy; asthma; diabetic mellitus;  
immune system disorder; hypersensitivity; anaphylaxis;  
blood group incompatibility; ss; human; PCR; primer.  
KM

Homo sapiens.  
OS

WO200280852-A2.  
PN

17-OCT-2002.  
PD

04-APR-2002; 2002WO-US010873.  
PF

04-APR-2001; 2001US-0281416P.  
PR

(DIGI-) DIGITAL GENE TECHNOLOGIES INC.  
PA

Brayden DJ, Byrne D, O'mahony DJ, Evans CF, Mah SP, Lo DD;  
PI

WPI; 2003-075470/07.  
DR

Novel isolated or purified polypeptide encoded by genes associated with  
intestinal epithelium or M cell development, differentiation or function,  
useful for treating autoimmune diseases and infectious diseases.  
PT

Disclosure; SEQ ID NO 543; 152PP; English.  
PS

The invention comprises DNA sequences which are associated with  
intestinal epithelium and peyer's patch M cells. The DNA sequences of the  
invention are useful for assessing, modifying, modulating or regulating  
intestinal epithelium or M cell development. The DNA sequences of the  
invention are also useful in the treatment of: inflammatory bowel  
disease, glutenenteropathy, infectious diseases, autoimmune diseases  
(e.g. haemolytic anaemia, rheumatoid arthritis, dermatitis, Grave's  
disease, multiple sclerosis, allergy, asthma and diabetic mellitus),  
diseases or disorders of the immune system, hypersensitivity,  
anaphylaxis, and blood group incompatibility. The present DNA sequence  
represents a PCR primer that was used to amplify an intestinal  
epithelium/peyer's patch M cell-associated DNA sequence of the invention.  
CC

Sequence 19 BP; 3 A; 5 C; 7 G; 4 T; 0 U; 0 Other;  
SQ

Query Match 1.9%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 638 TGTACCCAGGCTGGAGTG 656  
DB 1 TGTACCCAGGCTGGAGTG 19

## RESULT 662

ADM32300/C  
ID ADM32300 standard; DNA, 19 BP.  
XX  
AC ADM32300;  
XX

20-MAY-2004 (first entry)  
DT

Human interleukin-18 gene polymorphism related probe, SEQ ID NO 57.  
DE

human interleukin-18; IL-18; adult onset still disease; gene;  
single nucleotide polymorphism; ss; probe.  
KM

Homo sapiens.  
OS

Synthetic.  
XX

JP2004049136-A.  
PN

19-FEB-2004.  
PD

22-JUL-2002; 2002JP-00212550.  
PF

22-JUL-2002; 2002JP-00212550.  
PR

(SUGI/) SUGIURA S.  
PA

(HYUB-) HYUBITTO GENOMICS KK.  
PA

WPI; 2004-174121/17.  
DR

Claim 6; SEQ ID NO 57; 61PP; Japanese.  
PS

The invention relates to a novel method for detecting a gene polymorphism  
in a human interleukin (IL)-18 gene. The method involves detecting a 9  
base insertion between -6311 position and -6310 position, a polymorphism  
at positions -5890, -5316, -4762, -4675, -3268, -689 and -640 of a  
CC polynucleotide which consists of a fully defined sequence of 6640 base  
CC pairs as given in the specification, where in the 6640bp polynucleotide,  
the position 6575 is set to +1 from which numbering is performed. The  
CC method is useful for detecting gene polymorphism in IL-18 gene of human  
and for detecting adult onset still disease. This polynucleotide sequence  
represents a probe of the human interleukin-18 gene of the invention.  
CC

Sequence 19 BP; 4 A; 5 C; 7 G; 3 T; 0 U; 0 Other;  
SQ

Query Match 1.9%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 210 GGTGCTCGAAGTCCCGA 228  
DB 19 GGTGCTCGAAGTCCCGA 1

## RESULT 663

ADO80008  
ID ADO80008 standard; DNA, 19 BP.

ADO80008;  
AC

26-AUG-2004 (first entry)  
DT

CENPCL extend primer #59.  
DE

Cytostatic; Gene therapy; breast cancer; human; DGL; KIAA0783; DPF3;  
CENPCL; SNP; single nucleotide polymorphism; centromere protein C1;  
centromere autoantigen C1; chromosome 4q12-q13.3; extend; primer; ss.  
KM

Homo sapiens.  
OS

WO2004047514-A2.  
PN

## RESULT 664





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PD 22-OCT-1998.
XX
XX 15-APR-1998; 98MO-GB001102.
XX
XX 15-APR-1997; 97US-0043553P.
PR 05-JUN-1997; 97US-0048740P.
XX
XX (WELL ) WELLCOME TRUST LTD.
PA (MERI ) MERCK & CO INC.
XX
PI Todd JA, Hess JW, Caskey CT, Cox RD, Gerhold D, Hammond H;
PI Hey P, Kawaguchi Y, Merriman TR, Metzker ML, Nakagawa Y;
PI Phillips MS, Twells RCJ;
XX
XX WPI; 1998-594573/50.
XX
XX New isolated LDL-receptor related protein - used to develop products for
PT treating, e.g. elevated triglyceride levels, diabetes, autoimmune
PT disorders, inflammation or Alzheimer's disease.
XX
XX Claim 12; Page 111; 200pp; English.
XX
XX The present invention describes LRP5 (low density lipoprotein (LDL)
XX receptor related protein, previously designated LRP-3). AAV85823 to
XX AAV85900 represent SNP primers used for obtaining LRP5 cDNA. Nucleic acid
XX molecules (NMs) encoding LRP5 can be used for determining if an
XX individual is susceptible to insulin dependent diabetes mellitus (IDDM).
XX The NMs or proteins can be used for reducing triglyceride levels in the
XX serum of an individual. Therapies that affect LRP5 may also be useful in
XX the treatment of autoimmune diseases such as glomerulonephritis, diseases
XX and disorders involving disruption of endocytosis and/or antigen
XX presentation, cytokine clearance and/or inflammation, viral infection,
XX pathogenic bacterial toxin contamination, elevation of free fatty acids
XX or hypercholesterolemia, type 2 diabetes, osteoporosis, Alzheimer's
XX disease and cardiovascular disease. Products from the present invention
XX can also be used for detection, diagnosis and drug screening
XX
XX Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 1.9%; Score 19; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+03;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 668 TCTTGAGCTCAGTCAACCT 686
XX |||||
XX 2 TCTTGAGCTCAGTCAACCT 20
XX
XX Db
XX
XX RESULT 666
XX AA237713/C
XX ID AA237713 standard; DNA; 20 BP.
XX
XX AC AA237713;
XX
XX 07-JAN-2000 (first entry)
XX
XX Human mdm2 phosphorothioate oligodeoxynucleotide #243.
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
XX antisense; modulation; oligonucleotide; expression; inhibition;
XX hyperproliferation; blood cancer; brain cancer; breast cancer;
XX lung cancer; soft tissue cancer; psoriasis; fibrosis; atherosclerosis;
XX restenosis; ss.
XX
XX Synthetic.
XX OS Homo sapiens.
XX
XX PI WO9949065-A1.
XX
XX PN WO9949065-A1.
XX
XX PD 30-SEP-1999.
XX
XX PF 26-MAR-1999; 99WO-US006702.
XX
XX

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PR 26-MAR-1998; 98US-00048810.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowseart LM;
XX
XX WPI; 1999-610754/52.
XX
XX New antisense compounds used to treat eg. hyperproliferative conditions.
XX
XX Example 9; Page 54; 157pp; English.
XX
XX AA237473-237738 represent human mdm2 phosphorothioate oligonucleotides.
XX AA237471, AA237472, AA237739, AA237740 and AA237741 are used in the
XX exemplification of the present invention. The present invention describes
XX novel nucleotide antisense compounds, targeted to the 5' untranslated,
XX translation termination codon, or 3' untranslated region of a nucleic
XX acid encoding human mdm2, that modulates expression of human mdm2. The
XX oligonucleotides mediate their effect by antisense inhibition of
XX hyperproliferative gene expression. The antisense compound is used to
XX treat an animal having a disease or condition associated with mdm2,
XX particularly a hyperproliferative condition, more particularly cancer,
XX especially of the blood, brain, breast, lung or soft tissue, or
XX psoriasis, fibrosis, atherosclerosis or restenosis
XX
XX Sequence 20 BP; 3 A; 10 C; 4 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 1.9%; Score 19; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+03;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 644 CCAGGCTGAGTGCAGTGG 662
XX |||||
XX 20 CCAGGCTGAGTGCAGTGG 2
XX
XX Db
XX
XX RESULT 667
XX AA237720/C
XX ID AA237720 standard; DNA; 20 BP.
XX
XX AC AA237720;
XX
XX 07-JAN-2000 (first entry)
XX
XX Human mdm2 phosphorothioate oligodeoxynucleotide #250.
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
XX antisense; modulation; oligonucleotide; expression; inhibition;
XX hyperproliferation; blood cancer; brain cancer; breast cancer;
XX lung cancer; soft tissue cancer; psoriasis; fibrosis; atherosclerosis;
XX restenosis; ss.
XX
XX Synthetic.
XX OS Homo sapiens.
XX
XX PI WO9949065-A1.
XX
XX PN WO9949065-A1.
XX
XX PD 30-SEP-1999.
XX
XX PF 26-MAR-1999; 99WO-US006702.
XX
XX PR 26-MAR-1998; 98US-00048810.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX PI Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowseart LM;
XX
XX WPI; 1999-610754/52.
XX
XX New antisense compounds used to treat eg. hyperproliferative conditions.
XX
XX Example 9; Page 54; 157pp; English.
XX

```

CC AA237473-237738 represent human mdm2 phosphorothioate oligonucleotides.  
CC AA237471, AA237472, AA237739, AA237740 and AA237741 are used in the  
CC exemplification of the present invention. The present invention describes  
CC novel nucleotide antisense compounds, targeted to the 5' untranslated,  
CC translation termination codon, or 3' untranslated region of a nucleic  
CC acid encoding human mdm2, that modulates expression of human mdm2. The  
CC oligonucleotides mediate their effect by antisense inhibition of  
CC hyperproliferative gene expression. The antisense compound is used to  
CC treat an animal having a disease or condition associated with mdm2,  
CC particularly a hyperproliferative condition, more particularly cancer,  
CC especially of the blood, brain, breast, lung or soft tissue, or  
CC psoriasis, fibrosis, atherosclerosis or restenosis  
XX

XX Sequence 20 BP; 5 A; 2 C; 10 G; 3 T; 0 U; 0 Other;

Query Match 1.9%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03; Indels 0; Gaps 0;  
Matches 19; Conservative 0; Mismatches 0;

QY 536 TCCTGCTCAGCTCCCAA 554  
DB 20 TCCTGCTCAGCTCCCAA 2

RESULT 668  
AAF0874/c  
ID AAF0874 standard; DNA; 20 BP.

AC AAF0874;

DT 02-MAY-2001 (first entry)

XX Human mdm2 phosphorothioate oligonucleotide #248.

XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

XX Homo sapiens;

XX US6184212-B1.

PD 06-FEB-2001.

PF 26-MAR-1999; 99US-00280805.

PR 26-MAR-1998; 98US-00048810.

XX (ISIS-) ISIS PHARM INC.

PI Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowse LM;

DR WPI; 2001-190948/19.

XX Novel antisense compound 8-30 nucleobases in length targeted to a nucleic  
PT acid molecule encoding human mdm-2 useful for modulating the expression  
PT of human mdm-2 and reducing hyperproliferation of human cells.

XX Example 9; Col 33; 77pp; English.

XX The present invention relates to an antisense compound 8-30 nucleobases  
CC in length targeted to nucleobases 1-308 of the 5' untranslated region,  
CC 1776-1806 of the translation termination codon region or 1818-2370 of the  
CC 3' untranslated region of a nucleic acid molecule encoding human mdm-2.  
CC The invention is useful for reducing hyperproliferation of human cells,  
CC modulating the expression of mdm2 in human cells or tissues or in vitro.  
CC The hyperproliferative disorder includes cancer or psoriasis  
XX

XX Sequence 20 BP; 5 A; 2 C; 10 G; 3 T; 0 U; 0 Other;

Query Match 1.9%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 536 TCCTGCTCAGCTCCCAA 554

DB 20 TCCTGCTCAGCTCCCAA 2

RESULT 669  
AAF0867/c  
ID AAF0867 standard; DNA; 20 BP.

AC AAF0867;

DT 02-MAY-2001 (first entry)

XX Human mdm2 phosphorothioate oligonucleotide #241.

XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

XX Homo sapiens.

PD 06-FEB-2001.

PF 26-MAR-1999; 99US-00280805.

PR 26-MAR-1998; 98US-00048810.

XX (ISIS-) ISIS PHARM INC.

PI Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowse LM;

DR WPI; 2001-190948/19.

XX Novel antisense compound 8-30 nucleobases in length targeted to a nucleic  
PT acid molecule encoding human mdm-2 useful for modulating the expression  
PT of human mdm-2 and reducing hyperproliferation of human cells.

XX Example 9; Col 31; 77pp; English.

XX The present invention relates to an antisense compound 8-30 nucleobases  
CC in length targeted to nucleobases 1-308 of the 5' untranslated region,  
CC 1776-1806 of the translation termination codon region or 1818-2370 of the  
CC 3' untranslated region of a nucleic acid molecule encoding human mdm-2.  
CC The invention is useful for reducing hyperproliferation of human cells,  
CC modulating the expression of mdm2 in human cells or tissues or in vitro.  
CC The hyperproliferative disorder includes cancer or psoriasis  
XX

XX Sequence 20 BP; 3 A; 10 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 1.9%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03; Indels 0; Gaps 0;  
Matches 19; Conservative 0; Mismatches 0;

QY 644 CCAGGCTGAGTGCAGTGG 662  
DB 20 CCAGGCTGAGTGCAGTGG 2

RESULT 670

ID AAC88720 standard; DNA; 20 BP.

AC AAC88720;

DT 07-MAR-2001 (first entry)

XX Human catenin-binding zinc finger protein PCR primer FVR510F.

XX Catenin-binding zinc finger protein; cancer; neurological disorder;

XX drug screening; PCR primer; ss.

XX Homo sapiens.

XX BP1054059-A1.

```
XX 22-NOV-2000.
PD
XX 17-MAY-1999; 99EP-00201543.
PF
XX 17-MAY-1999; 99EP-00201543.
PR
XX (VLAA-) VLAAWS INTERUNIVERSITAIR INST BIOTECHNOG.
PA
XX Van Roy F, Vanlandeschoot A, Janssens B;
PI
XX WPI; 2001-033776/05.
DR
XX Nucleic acid or its fragments, useful for diagnosing and treating cancer
PT and neurological disorders, corresponds to a catenin-binding protein in
PT signal transduction and gene regulatory pathways.
PS Disclosure; Page 17; 71pp; English.
XX
XX The present invention is related to the coding sequence and protein
CC fragments of a human catenin-binding zinc finger protein. The coding
CC sequence was isolated from a human kidney cDNA library, but is expressed
CC in most human tissue. The sequences provided by the invention can be used
CC in the diagnosis and treatment of cancer and neurological disorders, and
CC in drug screening to identify compounds capable of the same
XX
SQ Sequence 20 BP; 5 A; 3 C; 8 G; 4 T; 0 U; 0 Other;
Query Match 1.9%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. NO. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 864 GCTGGATTACAGGCGTGA 882
DB 1 GCTGGATTACAGGCGTGA 19
RESULT 671
AADI2635
ID AADI2635 standard; DNA; 20 BP.
XX
AC AADI2635;
XX
DT 25-SEP-2001 (first entry)
XX
DE Human ANC_2H01 cDNA sequencing forward primer, FVR510F.
XX
KW Human; ANC_2H01 protein; catenin-binding protein; signal transduction;
KW gene regulation; zinc finger protein; alphan-catenin; drug screening;
KW therapy; cancer; neurological disorder; cytostatic; neuroprotective;
KW primer; ss.
XX
OS Homo sapiens.
XX
PN WO200147954-A2.
XX
PD 05-JUL-2001.
XX
PF 18-MAY-2000; 2000WO-EP004535.
XX
PR 23-DEC-1999; 99EP-00204512.
XX
PA (VLAA-) VLAAWS INTERUNIVERSITAIR INST BIOTECHNOG.
PI Van Roy F, Vanlandeschoot A, Janssens B;
DR WPI; 2001-418220/44.
XX
PT Novel recombinant nucleic acids useful for diagnosing, prognosing and/or
PT treating cancer and neurological disorders, corresponds to a protein
PT binding to alpha-catenin protein and with signal transduction function.
PS Disclosure; Page 66; 160pp; English.
```

```
XX The invention relates to human catenin-binding proteins and their
CC corresponding cDNA molecules which functions in signal transduction and
CC gene regulatory pathways. The invention also provides an isolated and/or
CC recombinant nucleic acid or its functional fragment, homologue or
CC derivative, corresponding to a alpha-catenin binding protein. The
CC invention also relates to a novel human zinc finger protein binding with
CC a member of the a-cattulin/vinculin family, preferably with a human
CC isoform of alpha N-catenin (neural form). The invention also relates to
CC the field of drug discovery, diagnosis, prognosis and treatment of cancer
CC and neurological disorders. The present sequence is a primer which is
XX used for sequencing human ANC_2H01 cDNA
SQ Sequence 20 BP; 5 A; 3 C; 8 G; 4 T; 0 U; 0 Other;
Query Match 1.9%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. NO. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 864 GCTGGATTACAGGCGTGA 882
DB 1 GCTGGATTACAGGCGTGA 19
RESULT 672
AAS29482/C
ID AAS29482 standard; DNA; 20 BP.
XX
AC AAS29482;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31620.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW anti arteriosclerotic; vasotropic; antisense; phosphorothioate; ss.
XX
OS Homo sapiens.
XX
PN US2001016575-A1.
XX
PD 23-AUG-2001.
XX
PF 02-JAN-2001; 2001US-00752983.
XX
PR 26-MAR-1998; 98US-00048810.
XX
PR 26-MAR-1999; 99US-00280805.
XX
PA (MIRA/) MIRAGLIA L J.
PA (NERO/) NERO P.
PA (GRAH/) GRAHAM M J.
PA (MONI/) MONIA B P.
PA (COWS/) COWSERT L M.
PI Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowsert LM;
DR WPI; 2001-535565/59.
XX
PT An antisense compound, useful for treating e.g. cancer, comprises
PT nucleobases targeted a region (e.g. translation termination codon region)
PT of a nucleic acid encoding human mdm2.
XX
XX Example 9; Page 18; 81pp; English.
```

CC The present invention relates to antisense compounds, 8-30 nucleobases in  
 CC length targeted to the 5' untranslated region, translation termination  
 CC codon region, 3' untranslated region, coding region or translation start  
 CC site of a nucleic acid encoding human mdm2, where the antisense compound  
 CC modulates the expression of human mdm2. The antisense oligonucleotides of  
 CC the invention are useful for encoding human mdm2 and for inhibiting the  
 CC expression of human mdm2. They may be used for creating an animal having  
 CC a disease or condition associated with amplification of mdm2 gene or  
 CC overexpression of mdm2 e.g. a hyperproliferative disorder such as cancer  
 CC (blood, brain, breast, lung, or a soft tissue cancer) and psoriasis,  
 CC fibrosis, atherosclerosis or restenosis, tumours, colorectal carcinoma  
 CC and chronic myelogenous leukemia. The antisense compound may be  
 CC administered with a chemotherapeutic agent to overcome drug resistance.  
 CC The antisense compound reduces hyperproliferation of human cells. The  
 CC method, which involves the use of the antisense compound, is also useful  
 CC for detecting the role of mdm2 expression in various cell functions and  
 CC physiological processes and useful in both clinical research and  
 CC diagnostic tools. AAS29242-AAS29507 represent the human mdm2 antisense  
 CC oligonucleotides of the present invention

SO Sequence 20 BP; 3 A; 10 C; 4 G; 3 T; 0 U; 0 Other;

QY Query Match 1.9%; Score 19; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred.No.1.2e+03;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 644 CCAGGCTGAGTGCAGTGG 662  
 20 CCAGGCTGAGTGCAGTGG 2

RESULT 673  
 AAS29489/c  
 ID AAS29489 standard; DNA; 20 BP.  
 AC AAS29489;  
 XX  
 XX 21-NOV-2001 (first entry)  
 DT  
 XX  
 DE Human mdm2 antisense oligonucleotide 31784.  
 XX  
 XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;  
 KW atherosclerosis; tumour; cytostatic; anti psoriatic;  
 KM anti arteriosclerotic; vasotropic; antisense; phosphorothioate; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH modified\_base 1..20  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= All phosphorothioate linkages,  
 FT additional bases 1-6 and bases 15-20 are 2'-O-  
 FT methoxyethyl bases, and bases 7-14 are deoxynucleotides"

US2001016575-A1.  
 PN  
 XX  
 PD 23-AUG-2001.  
 XX  
 XX 02-JAN-2001; 2001US-00752983.  
 PF  
 XX 26-MAR-1998; 98US-00048810.  
 PR 26-MAR-1999; 99US-00280805.  
 XX  
 XX (MIRA/) MIRAGLIA L J.  
 PA (NERO/) NERO P.  
 PA (GRAH/) GRAHAM M J.  
 PA (MONI/) MONIA B P.  
 PA (COMS/) COMSERT L M.  
 XX  
 PI Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowseert LM;  
 XX  
 DR WPI; 2001-535565/59.

XX An antisense compound, useful for treating e.g. cancer, comprises  
 PT nucleobases targeted a region (e.g. translation termination codon region)  
 PT of a nucleic acid encoding human mdm2.  
 PS Example 9; Page 18; 81pp; English.

CC The present invention relates to antisense compounds, 8-30 nucleobases in  
 CC length targeted to the 5' untranslated region, coding region or translation start  
 CC codon region, 3' untranslated region, coding region or translation start  
 CC site of a nucleic acid encoding human mdm2, where the antisense compound  
 CC modulates the expression of human mdm2. The antisense oligonucleotides of  
 CC the invention are useful for encoding human mdm2 and for inhibiting the  
 CC expression of human mdm2. They may be used for treating an animal having  
 CC a disease or condition associated with amplification of mdm2 gene or  
 CC overexpression of mdm2 e.g. a hyperproliferative disorder such as cancer  
 CC (blood, brain, breast, lung, or a soft tissue cancer) and psoriasis,  
 CC fibrosis, atherosclerosis or restenosis, tumours, colorectal carcinoma  
 CC and chronic myelogenous leukemia. The antisense compound may be  
 CC administered with a chemotherapeutic agent to overcome drug resistance.  
 CC The antisense compound reduces hyperproliferation of human cells. The  
 CC method, which involves the use of the antisense compound, is also useful  
 CC for detecting the role of mdm2 expression in various cell functions and  
 CC physiological processes and useful in both clinical research and  
 CC diagnostic tools. AAS29242-AAS29507 represent the human mdm2 antisense  
 CC oligonucleotides of the present invention

SO Sequence 20 BP; 5 A; 2 C; 10 G; 3 T; 0 U; 0 Other;

QY Query Match 1.9%; Score 19; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred.No.1.2e+03;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 536 TCCTGCTCAGCTCCCAA 554  
 20 TCCTGCTCAGCTCCCAA 2

RESULT 674  
 AAD12408/c  
 ID AAD12408 standard; DNA; 20 BP.  
 AC AAD12408;  
 XX  
 XX 25-SEP-2001 (first entry)  
 DT  
 XX  
 DE Human caspase 8 mRNA antisense compound ISIS 107686.  
 XX  
 XX Caspase 8; infection; inflammation; tumour; research reagent; cytostatic;  
 KW gene therapy; antisense; human; phosphorothioate; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH modified\_base 1..20  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "Phosphorothioate backbone"

modified\_base 1..5  
 FT /\*tag= b  
 FT /mod\_base= OTHER  
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"

modified\_base 2  
 FT /\*tag= d  
 FT /mod\_base= m5c  
 FT /\*tag= e  
 FT /mod\_base= m5c  
 FT /\*tag= f  
 FT /mod\_base= m5c  
 FT modified\_base 7

Query Match	1.9%; Score 19; DB 1; Length 20; Best Local Similarity 100.0%; Pred.No. 1.2e+03; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0
646 AGGCTGAGTGCAGTGGCG 664	
20 AGGCTGAGTGCAGTGGCG 2	
DB	
Result 675	
AA161524	
ID AA161524 standard; DNA; 20 BP.	
XX	
AC AA161524;	
XX	
DT 22-SEP-2003 (first entry)	
DE Human inhibitor-kappa B-R antisense oligonucleotide, ISIS #130449.	
XX	

Key	Location/Qualifiers
modified_base	1..20
/*tag= a	
/mod_base= OTHER	
/note= "Phosphorothioate backbone; All cytidine residues are 5-methylcytidines"	
modified_base	1..5
/*tag= b	
/mod_base= OTHER	
/note= "2'-methoxyethyl (2'-MOE) nucleotides"	
modified_base	16..20
/*tag= c	
/mod_base= OTHER	
/note= "2'-methoxyethyl (2'-MOE) nucleotides"	
WO2003042360-A2.	
22-MAY-2003.	
05-NOV-2002; 2002WO-US035597.	
13-NOV-2001; 2001US-00993731.	
(ISIS-) ISIS PHARM INC.	
Monia BP, Watt AT;	
WPI, 2003-468635/44.	
New antisense oligonucleotides targeted to nucleic acids encoding inhibitor-kappa B-R, useful for diagnosing or treating diseases associated with expression of inhibitor-kappa B-R, e.g., a heightened immune response or infection.	
Claim 3; Page 74; 108pp; English.	
The invention relates to antisense compounds targeted to a nucleic acid molecule encoding human inhibitor-kappa B-R (also known as I-kappaB, IKK $\beta$ , I-kappa-B-related, ikappa r, nuclear factor of kappa light polypeptides gene enhancer in B-cells inhibitor-like 2 and NF $\kappa$ B12) to inhibit its expression. Antisense compounds of the invention are useful for treating diseases or conditions associated with the expression of inhibitor-kappa B-R such as a heightened immune response involving increased cytokine expression, or a result of infection (e.g. bacterial, viral or parasitic). They are useful for diagnostics, therapeutics, prophylaxis e.g. to prevent or delay infection, inflammation or tumour formation, as research reagents and kits and in distinguishing between functions of various members of a biological pathway. They are also useful in antisense therapy. The present sequence is an oligonucleotide targeted to human inhibitor-kappa B-R DNA	
Sequence 20 BP; 4 A; 4 C; 9 G; 3 T; 0 U; 0 Other;	
Query Match	1.9%; Score 19; DB 1; Length 20;
Best Local Similarity	100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
645 CAGGCTGAGTCGACGTGC 663	
1 CAGGCTGAGTCGACGTGC 19	

```

AC  ADC65799;
XX
XX  18-DEC-2003 (first entry)
DT
XX
XX  Human TGF-beta receptor II targeted antisense oligonucleotide #76.
DE
XX
XX  human; antisense oligonucleotide;
XX  transforming growth factor beta receptor II; TGF-beta receptor II;
XX  hyperproliferative disorder; breast cancer; autoimmune disorder;
XX  rheumatoid arthritis; 2'-O-methoxyethyl gapper;
XX  phosphorothioate backbone; ss.
XX
XX  Homo sapiens.
OS
XX  WO2003000656-A2.
PN
XX
XX  03-JAN-2003.
PD
XX
XX  19-JUN-2002; 2002WO-US019665.
PF
XX
XX  21-JUN-2001; 2001US-00888361.
PR
XX
XX  (ISIS-) ISIS PHARM INC.
PA
XX
XX  Murray SF, Wyatt JR;
PI
XX
XX  WPI; 2003-175279/17.
DR
XX
XX  New compound having a sequence targeted to a nucleic acid encoding
XX  transforming growth factor beta-receptor II, useful for preparing a
XX  composition for treating hyperproliferative disorder e.g., lung, liver,
XX  colon or gastric cancer.
XX
XX  Example 15; SEQ ID NO 95; 141bp; English.
PS
XX
XX  The invention comprises antisense oligonucleotides that are targeted to
XX  the nucleic acid encoding transforming growth factor beta (TGF-beta)
XX  receptor II. The antisense oligonucleotides of the invention are useful
XX  for treating: hyperproliferative disorders (e.g. breast cancer), or an
XX  autoimmune disorder (e.g. rheumatoid arthritis). The present DNA sequence
XX  represents a 2'-O-methoxyethyl gapper oligonucleotide with a
XX  phosphorothioate backbone that is targeted to human TGF-beta receptor II.
XX
XX  Sequence 20 BP; 5 A; 9 C; 3 G; 3 T; 0 U; 0 Other;
SQ
XX
XX  Query Match 1.9%; Score 19; DB 1; Length 20;
XX  Best Local Similarity 100.0%; Pred. No. 1.2e+03;
XX  Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY  541 CCTCAGCCTCCCAAGTAGC 559
XX  |||||
XX  2 CCTCAGCCTCCCAAGTAGC 20
DB
XX
XX  RESULT 677
XX  ADD21685/c
XX  ADD21685 standard; DNA; 20 BP.
XX
XX  ADD21685;
XX
XX  15-JAN-2004 (first entry)
XX
XX  Human mdm2 antisense oligonucleotide #248.
DE
XX
XX  antisense oligonucleotide; human; mdm2; hyperproliferation;
XX  hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX  atherosclerosis; restenosis; apoptosis modulation; p21; ss;
XX  2'-methoxyethoxy-residue; phosphorothioate backbone.
XX
XX  Homo sapiens.
OS
XX
XX  WO2003048315-A2.
XX
XX  PN
XX
XX  12-JUN-2003.
XX
XX  02-DEC-2002; 2002WO-US038281.
XX
XX  04-DEC-2001; 2001US-00005344.
XX
XX  (ISIS-) ISIS PHARM INC.
XX
XX  Miraglia LJ, Nero PS, Graham MJ, Monia BP, Koller E, Chiang MY;
XX  Manoharan M;
XX
XX  WPI; 2003-577263/54.
XX
XX  Novel antisense compound targeted to 5' untranslated region, coding
XX  region, or intron:exon junction of nucleic acid molecule encoding mdm2,
XX  useful for treating e.g. cancer, psoriasis or restenosis by inhibiting
XX  mdm2 expression.
XX
XX  Example 9; SEQ ID NO 250; 289bp; English.
PS
XX
XX  The invention comprises antisense oligonucleotides which are targeted to
XX  the human mdm2 gene. The antisense oligonucleotides of the invention are
XX  useful for reducing hyperproliferation of human cells. The antisense
XX  oligonucleotides are also useful for treating: hyperproliferative
XX  disorders (e.g. cancer), psoriasis, fibrosis, atherosclerosis, or
XX  restenosis. The antisense oligonucleotides are also useful for modulating
XX  apoptosis, and for increasing expression of p21. The present DNA sequence
XX  represents a human mdm2 gene antisense oligonucleotide of the invention.
XX  The present sequence contains 2'-methoxyethoxy-residues and has a
XX  phosphorothioate backbone.
XX
XX  Sequence 20 BP; 5 A; 2 C; 10 G; 3 T; 0 U; 0 Other;
SQ
XX
XX  Query Match 1.9%; Score 19; DB 1; Length 20;
XX  Best Local Similarity 100.0%; Pred. No. 1.2e+03;
XX  Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY  536 TCCTGCCTCAGCCTCCCA 554
XX  |||||
XX  2 TCCTGCCTCAGCCTCCCA 2
DB
XX
XX  RESULT 678
XX  ADD21678/c
XX  ADD21678 standard; DNA; 20 BP.
XX
XX  ADD21678;
XX
XX  15-JAN-2004 (first entry)
XX
XX  Human mdm2 antisense oligonucleotide #241.
DE
XX
XX  antisense oligonucleotide; human; mdm2; hyperproliferation;
XX  hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX  atherosclerosis; restenosis; apoptosis modulation; p21; ss;
XX  2'-methoxyethoxy-residue; phosphorothioate backbone.
XX
XX  Homo sapiens.
OS
XX
XX  WO2003048315-A2.
XX
XX  PN
XX
XX  12-JUN-2003.
XX
XX  02-DEC-2002; 2002WO-US038281.
XX
XX  04-DEC-2001; 2001US-00005344.
XX
XX  (ISIS-) ISIS PHARM INC.
XX
XX  Miraglia LJ, Nero PS, Graham MJ, Monia BP, Koller E, Chiang MY;
XX  Manoharan M;
XX
XX  WPI; 2003-577263/54.
XX

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PD  12-JUN-2003.
XX
XX  02-DEC-2002; 2002WO-US038281.
XX
XX  04-DEC-2001; 2001US-00005344.
XX
XX  (ISIS-) ISIS PHARM INC.
XX
XX  Miraglia LJ, Nero PS, Graham MJ, Monia BP, Koller E, Chiang MY;
XX  Manoharan M;
XX
XX  WPI; 2003-577263/54.
XX
XX  Novel antisense compound targeted to 5' untranslated region, coding
XX  region, or intron:exon junction of nucleic acid molecule encoding mdm2,
XX  useful for treating e.g. cancer, psoriasis or restenosis by inhibiting
XX  mdm2 expression.
XX
XX  Example 9; SEQ ID NO 250; 289bp; English.
PS
XX
XX  The invention comprises antisense oligonucleotides which are targeted to
XX  the human mdm2 gene. The antisense oligonucleotides of the invention are
XX  useful for reducing hyperproliferation of human cells. The antisense
XX  oligonucleotides are also useful for treating: hyperproliferative
XX  disorders (e.g. cancer), psoriasis, fibrosis, atherosclerosis, or
XX  restenosis. The antisense oligonucleotides are also useful for modulating
XX  apoptosis, and for increasing expression of p21. The present DNA sequence
XX  represents a human mdm2 gene antisense oligonucleotide of the invention.
XX  The present sequence contains 2'-methoxyethoxy-residues and has a
XX  phosphorothioate backbone.
XX
XX  Sequence 20 BP; 5 A; 2 C; 10 G; 3 T; 0 U; 0 Other;
SQ
XX
XX  Query Match 1.9%; Score 19; DB 1; Length 20;
XX  Best Local Similarity 100.0%; Pred. No. 1.2e+03;
XX  Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY  536 TCCTGCCTCAGCCTCCCA 554
XX  |||||
XX  2 TCCTGCCTCAGCCTCCCA 2
DB
XX
XX  RESULT 678
XX  ADD21678/c
XX  ADD21678 standard; DNA; 20 BP.
XX
XX  ADD21678;
XX
XX  15-JAN-2004 (first entry)
XX
XX  Human mdm2 antisense oligonucleotide #241.
DE
XX
XX  antisense oligonucleotide; human; mdm2; hyperproliferation;
XX  hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX  atherosclerosis; restenosis; apoptosis modulation; p21; ss;
XX  2'-methoxyethoxy-residue; phosphorothioate backbone.
XX
XX  Homo sapiens.
OS
XX
XX  WO2003048315-A2.
XX
XX  PN
XX
XX  12-JUN-2003.
XX
XX  02-DEC-2002; 2002WO-US038281.
XX
XX  04-DEC-2001; 2001US-00005344.
XX
XX  (ISIS-) ISIS PHARM INC.
XX
XX  Miraglia LJ, Nero PS, Graham MJ, Monia BP, Koller E, Chiang MY;
XX  Manoharan M;
XX
XX  WPI; 2003-577263/54.
XX

```

XX Novel antisense compound targeted to 5' untranslated region, coding  
PT region, or intron/exon junction of nucleic acid molecule encoding mdm2,  
PT useful for treating e.g. cancer, psoriasis or restenosis by inhibiting  
PT mdm2 expression.

PS Claim 4; SEQ ID NO 243; 289bp; English.

XX The invention comprises antisense oligonucleotides which are targeted to  
CC the human mdm2 gene. The antisense oligonucleotides of the invention are  
CC useful for reducing hyperproliferation of human cells. The antisense  
CC oligonucleotides are also useful for treating: hyperproliferative  
CC disorders (e.g. cancer), psoriasis, fibrosis, atherosclerosis, or  
CC restenosis. The antisense oligonucleotides are also useful for modulating  
CC apoptosis, and for increasing expression of p21. The present DNA sequence  
CC represents a human mdm2 gene antisense oligonucleotide of the invention.  
CC The present sequence contains 2'-methoxyethoxy-residues and has a  
CC phosphorothioate backbone.

SQ Sequence 20 BP; 3 A; 10 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 1.9%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 644 CCAGCTGAGTGCAGTGG 662  
DB 20 CCAGCTGAGTGCAGTGG 2

RESULT 679  
ADD25037/C  
ID ADD25037 standard; DNA; 20 BP.

AC ADD25037;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Human caspase-8 antisense oligonucleotide ISIS 107686.

XX Caspase-8; cytostatic; immunosuppressant; anti-HIV; SBI;  
KW antisense gene therapy; apoptosis; hyperproliferative disorder;  
KW haematopoietic disorder; autoimmune disorder; viral infection; AIDS;  
KW neurological disorder; Alzheimer's disease; Parkinson's disease;  
KW amyotrophic lateral sclerosis; retinitis pigmentosa; blood cell disorder;  
KW cancer; human.  
XX  
XX  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH 1. 20  
FT modified\_base /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "Phosphorothioate backbone and all cytidines are 5  
FT -methylcytidines"  
FT 1..5  
FT modified\_base /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "2'-methoxyethyl residues"  
FT 16..20  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "2'-methoxyethyl residues"  
XX  
XX US2003083296-A1.  
XX  
XX PD 01-MAY-2003.  
XX  
XX PF 12-JUL-2002; 2002US-00181177.  
XX  
XX PR 19-JAN-2000; 2000US-00487445.  
XX  
XX PR 11-JAN-2001; 2001WO-US000955.  
XX

PA (ZHAN/) ZHANG H.  
PA (COMS/) COMSERT L M.  
XX  
XX Zhang H, Cowseert LM;  
PI WPI; 2003-810793/76.  
XX  
DR WPI; 2003-810793/76.  
XX  
XX New compound, particularly antisense oligonucleotides targeted to a  
PT nucleic acid encoding caspase 8, useful for treating a disease/condition  
PT associated with caspase 8, such as hyperproliferative or autoimmune  
PT disorders.

PS Example 15; SEQ ID NO 94; 59bp; English.

XX The invention relates to a compound 8-30 nucleobases in length targeted  
CC to, and which specifically hybridises with a nucleic acid molecule  
CC encoding caspase 8 (a protein involved in apoptosis) and inhibits the  
CC expression of caspase 8, i.e. an antisense oligonucleotide. Also included  
CC are a compound 8-30 nucleobases in length that specifically hybridises  
CC with at least an 8-nucleobase portion of an active site on a nucleic acid  
CC molecule encoding caspase 8, a composition comprising the compound and a  
CC carrier or diluent, inhibiting the expression of caspase 8 in cells or  
CC tissues (by contacting the cells or tissues with the compound so that  
CC expression of caspase 8 is inhibited) and treating an animal having a  
CC disease or condition associated with caspase 8 by administering to the  
CC animal a therapeutic or prophylactic amount of the compound so that  
CC expression of caspase 8 is inhibited. The compound, composition and  
CC methods are useful for treating a disease or condition associated with  
CC caspase 8, such as hyperproliferative, haematopoietic or autoimmune  
CC disorder, viral infection such as AIDS, neurological disorders (e.g.  
CC Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis,  
CC retinitis pigmentosa), blood cell disorders and cancer. They are also  
CC useful in research and diagnostics for modulating the expression of  
CC interleukin 8. The present sequence is a caspase-8 targeting antisense  
CC oligonucleotide of the invention.

SQ Sequence 20 BP; 4 A; 10 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 1.9%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 646 AGGCTGAGTGCAGTGGC 664  
DB 20 AGGCTGAGTGCAGTGGC 2

RESULT 680  
AB297910  
ID AB297910 standard; DNA; 20 BP.

AC AB297910;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Human RANTES oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX  
XX  
XX Homo sapiens.  
XX  
XX OS  
XX WO200285308-A2.  
XX  
XX PD 31-OCT-2002.  
XX  
XX PF 23-APR-2002; 2002WO-US013135.  
XX  
XX PR 24-APR-2001; 2001US-0286137P.  
XX



XX PA (EPIC-) EPIGENESIS PHARM INC.  
XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
XX PI Miller S, Tang L, Shahabuddin S;  
XX DR WPI; 2003-229219/22.  
XX PT Pharmaceutical composition for treating ailments associated with impaired  
XX PT respiration, has oligo(s) antisense to specific gene(s) or its  
XX PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
XX PT ubiquinone.  
XX PS Disclosure; SEQ ID NO 13152; 872bp; English.  
XX CC The invention relates to a novel pharmaceutical composition, which has a  
XX CC first active agent comprising an oligonucleotide antisense to the  
XX CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
XX CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
XX CC junctions of genes encoding a polypeptide associated with lung and/or  
XX CC nasal airway dysfunction and a second active agent comprising an  
XX CC antiinflammatory steroid and ubiquinone. A composition of the invention  
XX CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
XX CC immunosuppressive, and cytostatic activity. The composition may have a  
XX CC use in antisense gene therapy. The composition is useful for treating or  
XX CC preventing a respiratory, lung or malignant disease or condition, also  
XX CC for enhancing the prophylactic or therapeutic respiratory effect of an  
XX CC antiinflammatory steroid in a subject, for reducing or depleting levels  
XX CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
XX CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
XX CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
XX CC lung inflammation, lung allergies, or a respiratory disease or condition.  
XX CC Note: The sequence data for this patent is not represented in the printed  
XX CC specification, but was obtained in electronic format directly from WIPO  
XX CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 20 BP; 5 A; 4 C; 8 G; 3 T; 0 U; 0 Other;  
XX  
XX Query Match 1.9%; Score 19; DB 1; Length 20;  
XX Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 728 GAGTAGCTGGAGCTACAGG 746  
Db 2 GAGTAGCTGGAGCTACAGG 20  
RESULT 681  
AB298002  
ID AB298002 standard; DNA; 20 BP.  
XX AC AB298002;  
XX DT 17-OCT-2003 (first entry)  
XX DE Human RANTES oligonucleotide sequence.  
XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
XX KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
XX KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
XX KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
XX KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
XX KW lung inflammation; respiratory disease; ds.  
XX OS Homo sapiens.  
XX PN WO200285308-A2.  
XX PD 31-OCT-2002.  
XX PF 23-APR-2002; 2002WO-US013135.  
XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPIC-) EPIGENESIS PHARM INC.  
XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
XX PI Miller S, Tang L, Shahabuddin S;  
XX DR WPI; 2003-229219/22.  
XX PT Pharmaceutical composition for treating ailments associated with impaired  
XX PT respiration, has oligo(s) antisense to specific gene(s) or its  
XX PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
XX PT ubiquinone.  
XX PS Disclosure; SEQ ID NO 13244; 872bp; English.  
XX CC The invention relates to a novel pharmaceutical composition, which has a  
XX CC first active agent comprising an oligonucleotide antisense to the  
XX CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
XX CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
XX CC junctions of genes encoding a polypeptide associated with lung and/or  
XX CC nasal airway dysfunction and a second active agent comprising an  
XX CC antiinflammatory steroid and ubiquinone. A composition of the invention  
XX CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
XX CC immunosuppressive, and cytostatic activity. The composition may have a  
XX CC use in antisense gene therapy. The composition is useful for treating or  
XX CC preventing a respiratory, lung or malignant disease or condition, also  
XX CC for enhancing the prophylactic or therapeutic respiratory effect of an  
XX CC antiinflammatory steroid in a subject, for reducing or depleting levels  
XX CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
XX CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
XX CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
XX CC lung inflammation, lung allergies, or a respiratory disease or condition.  
XX CC Note: The sequence data for this patent is not represented in the printed  
XX CC specification, but was obtained in electronic format directly from WIPO  
XX CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 20 BP; 3 A; 5 C; 7 G; 5 T; 0 U; 0 Other;  
XX  
XX Query Match 1.9%; Score 19; DB 1; Length 20;  
XX Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 638 TGTCAACCCAGGCTGAGTG 656  
Db 2 TGTCAACCCAGGCTGAGTG 20  
RESULT 682  
ABD31033  
ID ABD31033 standard; DNA; 20 BP.  
XX AC ABD31033;  
XX DT 29-JUL-2004 (first entry)  
XX DE Human RANTES-derived oligonucleotide SEQ ID 13244.  
XX KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
XX KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
XX KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;  
XX KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
XX KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
XX KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
XX KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
XX KW pulmonary transplantation rejection; ss; primer.  
XX OS Homo sapiens.  
XX PN WO200285309-A2.  
XX PD 31-OCT-2002.  
XX PF 23-APR-2002; 2002WO-US013143.  
XX PR



ID ADJ59867 standard; DNA; 20 BP.  
XX  
AC ADJ59867;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Oligonucleotide associated to RANTES #116.  
XX  
XX Interleukin; IL-4 receptor; IL-5 receptor; lung disease;  
KW airway inflammation; allergy; asthma; impeded respiration;  
KW cystic fibrosis; acute respiratory distress syndrome;  
KW pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;  
KW ss.  
XX  
OS Homo sapiens.  
XX  
PN MO2004011613-A2.  
XX  
PD 05-FEB-2004.  
XX  
PF 25-JUL-2003; 2003WO-US023509.  
XX  
PR 29-JUL-2002; 2002US-0399076P.  
XX  
XX (EPIC-) EPIGENESIS PHARM INC.  
XX  
PI Nyce JW, Tang L, Sandrasagra A, Aguilar D, Miller S;  
PI Shababuddin S, Lu H, Cong H;  
DR WPI; 2004-203534/19.  
XX  
XX Novel single or multiple target oligonucleotide anti-sense to e.g.  
PT initiation codons and introns of respiratory disease-relevant genes e.g.,  
PT CCR1, RANTES, MCP4, useful for prophylaxis or treating respiratory  
PT disease e.g., asthma.  
XX  
PS Claim 2; SEQ ID NO 723; 85bp; English.  
XX  
XX The present invention relates to an oligonucleotide anti-sense to e.g.,  
CC initiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-  
CC end of nucleic acid target comprising gene(s) chosen from e.g.  
CC Interleukin (IL)-4 receptor, IL-5 receptor or salts of the  
CC oligonucleotide and optionally surfactant operatively linked to the  
CC oligonucleotide. The method is useful for preventing or treating a  
CC respiratory or lung disease, which involves administering to the airways  
CC of a subject an effective amount of an inhibitor. The oligonucleotide is  
CC useful for production of a medicament for the prevention and/or treatment  
CC of a respiratory or lung disease. The respiratory or lung disease is  
CC chosen from airway inflammation, allergy(ies), asthma, impeded  
CC respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases  
CC (COPD), allergic rhinitis (AR), acute respiratory distress syndrome  
CC (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway  
CC obstruction. The present sequence represents an oligonucleotide of the  
CC invention.  
XX  
SQ Sequence 20 BP; 3 A; 5 C; 7 G; 5 T; 0 U; 0 Other;  
XX  
Query Match 1.9%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03; Indels 0; Gaps 0;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 638 TGTCAACGAGCTGAGTG 656  
DB 2 TGTCAACGAGCTGAGTG 20  
XX  
RESULT 685  
ADJ59775  
ID ADJ59775 standard; DNA; 20 BP.  
XX  
AC ADJ59775;  
XX  
DT 06-MAY-2004 (first entry)

XX  
DE Oligonucleotide associated to RANTES #24.  
XX  
KW Interleukin; IL-4 receptor; IL-5 receptor; lung disease;  
KW airway inflammation; allergy; asthma; impeded respiration;  
KW cystic fibrosis; acute respiratory distress syndrome;  
KW pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;  
KW ss.  
XX  
OS Homo sapiens.  
XX  
PN MO2004011613-A2.  
XX  
PD 05-FEB-2004.  
XX  
PF 25-JUL-2003; 2003WO-US023509.  
XX  
PR 29-JUL-2002; 2002US-0399076P.  
XX  
XX (EPIC-) EPIGENESIS PHARM INC.  
XX  
PI Nyce JW, Tang L, Sandrasagra A, Aguilar D, Miller S;  
PI Shababuddin S, Lu H, Cong H;  
DR WPI; 2004-203534/19.  
XX  
XX Novel single or multiple target oligonucleotide anti-sense to e.g.  
PT initiation codons and introns of respiratory disease-relevant genes e.g.,  
PT CCR1, RANTES, MCP4, useful for prophylaxis or treating respiratory  
PT disease e.g., asthma.  
XX  
PS Claim 2; SEQ ID NO 631; 85bp; English.  
XX  
XX The present invention relates to an oligonucleotide anti-sense to e.g.,  
CC initiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-  
CC end of nucleic acid target comprising gene(s) chosen from e.g.  
CC Interleukin (IL)-4 receptor, IL-5 receptor or salts of the  
CC oligonucleotide and optionally surfactant operatively linked to the  
CC oligonucleotide. The method is useful for preventing or treating a  
CC respiratory or lung disease, which involves administering to the airways  
CC of a subject an effective amount of an inhibitor. The oligonucleotide is  
CC useful for production of a medicament for the prevention and/or treatment  
CC of a respiratory or lung disease. The respiratory or lung disease is  
CC chosen from airway inflammation, allergy(ies), asthma, impeded  
CC respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases  
CC (COPD), allergic rhinitis (AR), acute respiratory distress syndrome  
CC (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway  
CC obstruction. The present sequence represents an oligonucleotide of the  
CC invention.  
XX  
SQ Sequence 20 BP; 5 A; 4 C; 8 G; 3 T; 0 U; 0 Other;  
XX  
Query Match 1.9%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03; Indels 0; Gaps 0;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 728 GAGTAGCTGGAGCTACAGG 746  
DB 2 GAGTAGCTGGAGCTACAGG 20  
XX  
RESULT 686  
ADM14845/C  
ID ADM14845 standard; DNA; 20 BP.  
XX  
AC ADM14845;  
XX  
DT 01-JUL-2004 (first entry)  
XX  
DE Human mPGEs-1 chimeric antisense oligonucleotide SEQ ID NO:1032.  
XX  
KW chimeric; antisense oligonucleotide; phosphorothioate; human;  
KW microsomal prostaglandin H2 synthase; mPGEs-1; mPGEs-1 inhibitor;

KW microsome1 prostaglandin E2 synthase inhibitor; cytosstatic; antidiabetic;  
KW immunomodulator; carciant; neuroprotective; antiinflammatory;  
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;  
KW immunomodulatory; cardiovascular; gene therapy; inflammation;  
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;  
KW reperfusion injury; ophthalmic disorder; immunological disorder;  
KW cardiovascular disorder; neurological disorder; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
XX  
XX Key Location/Qualifiers  
FT modified\_base 1..20  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "phosphorothioate linkages and all cytidine  
FT residues are 5-methylcytidines"  
FT modified\_base 1..5  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "2'-O-methoxyethyls"  
FT modified\_base 16..20  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "2'-O-methoxyethyls"  
XX  
XX WO2004028458-A2.  
XX  
XX 08-APR-2004.  
XX  
XX 25-SEP-2003; 2003WO-US030374.  
XX  
XX 25-SEP-2002; 2002US-0413549P.  
XX  
XX (PBARA ) PHARMACIA CORP.  
XX  
XX Gierse JK;  
XX  
XX MPI; 2004-305094/28.  
XX  
XX  
XX New antisense compound, having a sequence targeted to a nucleic acid  
PT encoding mPGEs-1, useful for preparing a composition for treating e.g.,  
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or  
PT ischemia.  
XX  
XX  
XX Claim 4; SEQ ID NO 1032; 132pp; English.  
XX  
XX The present sequence represents a chimeric antisense oligonucleotide  
CC targeted to human microsome1 prostaglandin E2 synthase (mPGEs-1). The  
CC human mPGEs-1 gene is located on chromosome 9, more specifically to  
CC 9q34.3. The present invention also describes: (1) antisense compounds,  
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding  
CC mPGEs-1, which specifically hybridise with the nucleic acid mPGEs-1 and  
CC inhibit its expression; (2) a method of inhibiting the expression of  
CC mPGEs-1 in cells or tissues; and (3) a method of treating an animal  
CC having a disease or condition associated with mPGEs-1. mPGEs-1 chimeric  
CC antisense oligonucleotides and antisense compounds have cytosstatic,  
CC antidiabetic, immunomodulator, carciant, neuroprotective,  
CC antiinflammatory, nootropic, antiarthritic, vasotropic,  
CC ophthalmological, immunomodulatory and cardiovascular activities, and can  
CC be used as mPGEs-1 inhibitors and in gene therapy. The antisense compound  
CC can be used for preparing a composition for treating a disease or  
CC condition associated with mPGEs-1 e.g., inflammation, Alzheimer's  
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or  
CC ophthalmic, immunological, cardiovascular or neurological disorder.  
XX  
XX Sequence 20 BP; 3 A; 6 C; 8 G; 3 T; 0 U; 0 Other;  
XX  
XX  
XX Query Match 1.9%; Score 19; DB 1; Length 20;  
XX Best Local Similarity 100.0%; Pred No. 1.2e+03;  
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX 846 GCCTCGGCTCCCAAGTG 864

Db 19 GCCTCGGCTCCCAAGTG 1  
|||||  
RESULT 687  
ADM14508/C  
ID ADM14508 standard; DNA; 20 BP.  
XX  
XX ADM14508;  
XX  
XX 01-JUL-2004 (first entry)  
XX  
XX Human mPGEs-1 chimeric antisense oligonucleotide SEQ ID NO:695.  
XX  
XX chimeric; antisense oligonucleotide; phosphorothioate; human;  
XX microsome1 prostaglandin E2 synthase inhibitor; mPGEs-1 inhibitor;  
KW microsome1 prostaglandin E2 synthase inhibitor; cytosstatic; antidiabetic;  
KW immunomodulator; carciant; neuroprotective; antiinflammatory;  
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;  
KW immunomodulatory; cardiovascular; gene therapy; inflammation;  
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;  
KW reperfusion injury; ophthalmic disorder; immunological disorder;  
KW cardiovascular disorder; neurological disorder; ss.  
XX  
XX Homo sapiens.  
XX Synthetic.  
OS  
OS  
XX  
XX Key Location/Qualifiers  
FT modified\_base 1..20  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "phosphorothioate linkages and all cytidine  
FT residues are 5-methylcytidines"  
FT modified\_base 1..5  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "2'-O-methoxyethyls"  
FT modified\_base 16..20  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "2'-O-methoxyethyls"  
XX  
XX WO2004028458-A2.  
XX  
XX 08-APR-2004.  
XX  
XX 25-SEP-2003; 2003WO-US030374.  
XX  
XX 25-SEP-2002; 2002US-0413549P.  
XX  
XX (PBARA ) PHARMACIA CORP.  
XX  
XX Gierse JK;  
XX  
XX MPI; 2004-305094/28.  
XX  
XX  
XX New antisense compound, having a sequence targeted to a nucleic acid  
PT encoding mPGEs-1, useful for preparing a composition for treating e.g.,  
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or  
PT ischemia.  
XX  
XX  
XX Claim 4; SEQ ID NO 695; 132pp; English.  
XX  
XX The present sequence represents a chimeric antisense oligonucleotide  
CC targeted to human microsome1 prostaglandin E2 synthase (mPGEs-1). The  
CC human mPGEs-1 gene is located on chromosome 9, more specifically to  
CC 9q34.3. The present invention also describes: (1) antisense compounds,  
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding  
CC mPGEs-1, which specifically hybridise with the nucleic acid mPGEs-1 and  
CC inhibit its expression; (2) a method of inhibiting the expression of  
CC mPGEs-1 in cells or tissues; and (3) a method of treating an animal  
CC having a disease or condition associated with mPGEs-1. mPGEs-1 chimeric  
CC antisense oligonucleotides and antisense compounds have cytosstatic,  
CC

PT New antisense compound, having a sequence targeted to a nucleic acid

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FT /mod_base= OTHER
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[illegible]

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XX XX WO2004028458-A2.
XX XX
XX XX 08-APR-2004.
XX XX
XX XX 25-SEP-2003; 2003WO-US030374.
XX XX
XX XX 25-SEP-2002; 2002US-0413549P.
XX XX
XX XX (PHAA ) PHARMACIA CORP.
XX XX
XX XX Gierse JK;
XX XX
XX XX WPI; 2004-305094/28.
XX XX
XX XX New antisense compound, having a sequence targeted to a nucleic acid
XX XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX XX ischemia.
XX XX
XX XX Claim 4; SEQ ID NO 1199; 132pp; English.
XX XX
XX XX The present sequence represents a chimeric antisense oligonucleotide
XX XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX XX mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
XX XX inhibits its expression; (2) a method of inhibiting the expression of
XX XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX XX antisense oligonucleotides and antisense compounds have cytostatic,
XX XX antidiabetic, immunomodulatory, cardiant, neuroprotective,
XX XX antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
XX XX ophthalmological, immunomodulatory and cardiovascular activities, and can
XX XX be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX XX can be used for preparing a composition for treating a disease or
XX XX condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX XX disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
XX XX ophthalmic, immunological, cardiovascular or neurological disorder.
XX XX
XX XX Sequence 20 BP; 5 A; 7 C; 5 G; 3 T; 0 U; 0 Other;
XX XX
XX XX Query Match 1.9%; Score 19; DB 1; Length 20;
XX XX Best Local Similarity 100.0%; Pred. No. 1.2e+03;
XX XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
XX XX 721 GCTCTCTGAGTAGCTGGGA 739
XX XX |||||
XX XX Db 20 GCCTCTGAGTAGCTGGGA 2
XX XX
XX XX RESULT 690
XX XX ADM15357/C
XX XX ID ADM15357 standard; DNA; 20 BP.
XX XX
XX XX ADM15357;
XX XX
XX XX 01-JUL-2004 (first entry)
XX XX
XX XX Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:1544.
XX XX
XX XX chimeric; antisense oligonucleotide; phosphorochiaste; human;
XX XX microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
XX XX microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
XX XX immunomodulatory; cardiant; neuroprotective; antiinflammatory;
XX XX neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
XX XX immunomodulatory; cardiovascular; gene therapy; inflammation;
XX XX Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
XX XX reperfusion injury; ophthalmic disorder; immunological disorder;
XX XX cardiovascular disorder; neurological disorder; ss.
XX XX
XX XX Homo sapiens.
XX XX

```

```

OS Synthetic.
XX XX Location/Qualifiers
XX XX Key modified_base 1..20
XX XX FT modified_base 1..20
XX XX FT /tag= b
XX XX FT /mod_base= OTHER
XX XX FT /note= "phosphorochiaste linkages and all cytidine
XX XX FT residues are 5-methylcytidines"
XX XX FT modified_base 1..5
XX XX FT /tag= a
XX XX FT /mod_base= OTHER
XX XX FT /note= "2'-O-methoxyethyls"
XX XX FT modified_base 16..20
XX XX FT /tag= c
XX XX FT /mod_base= OTHER
XX XX FT /note= "2'-O-methoxyethyls"
XX XX
XX XX WO2004028458-A2.
XX XX
XX XX 08-APR-2004.
XX XX
XX XX 25-SEP-2003; 2003WO-US030374.
XX XX
XX XX 25-SEP-2002; 2002US-0413549P.
XX XX
XX XX (PHAA ) PHARMACIA CORP.
XX XX
XX XX Gierse JK;
XX XX
XX XX WPI; 2004-305094/28.
XX XX
XX XX New antisense compound, having a sequence targeted to a nucleic acid
XX XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX XX ischemia.
XX XX
XX XX Claim 4; SEQ ID NO 1544; 132pp; English.
XX XX
XX XX The present sequence represents a chimeric antisense oligonucleotide
XX XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX XX mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
XX XX inhibits its expression; (2) a method of inhibiting the expression of
XX XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX XX antisense oligonucleotides and antisense compounds have cytostatic,
XX XX antidiabetic, immunomodulatory, cardiant, neuroprotective,
XX XX antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
XX XX ophthalmological, immunomodulatory and cardiovascular activities, and can
XX XX be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX XX can be used for preparing a composition for treating a disease or
XX XX condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX XX disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
XX XX ophthalmic, immunological, cardiovascular or neurological disorder.
XX XX
XX XX Sequence 20 BP; 12 A; 3 C; 0 G; 5 T; 0 U; 0 Other;
XX XX
XX XX Query Match 1.9%; Score 19; DB 1; Length 20;
XX XX Best Local Similarity 100.0%; Pred. No. 1.2e+03;
XX XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
XX XX 769 TTTTGTATTTTGTAGTACA 787
XX XX |||||
XX XX Db 19 TTTTGTATTTTGTAGTACA 1
XX XX
XX XX RESULT 691
XX XX ADM15184/C
XX XX ID ADM15184 standard; DNA; 20 BP.
XX XX
XX XX ADM15184;
XX XX

```

XX 01-JUL-2004 (first entry)  
DT Human mPES-1 chimeric antisense oligonucleotide SEQ ID NO:1371.  
XX chimeric; antisense oligonucleotide; phosphorothioate; human;  
XX microosomal prostaglandin E2 synthase; mPES-1; mPES-1 inhibitor;  
XX microosomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;  
XX immunomodulator; cardiant; neuroprotective; antiinflammatory;  
XX neuroprotective; neurotrophic; antiarthritic; vasoregulatory; ophthalmological;  
XX immunomodulatory; cardiovascular; gene therapy; inflammation;  
XX Alzheimer's disease; arthritis; diabetes; cancer; ischemia;  
XX reperfusion injury; ophthalmic disorder; immunological disorder;  
XX cardiovascular disorder; neurological disorder; ss.  
XX Homo sapiens.  
OS Synthetic.  
XX Key Location/Qualifiers  
XX modified\_base 1..20  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "phosphorothioate linkages and all cytidine  
FT residues are 5-methylcytidines"  
FT modified\_base 1..5  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "2'-O-methoxyethyls"  
FT modified\_base 15..20  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "2'-O-methoxyethyls"  
XX WO2004028458-A2.  
XX 08-APR-2004.  
XX 25-SEP-2003; 2003WO-US030374.  
XX 25-SEP-2002; 2002US-0413549P.  
XX (PHAA ) PHARMACIA CORP.  
XX Gierse JK;  
XX WPI; 2004-305094/28.  
XX New antisense compound, having a sequence targeted to a nucleic acid  
XX encoding mPES-1, useful for preparing a composition for treating e.g.,  
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or  
XX ischemia.  
XX Claim 4; SEQ ID NO 1371; 132pp; English.  
XX The present sequence represents a chimeric antisense oligonucleotide  
XX targeted to human microosomal prostaglandin E2 synthase (mPES-1). The  
XX human mPES-1 gene is located on chromosome 9, more specifically to  
XX 9p34.3. The present invention also describes: (1) antisense compounds,  
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding  
XX mPES-1, which specifically hybridize with the nucleic acid mPES-1 and  
XX inhibits its expression; (2) a method of inhibiting the expression of  
XX mPES-1 in cells or tissues; and (3) a method of treating an animal  
XX having a disease or condition associated with mPES-1. mPES-1 chimeric  
XX antisense oligonucleotides and antisense compounds have cytostatic,  
XX antidiabetic, immunomodulator, cardiant, neuroprotective,  
XX antiinflammatory, neuroprotective, neurotrophic, antiarthritic, vasoregulatory,  
XX ophthalmological, immunomodulatory and cardiovascular activities, and can  
XX be used as mPES-1 inhibitors and in gene therapy. The antisense compound  
XX can be used for preparing a composition for treating a disease or  
XX condition associated with mPES-1 e.g., inflammation, Alzheimer's  
XX disease, arthritis, diabetes, cancer, ischemia or reperfusion injury, or  
XX ophthalmic, immunological, cardiovascular or neurological disorder.

XX SQ Sequence 20 BP; 10 A; 4 C; 1 G; 5 T; 0 U; 0 Other;  
XX Query Match 1.9%; Score 19; DB 1; Length 20;  
XX Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 771 TTTGATTCTTGTAGTACAGA 789  
XX |||||  
XX Db 20 TTGTTATTTTGTAGTACAGA 2  
XX  
XX RESULT 692  
XX ADO45265  
XX ID ADO45265 standard; DNA; 20 BP.  
XX  
XX ADO45265;  
XX  
XX 15-JUL-2004 (first entry)  
XX  
XX Human oligonucleotide #631.  
XX  
XX Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;  
XX CCR1; CCR3; Eotaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;  
XX tryptase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease;  
XX lung disease; hyper-responsiveness; adenosis; adenosis A receptor;  
XX asthma; lung allergy; inflammation; inflammatory disease; cystic fibrosis; CF;  
XX airway inflammation; allergy; impeded respiration; allergic rhinitis;  
XX chronic obstructive pulmonary disease; COPD; allergic rhinitis;  
XX acute respiratory distress syndrome; pulmonary hypertension;  
XX lung inflammation; bronchitis; airway obstruction; bronchoconstriction.  
XX  
XX Homo sapiens.  
XX  
XX US2004049022-A1.  
XX  
XX 11-MAR-2004.  
XX  
XX 25-JUL-2003; 2003US-00627930.  
XX  
XX 23-APR-2002; 2002WO-US013135.  
XX 23-APR-2002; 2002WO-US013143.  
XX  
XX (NYCE/) NYCE J W.  
XX (SAND/) SANDRASAGRA A.  
XX (TANG/) TANG L.  
XX (AGUI/) AGUILAR D.  
XX (MILL/) MILLER S.  
XX (SHAH/) SHAHABUDDIN S.  
XX (LUHH/) LU H.  
XX (CONG/) CONG H.  
XX  
XX NYCE JW, Sandrasagra A, Tang L, Aguilar D, Miller S;  
XX Shahabuddin S, Lu H, Cong H;  
XX WPI; 2004-293804/27.  
XX  
XX Novel single or multiple target oligonucleotide anti-sense to e.g.  
XX initiation codon, intron of respiratory disease-relevant gene e.g. CCR1,  
XX RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.  
XX asthma.  
XX  
XX Claim 2; SEQ ID NO 631; 174pp; English.  
XX  
XX The invention relates to oligonucleotides anti-sense to an initiation  
XX codon, coding region, 5' or 3' intron-exon junction, intron or region  
XX with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target  
XX chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)  
XX -5 receptor, CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,  
XX tryptase a, tryptase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention  
XX also relates to a method of screening a candidate compound that binds to  
XX one or more nucleic acid target(s) or expressed product(s), for the  
XX prevention and/or treatment of a respiratory or lung disease. The  
XX oligonucleotides are useful for reducing or inhibiting expression of a



CC gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,  
 CC CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, tryptase a,  
 CC tryptase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are  
 CC useful for preventing or treating a respiratory or lung disease. The  
 CC respiratory or lung disease is associated with hyper-responsiveness to  
 CC and/or increased levels of, adenosine and/or levels of adenosine A  
 CC receptor(s), and/or asthma and/or lung allergies associated with  
 CC inflammation or an inflammatory disease. The respiratory or lung disease  
 CC is chosen from allergy inflammation, allergy, asthma, impeded respiration,  
 CC cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),  
 CC allergic rhinitis, acute respiratory distress syndrome, pulmonary  
 CC hypertension, lung inflammation, bronchitis, airway obstruction or  
 CC bronchoconstriction. This sequence represents an oligonucleotide of the  
 CC invention.

CC Sequence 20 BP; 5 A; 4 C; 8 G; 3 T; 0 U; 0 Other;

CC Query Match 1.9%; Score 19; DB 1; Length 20;

CC Best Local Similarity 100.0%; Pred. No. 1.2e+03;

CC Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Db 728 GAGTAGCTGGGACTACAGG 746

2 GAGTAGCTGGGACTACAGG 20

RESULT 693

AD045357

ID AD045357 standard; DNA; 20 BP.

AC AD045357;

DT 15-JUL-2004 (first entry)

DE Human oligonucleotide #723.

XX Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;  
 XX CCR1; CCR3; Eotaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;  
 XX tryptase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease;  
 XX lung disease; hyper-responsiveness; adenosine; adenosine A receptor;  
 XX asthma; lung allergy; inflammation; inflammatory disease;  
 XX airway inflammation; allergy; impeded respiration; cystic fibrosis; CF;  
 XX chronic obstructive pulmonary disease; COPD; allergic rhinitis;  
 XX acute respiratory distress syndrome; pulmonary hypertension;  
 XX lung inflammation; bronchitis; airway obstruction; bronchoconstriction.

XX Homo sapiens.

OS US2004049022-A1.

PN 11-MAR-2004.

PD 25-JUL-2003; 2003US-00627930.

PF 23-APR-2002; 2002WO-US013135.

PR 23-APR-2002; 2002WO-US013143.

XX (NYCE/) NYCE J W.

XX (SAND/) SANDRASAGRA A.

XX (TANG/) TANG L.

XX (AGUI/) AGUILAR D.

XX (MILL/) MILLER S.

XX (SHAH/) SHAHABUDDIN S.

XX (LUHR/) LU H.

XX (CONG/) CONG H.

XX NYCE JW, Sandrasagra A, Tang L, Aguilar D, Miller S;  
 XX PI Shahabuddin S, Lu H, Cong H;  
 XX DR WPI; 2004-293804/27.

XX Novel single or multiple target oligonucleotide anti-sense to e.g. CCR1,  
 PT initiation codon, intron of respiratory disease-relevant gene e.g. CCR1,

PT RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.  
 PT asthma.

PS Claim 2; SEQ ID NO 723; 174bp; English.

XX The invention relates to oligonucleotides anti-sense to an initiation  
 CC codon, coding region, 5' or 3' intron-exon junction, intron or region  
 CC with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target  
 CC chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)-  
 CC 5 receptor, CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,  
 CC tryptase a, tryptase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention  
 CC also relates to a method of screening a candidate compound that binds to  
 CC one or more nucleic acid target(s) or expressed product(s), for the  
 CC prevention and/or treatment of a respiratory or lung disease. The  
 CC oligonucleotides are useful for reducing or inhibiting expression of a  
 CC gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,  
 CC CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, tryptase a,  
 CC tryptase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are  
 CC useful for preventing or treating a respiratory or lung disease. The  
 CC respiratory or lung disease is associated with hyper-responsiveness to  
 CC and/or increased levels of, adenosine and/or levels of adenosine A  
 CC receptor(s), and/or asthma and/or lung allergies associated with  
 CC inflammation or an inflammatory disease. The respiratory or lung disease  
 CC is chosen from allergy inflammation, allergy, asthma, impeded respiration,  
 CC cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),  
 CC allergic rhinitis, acute respiratory distress syndrome, pulmonary  
 CC hypertension, lung inflammation, bronchitis, airway obstruction or  
 CC bronchoconstriction. This sequence represents an oligonucleotide of the  
 CC invention.

CC Sequence 20 BP; 3 A; 5 C; 7 G; 5 T; 0 U; 0 Other;

CC Query Match 1.9%; Score 19; DB 1; Length 20;

CC Best Local Similarity 100.0%; Pred. No. 1.2e+03;

CC Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Db 638 TGTACCCAGCGCTGAGTG 656

2 TGTACCCAGCGCTGAGTG 20

RESULT 694

ADP08716

ID ADP08716 standard; DNA; 20 BP.

AC ADP08716;

DT 26-AUG-2004 (first entry)

DE Extend primer 53 used to genotype human glycoprotein VI polymorphism.

XX breast cancer; cytostatic; gene therapy; human; platelet glycoprotein VI;  
 XX GW6; GPIV; GPIIb/IIIa; chromosome 19q13.4; ss; PCR; primer; SNP;

XX single nucleotide polymorphism.

XX Homo sapiens.

OS WO2004047767-A2.

PN 10-JUN-2004.

PD 25-NOV-2003; 2003WO-US037966.

PF 25-NOV-2002; 2002US-0429136P.

PR 24-JUL-2003; 2003US-0490234P.

XX (SEQU-) SEQUENOM INC.

XX Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;  
 XX PI WPI; 2004-441082/41.

XX Identifying a subject at risk of breast cancer by detecting the presence



PT or absence of one or more nucleotide polymorphic variations, useful for  
PT diagnosing, preventing and/or treating breast cancer.  
XX  
XX Example 3; Page 83; 286pp; English.  
XX  
CC The invention relates to a novel method for identifying a subject at risk  
CC of breast cancer which comprises detecting the presence or absence of one  
CC or more polymorphic variations associated with breast cancer in a nucleic  
CC acid sample from a subject. The method of the invention has cytostatic  
CC applications and may be useful for identifying a risk of breast cancer,  
CC as well as therapeutic and prophylactic treatments that specifically  
CC target breast cancer, such as gene therapy. The current sequence is that  
CC of an extend primer of the invention which was used to genotype single  
CC nucleotide polymorphisms within human glycoprotein VI (platelet) (GPI,  
CC GPIV/GPVI) DNA which is located at chromosomal position 19q13.4.  
XX  
SQ Sequence 20 BP; 3 A; 6 C; 6 G; 5 T; 0 U; 0 Other;  
  
Query Match 1.9%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 719 CAGCCTCCGAGTAGCTGG 737  
DB 2 CAGCCTCCGAGTAGCTGG 20  
  
RESULT 695  
ADG30202/C  
ID ADG30202 standard; RNA; 21 BP.  
XX  
AC ADG30202;  
XX  
DT 26-FEB-2004 (first entry)  
XX  
DE PKR-targeted siNA DNA-RNA hybrid - SEQ ID 768.  
XX  
XX double-stranded short interfering nucleic acid; siNA;  
KM antiarteriosclerotic; neuroprotective; neurotropic; antiparkinsonian;  
KM anticonvulsant; pulmonary disease; resenosis; atherosclerosis;  
KM Alzheimer's; Parkinson's; epilepsy; dementia; huntington's;  
KM amyotrophic lateral sclerosis; gene therapy; ss; DNA-RNA hybrid; PKR.  
XX  
OS Unidentified.  
OS Synthetic.  
XX  
XX WO2003074654-A2.  
XX  
PD 12-SEP-2003.  
XX  
PF 20-FEB-2003; 2003WO-US005028.  
XX  
XX 20-FEB-2002; 2002US-0358580P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 06-JUN-2002; 2002US-036782P.  
PR 29-AUG-2002; 2002US-0406784P.  
PR 05-SEP-2002; 2002US-0408378P.  
PR 09-SEP-2002; 2002US-0409293P.  
PR 15-JAN-2003; 2003US-0440129P.  
XX  
XX (SIRN-) SIRNA THERAPEUTICS INC.  
XX  
XX Mcswigen J, Beigelman L, Chowrira B, Pavco P, Fossnaugh K;  
PI Jamison S, Usman N, Thompson J;  
XX  
XX WPI; 2003-731676/69.  
XX  
XX New double-stranded short interfering nucleic acid molecule, useful for  
PT down-regulating the expression of an endogenous mammalian target gene or  
PT for treating diseases that respond to modulation of gene expression or  
PT activity.  
XX  
XX Example 24; SEQ ID NO 768; 593pp; English.  
PS

XX  
CC The invention relates to a double-stranded short interfering nucleic acid  
CC (siNA) molecule that down-regulates expression of an endogenous mammalian  
CC target gene comprising one or more chemical modifications and each strand  
CC of the double-stranded siNA comprises about 21 nucleotides. The siNA of  
CC the invention demonstrates antiarteriosclerotic, neuroprotective,  
CC neurotropic, antiparkinsonian and anticonvulsant activities and may be  
CC useful for down-regulating the expression of an endogenous mammalian  
CC target gene and therefore in the treatment of any disease or condition  
CC that responds to modulation of gene expression or activity in a cell,  
CC tissue or organism. The disease or condition may include pulmonary  
CC diseases such as resenosis, atherosclerosis, Alzheimer's disease,  
CC Parkinson's disease, epilepsy, dementia, huntington's disease or  
CC amyotrophic lateral sclerosis. Furthermore, the siNA may be utilized for  
CC gene therapy applications. The current sequence is that of the siNA DNA-  
CC RNA hybrid of the invention.  
XX  
SQ Sequence 21 BP; 5 A; 3 C; 7 G; 2 T; 4 U; 0 Other;  
  
Query Match 1.9%; Score 19; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1117 GGTCGAACCTCCTGACCT 1135  
DB 19 GGTCGAACCTCCTGACCT 1  
  
RESULT 696  
ADL25334/C  
ID ADL25334 standard; DNA; 21 BP.  
XX  
XX ADL25334;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Intestinal epithelium/peyer's patch M cell-associated PCR primer #479.  
XX  
XX Intestinal epithelium cell development; peyer's patch M cell development;  
KM inflammatory bowel disease; gluteenteropathy; infectious disease;  
KM autoimmune disease; haemolytic anaemia; rheumatoid arthritis; dermatitis;  
KM Grave's disease; multiple sclerosis; allergy; asthma; diabetic mellitus;  
KM immune system disorder; hypersensitivity; anaphylaxis;  
KM blood group incompatibility; ss; PCR; primer.  
XX  
XX Macaca fascicularis.  
XX  
XX WO200280852-A2.  
XX  
PN 17-OCT-2002.  
XX  
PD 04-APR-2002; 2002WO-US010873.  
XX  
PF 04-APR-2001; 2001US-0281416P.  
XX  
PR (DIGI-) DIGITAL GENE TECHNOLOGIES INC.  
XX  
XX Brayden DJ, Byrne D, O'mahony DJ, Evans CF, Mah SP, Lo DD;  
PI WPI; 2003-075470/07.  
XX  
XX Novel isolated or purified polypeptide encoded by genes associated with  
PT intestinal epithelium or M cell development, differentiation or function,  
PT useful for treating autoimmune diseases and infectious diseases.  
XX  
XX Disclosure; SEQ ID NO 844; 152pp; English.  
XX  
XX The invention comprises DNA sequences which are associated with  
CC intestinal epithelium and peyer's patch M cells. The DNA sequences of the  
CC invention are useful for assessing, modifying, modulating or regulating  
CC intestinal epithelium or M cell development. The DNA sequences of the  
CC invention are also useful in the treatment of: inflammatory bowel  
CC disease, gluteenteropathy, infectious diseases, autoimmune diseases

CC (e.g. haemolytic anaemia, rheumatoid arthritis, dermatitis, Grave's  
CC disease, multiple sclerosis, allergy, asthma and diabetic mellitus),  
CC disease or disorders of the immune system, hypersensitivity,  
CC anaphylaxis, and blood group incompatibility. The present DNA sequence  
CC represents a PCR primer that was used to amplify an intestinal  
CC epithelium/peyer's patch M cell-associated DNA sequence of the invention.  
SQ Sequence 21 BP; 8 A; 3 C; 9 G; 1 T; 0 U; 0 Other;

Query Match 1.9%; Score 19; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1008 TTCTCTGCTCAGCCTCC 1026  
DB 21 TTCTCTGCTCAGCCTCC 3

RESULT 697

AA225166  
ID AA225166 standard; DNA; 22 BP.

AC AA225166;

DT 13-DEC-1999 (first entry)

DE Human short interspersed repetitive element PCR primer #24.

XX Human; short interspersed repetitive element; SINE; PCR; primer;  
XX Oncohychnus; restriction primer; short interspersed repeated sequence;  
KW eukaryote; restricted polymerase chain reaction fingerprinting;  
KW identification; DNA specimen; discrimination; ss.

OS Synthetic.

OS Homo sapiens.

XX JP2913035-B1.

XX 28-JUN-1999.

XX 10-JUL-1998; 98JP-00195692.

XX 10-JUL-1998; 98JP-00195692.

XX (NORQ ) NORINSUISANSHO SUISANCHO YOSHOKU KENKYUSHOCHO.

XX WPI; 1999-583348/50.

XX Restriction primer for distinguishing individuals with short interspersed  
XX repeated sequence of eukaryotes by restricted polymerase chain reaction  
XX fingerprinting.

PS Claim 6; Page 4; 17pp; Japanese.

XX The present invention describes a restriction primer for eukaryotic short  
CC interspersed repeated sequences (SINE), which has one or more additional  
CC bases that are a mismatch to, or are unrelated to, the 3'-terminal end of  
CC the SINE. The annealing temperature of the primer to the DNA sequence is  
CC kept higher than the fusion temperature of the primer during polymerase  
CC chain reaction (PCR). The PCR fragments obtained are subjected to  
CC electrophoresis to obtain a fingerprint. By comparing the polymorphs from  
CC the electrophoresis band pattern, eukaryotic individuals are  
CC distinguished. The primer is used for amplifying a eukaryotic  
CC deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by  
CC polymerase chain reaction (PCR) fingerprinting. In particular it may be  
CC used for individual identification of humans for medical and legal  
CC applications and ecological studies. DNA specimens in traces  
CC (approximately 10 ng in mass) can be used for individual discrimination  
CC of eukaryotes using the primer in a polymerase chain reaction (PCR).  
CC AA225143 to AA225191 represent specifically claimed examples of primers  
CC from the present invention

SQ Sequence 22 BP; 5 A; 6 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 1.9%; Score 19; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 869 GATTACAGGCGGTGAGCCAC 887  
DB 1 GATTACAGGCGGTGAGCCAC 19

RESULT 698

AA225157  
ID AA225157 standard; DNA; 22 BP.

AC AA225157;

DT 13-DEC-1999 (first entry)

DE Human short interspersed repetitive element PCR primer #15.

XX Human; short interspersed repetitive element; SINE; PCR; primer;  
XX Oncohychnus; restriction primer; short interspersed repeated sequence;  
KW eukaryote; restricted polymerase chain reaction fingerprinting;  
KW identification; DNA specimen; discrimination; ss.

OS Synthetic.

OS Homo sapiens.

XX JP2913035-B1.

XX 28-JUN-1999.

XX 10-JUL-1998; 98JP-00195692.

XX 10-JUL-1998; 98JP-00195692.

XX (NORQ ) NORINSUISANSHO SUISANCHO YOSHOKU KENKYUSHOCHO.

XX WPI; 1999-583348/50.

XX Restriction primer for distinguishing individuals with short interspersed  
XX repeated sequence of eukaryotes by restricted polymerase chain reaction  
XX fingerprinting.

PS Claim 6; Page 3; 17pp; Japanese.

XX The present invention describes a restriction primer for eukaryotic short  
CC interspersed repeated sequences (SINE), which has one or more additional  
CC bases that are a mismatch to, or are unrelated to, the 3'-terminal end of  
CC the SINE. The annealing temperature of the primer to the DNA sequence is  
CC kept higher than the fusion temperature of the primer during polymerase  
CC chain reaction (PCR). The PCR fragments obtained are subjected to  
CC electrophoresis to obtain a fingerprint. By comparing the polymorphs from  
CC the electrophoresis band pattern, eukaryotic individuals are  
CC distinguished. The primer is used for amplifying a eukaryotic  
CC deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by  
CC polymerase chain reaction (PCR) fingerprinting. In particular it may be  
CC used for individual identification of humans for medical and legal  
CC applications and ecological studies. DNA specimens in traces  
CC (approximately 10 ng in mass) can be used for individual discrimination  
CC of eukaryotes using the primer in a polymerase chain reaction (PCR).  
CC AA225143 to AA225191 represent specifically claimed examples of primers  
CC from the present invention

SQ Sequence 22 BP; 7 A; 5 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 1.9%; Score 19; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 869 GATTACAGGCGGTGAGCCAC 887  
DB 1 GATTACAGGCGGTGAGCCAC 19

```

RESULT 699
AAZ25158
ID AAZ25158 standard; DNA; 22 BP.
XX
XX
AC AAZ25158;
XX
DT 13-DEC-1999 (first entry)
XX
DE Human short interspersed repetitive element PCR primer #16.
XX
XX Human; short interspersed repetitive element; SINE; PCR; primer;
KW Oncohychnus; restriction primer; short interspersed repeated sequence;
KW eukaryote; restricted polymerase chain reaction fingerprinting;
KW identification; DNA specimen; discrimination; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX JP2913035-B1.
XX
XX 28-JUN-1999.
XX
XX 10-JUL-1998; 98JP-00195692.
XX
XX 10-JUL-1998; 98JP-00195692.
XX
XX (NORQ ) NORINSUISANSHO SUISANCHO YOSHOKU KENKYUSHOCHO.
XX
XX WPI; 1999-583348/50.
XX
XX Restriction primer for distinguishing individuals with short interspersed
PT repeated sequence of eukaryotes by restricted polymerase chain reaction
PT fingerprinting.
XX
XX Claim 6; Page 3; 17pp; Japanese.
XX
XX The present invention describes a restriction primer for eukaryotic short
CC interspersed repeated sequences (SINE), which has one or more additional
CC bases that are a mismatch to, or are unrelated to, the 3'-terminal end of
CC the SINE. The annealing temperature of the primer to the DNA sequence is
CC kept higher than the fusion temperature of the primer during polymerase
CC chain reaction (PCR). The PCR fragments obtained are subjected to
CC electrophoresis to obtain a fingerprint. By comparing the polymorphs from
CC the electrophoresis band pattern, eukaryotic individuals are
CC distinguished. The primer is used for amplifying a eukaryotic
CC deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by
CC polymerase chain reaction (PCR) fingerprinting. In particular it may be
CC used individual identification of humans for medical and legal
CC applications and ecological studies. DNA specimens in traces
CC (approximately 10 ng in mass) can be used for individual discrimination
CC of eukaryotes using the primer in a polymerase chain reaction (PCR).
CC AAZ25143 to AAZ25191 represent specifically claimed examples of primers
CC from the present invention
XX
XX Sequence 22 BP; 6 A; 5 C; 7 G; 4 T; 0 U; 0 Other;
XX
Query Match 1.9%; Score 19; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 869 GATTACAGGCGGTGAGCCAC 887
DB 1 GATTACAGGCGGTGAGCCAC 19

```

```

DT 13-DEC-1999 (first entry)
XX
XX Human short interspersed repetitive element PCR primer #28.
DE
XX
XX Human; short interspersed repetitive element; SINE; PCR; primer;
KW Oncohychnus; restriction primer; short interspersed repeated sequence;
KW eukaryote; restricted polymerase chain reaction fingerprinting;
KW identification; DNA specimen; discrimination; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX JP2913035-B1.
XX
XX 28-JUN-1999.
XX
XX 10-JUL-1998; 98JP-00195692.
XX
XX 10-JUL-1998; 98JP-00195692.
XX
XX 10-JUL-1998; 98JP-00195692.
XX
XX (NORQ ) NORINSUISANSHO SUISANCHO YOSHOKU KENKYUSHOCHO.
XX
XX WPI; 1999-583348/50.
XX
XX Restriction primer for distinguishing individuals with short interspersed
PT repeated sequence of eukaryotes by restricted polymerase chain reaction
PT fingerprinting.
XX
XX Claim 6; Page 4; 17pp; Japanese.
XX
XX The present invention describes a restriction primer for eukaryotic short
CC interspersed repeated sequences (SINE), which has one or more additional
CC bases that are a mismatch to, or are unrelated to, the 3'-terminal end of
CC the SINE. The annealing temperature of the primer to the DNA sequence is
CC kept higher than the fusion temperature of the primer during polymerase
CC chain reaction (PCR). The PCR fragments obtained are subjected to
CC electrophoresis to obtain a fingerprint. By comparing the polymorphs from
CC the electrophoresis band pattern, eukaryotic individuals are
CC distinguished. The primer is used for amplifying a eukaryotic
CC deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by
CC polymerase chain reaction (PCR) fingerprinting. In particular it may be
CC used individual identification of humans for medical and legal
CC applications and ecological studies. DNA specimens in traces
CC (approximately 10 ng in mass) can be used for individual discrimination
CC of eukaryotes using the primer in a polymerase chain reaction (PCR).
CC AAZ25143 to AAZ25191 represent specifically claimed examples of primers
CC from the present invention
XX
XX Sequence 22 BP; 5 A; 5 C; 7 G; 5 T; 0 U; 0 Other;
XX
Query Match 1.9%; Score 19; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 869 GATTACAGGCGGTGAGCCAC 887
DB 1 GATTACAGGCGGTGAGCCAC 19

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```

RESULT 700
AAZ25170
ID AAZ25170 standard; DNA; 22 BP.
XX
XX AAZ25170;
XX

```

```

RESULT 701
AAZ25172
ID AAZ25172 standard; DNA; 22 BP.
XX
XX AAZ25172;
XX
XX 13-DEC-1999 (first entry)
XX
XX Human short interspersed repetitive element PCR primer #30.
DE
XX
XX Human; short interspersed repetitive element; SINE; PCR; primer;
KW Oncohychnus; restriction primer; short interspersed repeated sequence;
KW eukaryote; restricted polymerase chain reaction fingerprinting;
KW identification; DNA specimen; discrimination; ss.

```

```
XX OS Synthetic.
XX OS Homo sapiens.
XX XX JP2913035-B1.
XX XX 28-JUN-1999.
XX XX 10-JUL-1998; 98JP-00195692.
XX XX 10-JUL-1998; 98JP-00195692.
XX XX 10-JUL-1998; 98JP-00195692.
XX XX (NORO ) NORINSUISANSHO SUISANCHO YOSHOKU KENKYUSHOCHO.
XX XX WPI; 1999-583348/50.
XX XX Restriction primer for distinguishing individuals with short interspersed
XX XX repeated sequence of eukaryotes by restricted polymerase chain reaction
XX XX fingerprinting.
XX XX Claim 6; Page 4; 17pp; Japanese.
XX XX The present invention describes a restriction primer for eukaryotic short
XX XX interspersed repeated sequences (SINE), which has one or more additional
XX XX bases that are a mismatch to, or are unrelated to, the 3'-terminal end of
XX XX the SINE. The annealing temperature of the primer to the DNA sequence is
XX XX kept higher than the fusion temperature of the primer during polymerase
XX XX chain reaction (PCR). The PCR fragments obtained are subjected to
XX XX electrophoresis to obtain a fingerprint. By comparing the polymorphs from
XX XX the electrophoresis band pattern, eukaryotic individuals are
XX XX distinguished. The primer is used for amplifying a eukaryotic
XX XX deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by
XX XX polymerase chain reaction (PCR) fingerprinting. In particular it may be
XX XX used individual identification of humans for medical and legal
XX XX applications and ecological studies. DNA specimens in traces
XX XX (approximately 10 ng in mass) can be used for individual discrimination
XX XX of eukaryotes using the primer in a polymerase chain reaction (PCR).
XX XX AA25143 to AA25191 represent specifically claimed examples of primers
XX XX from the present invention
XX XX Sequence 22 BP; 6 A; 6 C; 6 G; 4 T; 0 U; 0 Other;
XX XX
XX XX Query Match 1.9%; Score 19; DB 1; Length 22;
XX XX Best Local Similarity 100.0%; Pred. No. 1.3e+03;
XX XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 869 GATTACAGCGGTGAGCCAC 887
DB 1 GATTACAGCGGTGAGCCAC 19
RESULT 702
AA25159
ID AA25159 standard; DNA; 22 BP.
XX AC AA25159;
XX XX
XX XX 13-DEC-1999 (first entry)
XX XX Human short interspersed repetitive element PCR primer #17.
XX XX Human; short interspersed repetitive element; SINE; PCR; primer;
XX XX Oncomychnus; restriction primer; short interspersed repeated sequence;
XX XX eukaryote; restricted polymerase chain reaction fingerprinting;
XX XX identification; DNA specimen; discrimination; ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX XX JP2913035-B1.
XX XX 28-JUN-1999.
XX XX
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```
PF 10-JUL-1998; 98JP-00195692.
XX XX 10-JUL-1998; 98JP-00195692.
XX XX (NORO ) NORINSUISANSHO SUISANCHO YOSHOKU KENKYUSHOCHO.
XX XX WPI; 1999-583348/50.
XX XX Restriction primer for distinguishing individuals with short interspersed
XX XX repeated sequence of eukaryotes by restricted polymerase chain reaction
XX XX fingerprinting.
XX XX Claim 6; Page 3; 17pp; Japanese.
XX XX The present invention describes a restriction primer for eukaryotic short
XX XX interspersed repeated sequences (SINE), which has one or more additional
XX XX bases that are a mismatch to, or are unrelated to, the 3'-terminal end of
XX XX the SINE. The annealing temperature of the primer to the DNA sequence is
XX XX kept higher than the fusion temperature of the primer during polymerase
XX XX chain reaction (PCR). The PCR fragments obtained are subjected to
XX XX electrophoresis to obtain a fingerprint. By comparing the polymorphs from
XX XX the electrophoresis band pattern, eukaryotic individuals are
XX XX distinguished. The primer is used for amplifying a eukaryotic
XX XX deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by
XX XX polymerase chain reaction (PCR) fingerprinting. In particular it may be
XX XX used individual identification of humans for medical and legal
XX XX applications and ecological studies. DNA specimens in traces
XX XX (approximately 10 ng in mass) can be used for individual discrimination
XX XX of eukaryotes using the primer in a polymerase chain reaction (PCR).
XX XX AA25143 to AA25191 represent specifically claimed examples of primers
XX XX from the present invention
XX XX Sequence 22 BP; 7 A; 6 C; 6 G; 3 T; 0 U; 0 Other;
XX XX
XX XX Query Match 1.9%; Score 19; DB 1; Length 22;
XX XX Best Local Similarity 100.0%; Pred. No. 1.3e+03;
XX XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 869 GATTACAGCGGTGAGCCAC 887
DB 1 GATTACAGCGGTGAGCCAC 19
RESULT 703
AA25163
ID AA25163 standard; DNA; 22 BP.
XX AC AA25163;
XX XX
XX XX 13-DEC-1999 (first entry)
XX XX Human short interspersed repetitive element PCR primer #21.
XX XX Human; short interspersed repetitive element; SINE; PCR; primer;
XX XX Oncomychnus; restriction primer; short interspersed repeated sequence;
XX XX eukaryote; restricted polymerase chain reaction fingerprinting;
XX XX identification; DNA specimen; discrimination; ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX XX JP2913035-B1.
XX XX 28-JUN-1999.
XX XX 10-JUL-1998; 98JP-00195692.
XX XX 10-JUL-1998; 98JP-00195692.
XX XX 10-JUL-1998; 98JP-00195692.
XX XX (NORO ) NORINSUISANSHO SUISANCHO YOSHOKU KENKYUSHOCHO.
XX XX WPI; 1999-583348/50.
XX XX
```

PT Restriction primer for distinguishing individuals with short interspersed  
PT repeated sequence of eukaryotes by restricted polymerase chain reaction  
PT fingerprinting.  
XX  
XX  
PS Claim 6; Page 3; 17pp; Japanese.  
XX  
XX The present invention describes a restriction primer for eukaryotic short  
CC interspersed repeated sequences (SINE), which has one or more additional  
CC bases that are a mismatch to, or are unrelated to, the 3'-terminal end of  
CC the SINE. The annealing temperature of the primer to the DNA sequence is  
CC kept higher than the fusion temperature of the primer during polymerase  
CC chain reaction (PCR). The PCR fragments obtained are subjected to  
CC electrophoresis to obtain a fingerprint. By comparing the polymorphs from  
CC the electrophoresis band pattern, eukaryotic individuals are  
CC distinguished. The primer is used for amplifying a eukaryotic  
CC deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by  
CC polymerase chain reaction (PCR) fingerprinting. In particular it may be  
CC used for individual identification of humans for medical and legal  
CC applications and ecological studies. DNA specimens in traces  
CC (approximately 10 ng in mass) can be used for individual discrimination  
CC of eukaryotes using the primer in a polymerase chain reaction (PCR).  
CC AA25143 to AA25191 represent specifically claimed examples of primers  
CC from the present invention  
XX  
XX  
SQ Sequence 22 BP; 6 A; 5 C; 7 G; 4 T; 0 U; 0 Other;  
  
Query Match 1.9%; Score 19; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 869 GATTACAGCGGTGAGCCAC 887  
Db 1 GATTACAGCGGTGAGCCAC 19  
|||||  
|  
RESULT 704  
AA25169  
ID AA25169 standard; DNA; 22 BP.  
XX  
XX AA25169;  
XX  
XX 13-DEC-1999 (first entry)  
XX  
XX Human short interspersed repetitive element PCR primer #27.  
XX  
XX Human; short interspersed repetitive element; SINE; PCR; primer;  
XX Oncohychnus; restriction primer; short interspersed repeated sequence;  
XX eukaryote; restricted polymerase chain reaction fingerprinting;  
XX identification; DNA specimen; discrimination; ss.  
XX  
XX Synthetic.  
XX Homo sapiens.  
XX  
XX JP2913035-B1.  
XX  
XX 28-JUN-1999.  
XX  
XX 10-JUL-1998; 98BP-00195692.  
XX  
XX 10-JUL-1998; 98BP-00195692.  
XX  
XX (NORQ ) NORINSUISANSHO SUISANCHO YOSHOKU KENKYUSHOCHO.  
XX  
XX WPI; 1999-583348/50.  
XX  
XX Restriction primer for distinguishing individuals with short interspersed  
PT repeated sequence of eukaryotes by restricted polymerase chain reaction  
PT fingerprinting.  
XX  
XX Claim 6; Page 4; 17pp; Japanese.  
XX  
XX The present invention describes a restriction primer for eukaryotic short  
CC interspersed repeated sequences (SINE), which has one or more additional

CC bases that are a mismatch to, or are unrelated to, the 3'-terminal end of  
CC the SINE. The annealing temperature of the primer to the DNA sequence is  
CC kept higher than the fusion temperature of the primer during polymerase  
CC chain reaction (PCR). The PCR fragments obtained are subjected to  
CC electrophoresis to obtain a fingerprint. By comparing the polymorphs from  
CC the electrophoresis band pattern, eukaryotic individuals are  
CC distinguished. The primer is used for amplifying a eukaryotic  
CC deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by  
CC polymerase chain reaction (PCR) fingerprinting. In particular it may be  
CC used for individual identification of humans for medical and legal  
CC applications and ecological studies. DNA specimens in traces  
CC (approximately 10 ng in mass) can be used for individual discrimination  
CC of eukaryotes using the primer in a polymerase chain reaction (PCR).  
CC AA25143 to AA25191 represent specifically claimed examples of primers  
CC from the present invention  
XX  
XX  
SQ Sequence 22 BP; 6 A; 5 C; 6 G; 5 T; 0 U; 0 Other;  
  
Query Match 1.9%; Score 19; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 869 GATTACAGCGGTGAGCCAC 887  
Db 1 GATTACAGCGGTGAGCCAC 19  
|||||  
|  
RESULT 705  
AA25171  
ID AA25171 standard; DNA; 22 BP.  
XX  
XX AA25171;  
XX  
XX 13-DEC-1999 (first entry)  
XX  
XX Human short interspersed repetitive element PCR primer #29.  
XX  
XX Human; short interspersed repetitive element; SINE; PCR; primer;  
XX Oncohychnus; restriction primer; short interspersed repeated sequence;  
XX eukaryote; restricted polymerase chain reaction fingerprinting;  
XX identification; DNA specimen; discrimination; ss.  
XX  
XX Synthetic.  
XX Homo sapiens.  
XX  
XX JP2913035-B1.  
XX  
XX 28-JUN-1999.  
XX  
XX 10-JUL-1998; 98BP-00195692.  
XX  
XX 10-JUL-1998; 98BP-00195692.  
XX  
XX (NORQ ) NORINSUISANSHO SUISANCHO YOSHOKU KENKYUSHOCHO.  
XX  
XX WPI; 1999-583348/50.  
XX  
XX Restriction primer for distinguishing individuals with short interspersed  
PT repeated sequence of eukaryotes by restricted polymerase chain reaction  
PT fingerprinting.  
XX  
XX Claim 6; Page 4; 17pp; Japanese.  
XX  
XX The present invention describes a restriction primer for eukaryotic short  
CC interspersed repeated sequences (SINE), which has one or more additional  
CC bases that are a mismatch to, or are unrelated to, the 3'-terminal end of  
CC the SINE. The annealing temperature of the primer to the DNA sequence is  
CC kept higher than the fusion temperature of the primer during polymerase  
CC chain reaction (PCR). The PCR fragments obtained are subjected to  
CC electrophoresis to obtain a fingerprint. By comparing the polymorphs from  
CC the electrophoresis band pattern, eukaryotic individuals are  
CC distinguished. The primer is used for amplifying a eukaryotic  
CC deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by

CC polymerase chain reaction (PCR) fingerprinting. In particular it may be  
CC used individual identification of humans for medical and legal  
CC applications and ecological studies. DNA specimens in traces  
CC (approximately 10 ng in mass) can be used for individual discrimination  
CC of eukaryotes using the primer in a polymerase chain reaction (PCR).  
CC AA25143 to AA25191 represent specifically claimed examples of primers  
CC from the present invention  
CC  
XX  
SQ Sequence 22 BP; 6 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 1.9%; Score 19; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 869 GATTACAGCGGTGAGCCAC 887  
|||||  
1 GATTACAGCGGTGAGCCAC 19

RESULT 706  
AA25160  
ID AA25160 standard; DNA; 22 BP.

AC AA25160;  
XX  
DT 13-DEC-1999 (first entry)

DE Human short interspersed repetitive element PCR primer #18.

XX Human; short interspersed repetitive element; SINE; PCR; primer;  
KM Oncorhynchus; restriction primer; short interspersed repeated sequence;  
KM eukaryote; restricted polymerase chain reaction fingerprinting;  
KM identification; DNA specimen; discrimination; ss.

OS Synthetic.  
OS Homo sapiens.

XX JP2913035-B1.

XX 28-JUN-1999.

XX 10-JUL-1998; 98JP-00195692.

XX 10-JUL-1998; 98JP-00195692.

XX (NORQ) NORINSUISANSO SUIANCHO YOSHOKU KENKYUSHOCHO.

XX WPI, 1999-583348/50.

PT Restriction primer for distinguishing individuals with short interspersed  
PT repeated sequence of eukaryotes by restricted polymerase chain reaction  
PT fingerprinting.

PS Claim 6; Page 3; 17pp; Japanese.

XX The present invention describes a restriction primer for eukaryotic short  
XX interspersed repeated sequences (SINE), which has one or more additional  
XX bases that are a mismatch to, or are unrelated to, the 3'-terminal end of  
XX the SINE. The annealing temperature of the primer to the DNA sequence is  
XX kept higher than the fusion temperature of the primer during polymerase  
XX chain reaction (PCR). The PCR fragments obtained are subjected to  
XX electrophoresis to obtain a fingerprint. By comparing the polymorphs from  
XX the electrophoresis band pattern, eukaryotic individuals are  
XX distinguished. The primer is used for amplifying a eukaryotic  
XX deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by  
XX polymerase chain reaction (PCR) fingerprinting. In particular it may be  
XX used individual identification of humans for medical and legal  
XX applications and ecological studies. DNA specimens in traces  
XX (approximately 10 ng in mass) can be used for individual discrimination  
XX of eukaryotes using the primer in a polymerase chain reaction (PCR).  
XX AA25143 to AA25191 represent specifically claimed examples of primers  
XX from the present invention

SQ Sequence 22 BP; 6 A; 6 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 1.9%; Score 19; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 869 GATTACAGCGGTGAGCCAC 887  
|||||  
1 GATTACAGCGGTGAGCCAC 19

RESULT 707  
AA25164  
ID AA25164 standard; DNA; 22 BP.

AC AA25164;  
XX  
DT 13-DEC-1999 (first entry)

DE Human short interspersed repetitive element PCR primer #22.

XX Human; short interspersed repetitive element; SINE; PCR; primer;  
KM Oncorhynchus; restriction primer; short interspersed repeated sequence;  
KM eukaryote; restricted polymerase chain reaction fingerprinting;  
KM identification; DNA specimen; discrimination; ss.

OS Synthetic.  
OS Homo sapiens.

XX JP2913035-B1.

XX 28-JUN-1999.

XX 10-JUL-1998; 98JP-00195692.

XX 10-JUL-1998; 98JP-00195692.

XX (NORQ) NORINSUISANSO SUIANCHO YOSHOKU KENKYUSHOCHO.

XX WPI, 1999-583348/50.

PT Restriction primer for distinguishing individuals with short interspersed  
PT repeated sequence of eukaryotes by restricted polymerase chain reaction  
PT fingerprinting.

PS Claim 6; Page 3; 17pp; Japanese.

XX The present invention describes a restriction primer for eukaryotic short  
XX interspersed repeated sequences (SINE), which has one or more additional  
XX bases that are a mismatch to, or are unrelated to, the 3'-terminal end of  
XX the SINE. The annealing temperature of the primer to the DNA sequence is  
XX kept higher than the fusion temperature of the primer during polymerase  
XX chain reaction (PCR). The PCR fragments obtained are subjected to  
XX electrophoresis to obtain a fingerprint. By comparing the polymorphs from  
XX the electrophoresis band pattern, eukaryotic individuals are  
XX distinguished. The primer is used for amplifying a eukaryotic  
XX deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by  
XX polymerase chain reaction (PCR) fingerprinting. In particular it may be  
XX used individual identification of humans for medical and legal  
XX applications and ecological studies. DNA specimens in traces  
XX (approximately 10 ng in mass) can be used for individual discrimination  
XX of eukaryotes using the primer in a polymerase chain reaction (PCR).  
XX AA25143 to AA25191 represent specifically claimed examples of primers  
XX from the present invention

SQ Sequence 22 BP; 5 A; 5 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 1.9%; Score 19; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 869 GATTACAGCGGTGAGCCAC 887  
|||||

DB 1 GATTACAGCGGTGAGCCAC 19

## RESULT 708

AAZ25165  
AAZ25165 standard; DNA, 22 BP.

AC AAZ25165;

DT 13-DEC-1999 (first entry)

DE Human short interspersed repetitive element PCR primer #23.

XX Human; short interspersed repetitive element; SINE; PCR; primer;

KW Oncohyunchus; restriction primer; short interspersed repeated sequence;  
KW eukaryote; restriction polymerase chain reaction fingerprinting;  
KW identification; DNA specimen; discrimination; ss.

OS Synthetic.

OS Homo sapiens.

XX JP2913035-B1.

PD 28-JUN-1999.

XX 10-JUL-1998; 98JP-00195692.

PR 10-JUL-1998; 98JP-00195692.

XX (NORO) NORINSUISANSHO SUISANCHO YOSHOKU KENKYUSHOCHO.

DR WPI; 1999-58348/50.

PT Restriction primer for distinguishing individuals with short interspersed  
PT repeated sequence of eukaryotes by restricted polymerase chain reaction  
PT fingerprinting.

PS Claim 6; Page 4; 17pp; Japanese.

XX The present invention describes a restriction primer for eukaryotic short  
CC interspersed repeated sequences (SINE), which has one or more additional  
CC bases that are a mismatch to, or are unrelated to, the 3'-terminal end of  
CC the SINE. The annealing temperature of the primer to the DNA sequence is  
CC kept higher than the fusion temperature of the primer during polymerase  
CC chain reaction (PCR). The PCR fragments obtained are subjected to  
CC electrophoresis to obtain a fingerprint. By comparing the polymorphs from  
CC the electrophoresis band pattern, eukaryotic individuals are  
CC distinguished. The primer is used for amplifying a eukaryotic  
CC deoxyribonucleic acid (DNA) sequence, pinched between SINE sequences by  
CC polymerase chain reaction (PCR) fingerprinting. In particular it may be  
CC used, individual identification of humans for medical and legal  
CC applications and ecological studies. DNA specimens in traces  
CC (approximately 10 ng in mass) can be used for individual discrimination  
CC of eukaryotes using the primer in a polymerase chain reaction (PCR).  
CC AAZ25143 to AAZ25191 represent specifically claimed examples of primers  
CC from the present invention

XX Sequence 22 BP; 6 A; 6 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 1.9%; Score 19; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 869 GATTACAGCGGTGAGCCAC 887

DB 1 GATTACAGCGGTGAGCCAC 19

RESULT 709  
ADG30198  
ID ADG30198 standard; RNA, 23 BP.  
XX  
AC ADG30198;

XX 26-FEB-2004 (first entry)

DT PKR-targeted siNA DNA-RNA hybrid - SEQ ID 764.

XX double-stranded short interfering nucleic acid; siNA;  
DE antiarteriosclerotic; neuroprotective; neurotropic; antiparkinsonian;  
KW anticonvulsant; pulmonary disease; restenosis; atherosclerosis;  
KW Alzheimer's; Parkinson's; epilepsy; dementia; Huntington's;  
KW amyotrophic lateral sclerosis; gene therapy; ss; DNA-RNA hybrid; PKR.

XX Unidentified.

OS Synthetic.

XX WO2003074654-A2.

XX 12-SEP-2003.

XX 20-FEB-2003; 2003WO-US005028.

XX 20-FEB-2002; 2002US-0358580P.

XX 11-MAR-2002; 2002US-0363124P.

XX 06-JUN-2002; 2002US-0386782P.

XX 29-AUG-2002; 2002US-0406784P.

XX 05-SEP-2002; 2002US-0408378P.

XX 09-SEP-2002; 2002US-0409293P.

XX 15-JAN-2003; 2003US-0440129P.

XX (SINR-) SINRA THERAPEUTICS INC.

XX Mcswigen J, Beigelman L, Chowitra B, Payco P, Fossnagh K,

XX Jamison S, Ueman N, Thompson J;

XX WPI; 2003-731676/69.

PT New double-stranded short interfering nucleic acid molecule, useful for  
PT down-regulating the expression of an endogenous mammalian target gene or  
PT for treating diseases that respond to modulation of gene expression or  
PT activity.

PS Example 24; SEQ ID NO 764; 593pp; English.

XX The invention relates to a double-stranded short interfering nucleic acid  
CC (siNA) molecule that down-regulates expression of an endogenous mammalian  
CC target gene comprising one or more chemical modifications and each strand  
CC of the double-stranded siNA comprises about 21 nucleotides. The siNA of  
CC the invention demonstrates antiarteriosclerotic, neuroprotective,  
CC neurotropic, antiparkinsonian and anticonvulsant activities and may be  
CC useful for down-regulating the expression of an endogenous mammalian  
CC target gene and therefore in the treatment of any disease or condition  
CC that responds to modulation of gene expression or activity in a cell,  
CC tissue or organism. The disease or condition may include pulmonary  
CC diseases such as restenosis, atherosclerosis, Alzheimer's disease or  
CC Parkinson's disease, epilepsy, dementia, Huntington's disease or  
CC amyotrophic lateral sclerosis. Furthermore, the siNA may be utilized for  
CC gene therapy applications. The current sequence is that of the siNA DNA-  
CC RNA hybrid of the invention.

XX Sequence 23 BP; 4 A; 7 C; 3 G; 2 T; 5 U; 2 Other;

Query Match 1.9%; Score 19; DB 1; Length 23;  
Best Local Similarity 73.7%; Pred. No. 1.4e+03;  
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1117 GGTCGAACCTCGACCT 1135

DB 2 GGUCUCAACUCCUGACCU 20

RESULT 710  
AAT39493  
ID AAT39493 standard; DNA, 22 BP.  
XX

AC AAT39493;  
 XX  
 DT 21-MAY-1997 (first entry)  
 XX  
 DE Steroidogenesis acute regulatory protein exon 4 PCR primer EX4S.  
 XX  
 KW Human; steroidogenesis; acute regulatory protein; hSTAR; analysis;  
 KW mutation; detection; prenatal; genetic defect; congenital; protein;  
 KW lipid adrenal hyperplasia; treatment; prevention; gene;  
 KW replacement therapy; hypercholesterolemia; primer; PCR;  
 KW polymerase chain reaction; exon 4; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN MO962938-A1.  
 XX  
 PD 26-SEP-1996.  
 XX  
 PF 22-MAR-1996; 96WO-US003896.  
 XX  
 PR 23-MAR-1995; 95US-00410540.  
 XX  
 PA (RBGC) UNIV CALIFORNIA.  
 PA (UYPE-) UNIV PENNSYLVANIA.  
 XX  
 PI Miller WL, Iain D, Straus JF;  
 XX  
 DR WPI; 1996-443130/44.  
 XX  
 PT Isolated human steroidogenesis acute regulatory protein gene - used for  
 PT detection of mutation(s) of this gene that cause congenital lipid  
 PT adrenal hyperplasia.  
 XX  
 PS Disclosure; Page 36; 89pp; English.  
 XX  
 CC The present sequence is a PCR primer for exon 4 of the human  
 CC steroidogenesis acute regulatory protein (hSTAR) gene. The hSTAR gene can  
 CC be analysed for mutations to detect (e.g. prenatally) genetic defects  
 CC associated with congenital lipid adrenal hyperplasia (CAH), or its  
 CC transmission to children. CAH can be treated by protein or gene  
 CC replacement therapy, which can also be used to prevent or treat  
 CC hypercholesterolemia. A human adrenal cortex cDNA library was screened  
 CC with a mouse Star probe to isolate a 1.6 kb insert, including an ORF for  
 CC a 285 residue protein. When it was cloned into pSPORT and expressed in  
 CC COS-1 cells cotransfected with pPA50sec abd pADX, it increased the level  
 CC of pregnenolone synthesis from cholesterol or 20-alpha-hydroxycholesterol  
 CC  
 XX  
 SQ Sequence 22 BP; 5 A; 3 C; 8 G; 6 T; 0 U; 0 Other;  
 XX  
 Query Match 1.9%; Score 18.8; DB 1; Length 22;  
 Best Local Similarity 90.9%; Pred. No. 1.3e+03;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 XX  
 QY 863 TGCTGGATTACAGCGTGAGC 884  
 |||||  
 DB 1 TGCTGGATTATAGCGGTGAAC 22  
 |||||  
 RESULT 711  
 AAX83018  
 ID AAX83018 standard; DNA; 22 BP.  
 XX  
 AC AAX83018;  
 XX  
 DT 31-AUG-1999 (first entry)  
 XX  
 DE Primer K to isolate human WRN gene 5' exons.  
 XX  
 KW Human; WRN; Werner's syndrome; detection; diagnosis; autosomal;  
 KW recessive disorder; phenotype; primer; RT-PCR; amplification; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.

XX  
 XX MO9724435-A1.  
 XX  
 PD 10-JUL-1997.  
 XX  
 PF 30-DEC-1996; 96WO-US020785.  
 XX  
 PR 29-DEC-1995; 95US-0009409P.  
 XX  
 PR 29-DEC-1995; 95US-00580539.  
 PR 30-JAN-1996; 96US-0010835P.  
 PR 30-JAN-1996; 96US-00594242.  
 PR 12-APR-1996; 96US-00632175.  
 XX  
 PA (DARW-) DARWIN MOLECULAR CORP.  
 XX  
 PI Oshima J, Fu Y, Yu C, Mulligan J, Schellenberg GD;  
 XX  
 DR WPI; 1997-363671/33.  
 XX  
 PT Isolated nucleic acid molecule encoding the WRN gene product - useful for  
 PT detection and treatment of Werner's syndrome, and related diseases.  
 XX  
 PS Example 2; Page 41; 153pp; English.  
 XX  
 CC Primers AAX83008-X83064 were used to RT-PCR amplify exons from the 5' and  
 CC 3' ends of the human WRN gene (AAX83003) which encodes a protein related  
 CC to Werner's syndrome. The products can be used for the detection and  
 CC treatment of Werner's syndrome (WS), an autosomal recessive disorder with  
 CC a complex phenotype, as well as related diseases  
 CC  
 XX  
 SQ Sequence 22 BP; 5 A; 4 C; 7 G; 6 T; 0 U; 0 Other;  
 XX  
 Query Match 1.9%; Score 18.8; DB 1; Length 22;  
 Best Local Similarity 90.9%; Pred. No. 1.3e+03;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 XX  
 QY 479 AGTGACGTGTGTGATCAGC 500  
 |||||  
 DB 1 AGTGACGTGTGTATCATCAGC 22  
 |||||  
 RESULT 712  
 AAC69375/C  
 ID AAC69375 standard; DNA; 22 BP.  
 XX  
 AC AAC69375;  
 XX  
 DT 29-JAN-2001 (first entry)  
 XX  
 DE Human ABC1 BAC contig polymorphic site, SEQ ID NO:274.  
 XX  
 KW Human ABC1 cholesterol transporter; chromosome 9q31;  
 KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;  
 KW Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;  
 KW cardiovascular disease; coronary artery disease; coronary restenosis;  
 KW cerebrovascular disease; peripheral vascular disease;  
 KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;  
 KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;  
 KW prognosis; prophylaxis; drug screening; transgenic animal; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200055318-A2.  
 XX  
 PD 21-SEP-2000.  
 XX  
 PF 15-MAR-2000; 2000WO-IB000532.  
 XX  
 PR 15-MAR-1999; 99US-0124702P.  
 PR 08-JUN-1999; 99US-0138048P.  
 PR 17-JUN-1999; 99US-0139600P.  
 PR 01-SEP-1999; 99US-0151977P.  
 XX





```

RESULT 714
AAF84349/C
ID AAF84349 standard; DNA; 22 BP.
XX
XX AAF84349;
AC
XX 20-JUN-2001 (first entry)
XX
XX Human CYP2C181 PCR primer #5.
DE
XX
XX Gene polymorphism; drug-metabolising enzyme; PCR primer; CYP2C181; ss.
XX
XX Homo sapiens.
OS
XX JF2001017185-A.
PN
XX 23-JAN-2001.
PD
XX 10-DEC-1999; 99JP-00351610.
PF
XX 19-MAR-1999; 99JP-00076592.
PR
XX 06-MAY-1999; 99JP-00125918.
PA
XX (SARA ) OTSUKA PHARM CO LTD.
XX
XX WPI; 2001-285409/30.
DR
XX
XX Detection of gene polymorphism of drug-metabolising enzymes useful for
PT diagnosis and testing comprises carrying out polymerase chain reaction.
XX
XX Example 1; Page 13; 27pp; Japanese.
XX
XX The present invention relates to a kit and method for the detection of
CC gene polymorphisms of drug-metabolising enzyme genes. The kit contains a
CC polymerase chain reaction (PCR) buffer solution containing DNA polymerase
CC and NTP, a normal forward primer, a mutated forward primer, a reverse
CC primer and a fluorescence-labelling probe. The method involves carrying
CC out PCR on sample DNA, containing a drug-metabolising enzyme gene,
CC together with PCR buffer, the normal forward primer, the reverse primer
CC and the fluorescence-labelling probe (step A); and carrying out PCR on
CC the sample DNA together with PCR buffer, the mutated forward primer, the
CC reverse primer and the fluorescence-labelling probe (step B), and a step
CC of comparing the result of step A with that of step B. The present
CC sequence is a primer for human CYP2C181, which was used to illustrate the
CC present invention
XX
XX SQ Sequence 22 BP; 5 A; 7 C; 3 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 1.9%; Score 18.8; DB 1; Length 22;
XX Best Local Similarity 90.9%; Pred. No. 1.3e+03;
XX Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 861 AGTCTGGGATTACAGCGCTGA 882
XX | | | | | | | | | | | | | | | | | | | |
XX | | | | | | | | | | | | | | | | | | | |
DB 22 AATGCTGGGATTACAGGCATGA 1
XX
XX RESULT 715
XX AAF29797/C
XX ID AAF29797 standard; DNA; 22 BP.
XX
XX AAF29797;
AC
XX 09-APR-2001 (first entry)
XX
XX Presentline-1 gene promoter PCR primer Prom22R.
DE
XX
XX Human; PSEN1; Alzheimer's disease; polymorphism; diagnosis;
KM Presentline-1; chromosome 14; PCR primer; ss.
XX
XX Homo sapiens.
XX

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PN WO200079000-A1.
XX
XX 28-DEC-2000.
PD
XX
XX 22-JUN-2000; 2000WO-EP005942.
PF
XX
XX 22-JUN-1999; 99EP-00201991.
PR
XX (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX
XX Theuns J, Cruts M, Van Broeckhoven C;
XX
XX WPI; 2001-071402/08.
DR
XX
XX Determining whether a human subject has or is at risk of developing (early
PT -onset) Alzheimer's disease comprises detecting the presence/absence of a
PT genetic lesion in the presentlin-1 gene.
XX
XX Example 1; Page 45; 56pp; English.
XX
XX The present invention describes a method for determining the presence of
CC or susceptibility to Alzheimer's disease in humans, involving detecting a
CC genetic lesion in the presentlin-1 (PSN1) gene, found on chromosome 14.
CC The genetic lesion is a polymorphism in the promoter or upstream
CC regulatory region of the gene. The invention also describes transgenic
CC animals which can be used to identify compounds useful in treating
CC Alzheimer's disease
XX
XX SQ Sequence 22 BP; 9 A; 7 C; 2 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 1.9%; Score 18.8; DB 1; Length 22;
XX Best Local Similarity 90.9%; Pred. No. 1.3e+03;
XX Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 174 TTTTACAGAGAGGACTTC 195
XX | | | | | | | | | | | | | | | | | | | |
DB 22 TTTTAGTAGAGACGGGTTTC 1
XX
XX RESULT 716
XX AAD31453/C
XX ID AAD31453 standard; DNA; 22 BP.
XX
XX AAD31453;
AC
XX 31-MAY-2002 (first entry)
XX
XX Human chromosome 17 92Kb gene fragment amplifying PCR primer, wt1R.
XX
XX Human; Van Buchem's disease; genomic deletion; craniofacial hypertrophy;
KM autosomal recessive disorder; chromosome 17; chromosome 17q21;
KM bone dysplasia; 92Kb gene fragment; PCR primer; ss.
XX
XX Homo sapiens.
OS
XX WO200210455-A2.
PN
XX 07-FEB-2002.
PD
XX 30-JUL-2001; 2001WO-US023968.
PF
XX 28-JUL-2000; 2000US-0221855P.
PR
XX 06-JUL-2001; 2001US-0303386P.
PA
XX (CELL-) CELLTECH R & D INC.
XX (STRA-) STRAHLING HAMPTON K.
XX
XX Brunkow ME, Prohl S, Paepel B;
XX
XX WPI; 2002-227089/28.
DR
XX
XX Methods for identifying subjects who are afflicted with or carriers of
PT diseases associated with genomic deletion(s), e.g. Van Buchem's disease,

```

PT by determining the presence of a deletion in the 92 kb region of human  
 PT chromosome 17 at 17q21.  
 XX  
 PS Example 3; Page 26; 109pp; English.  
 XX  
 CC The present invention relates to methods for distinguishing between  
 CC individuals homozygous for and therefore afflicted with Van Buchem's  
 CC disease, individuals heterozygous for and therefore carriers of Van  
 CC Buchem's disease and individuals who are not afflicted with Van Buchem's  
 CC disease comprise identifying a large genomic deletion in chromosome 17 at  
 CC 17q21. The method is useful for identifying individuals who are afflicted  
 CC with or carriers of diseases associated with one or more genomic  
 CC deletion, particularly Van Buchem's disease, which is a rare autosomal  
 CC recessive disorder that results in a bone dysplasia referred to a  
 CC craniotubular hypotosis. The present sequence is a PCR primer used to  
 CC amplify 92Kb gene fragment in human chromosome 17 at 17q21  
 XX  
 SQ Sequence 22 BP; 7 A; 2 C; 10 G; 3 T; 0 U; 0 Other;  
 Query Match 1.9%; Score 18.8; DB 1; Length 22;  
 Best Local Similarity 90.9%; Pred. No. 1.3e+03;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 532 ATCCTCTGCTCAGCTCCCA 553  
 DB 22 ATCTCTTGCTCAGCTCCCA 1  
 RESULT 717  
 AAD31457/c  
 ID AAD31457 standard; DNA; 22 BP.  
 XX  
 AC AAD31457;  
 XX  
 DT 31-MAY-2002 (first entry)  
 XX  
 DE Human chromosome 17 92Kb gene fragment amplifying PCR primer, wt3r.  
 XX  
 KM Human; Van Buchem's disease; genomic deletion; craniotubular hypotosis;  
 KM autosomal recessive disorder; chromosome 17; chromosome 17q21;  
 KM bone dysplasia; 92Kb gene fragment; PCR primer; ss.  
 XX  
 OS Homo sapiens.  
 OS  
 PN WC0200210455-A2.  
 XX  
 PD 07-FEB-2002.  
 XX  
 PF 30-JUL-2001; 2001WO-US023368.  
 XX  
 PR 28-JUL-2000; 2000US-0221855P.  
 PR 06-JUL-2001; 2001US-0303386P.  
 XX  
 PA (CELL-) CELLTECH R & D INC.  
 PA (STRA/) STRAHLING HAMPTON K.  
 XX  
 PI Brunkow ME, Proll S, Paepfer B;  
 DR WPI; 2002-227089/28.  
 XX  
 DR Methods for identifying subjects who are afflicted with or carriers of  
 PT diseases associated with genomic deletion(s), e.g. Van Buchem's disease,  
 PT by determining the presence of a deletion in the 92 kb region of human  
 PT chromosome 17 at 17q21.  
 XX  
 PS Example 3; Page 26; 109pp; English.  
 XX  
 CC The present invention relates to methods for distinguishing between  
 CC individuals homozygous for and therefore afflicted with Van Buchem's  
 CC disease, individuals heterozygous for and therefore carriers of Van  
 CC Buchem's disease and individuals who are not afflicted with Van Buchem's  
 CC disease comprise identifying a large genomic deletion in chromosome 17 at  
 CC 17q21. The method is useful for identifying individuals who are afflicted

CC with or carriers of diseases associated with one or more genomic  
 CC deletion, particularly Van Buchem's disease, which is a rare autosomal  
 CC recessive disorder that results in a bone dysplasia referred to a  
 CC craniotubular hypotosis. The present sequence is a PCR primer used to  
 CC amplify 92Kb gene fragment in human chromosome 17 at 17q21  
 XX  
 SQ Sequence 22 BP; 7 A; 2 C; 10 G; 3 T; 0 U; 0 Other;  
 Query Match 1.9%; Score 18.8; DB 1; Length 22;  
 Best Local Similarity 90.9%; Pred. No. 1.3e+03;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 532 ATCCTCTGCTCAGCTCCCA 553  
 DB 22 ATCTCTTGCTCAGCTCCCA 1  
 RESULT 718  
 ADL66998/c  
 ID ADL66998 standard; DNA; 22 BP.  
 XX  
 AC ADL66998;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE Multiplex PCR primer #2.  
 XX  
 KM DNA polymerase; anti-DNAp antibody; reverse transcriptase;  
 KM anti-RT antibody; single strand binding protein; SSB; ss; primer.  
 XX  
 OS Synthetic.  
 OS  
 PN WC02004022770-A2.  
 XX  
 PD 18-MAR-2004.  
 XX  
 PF 05-SEP-2003; 2003WO-US027705.  
 XX  
 PR 05-SEP-2002; 2002US-0408609P.  
 PR 19-NOV-2002; 2002US-0427867P.  
 XX  
 PA (INVT-) INVITROGEN CORP.  
 XX  
 PI Park K;  
 PI  
 DR WPI; 2004-248479/23.  
 XX  
 DR New compositions comprising one or more anti-reverse transcriptase  
 PT antibodies, anti-DNA polymerases or single strand binding proteins,  
 PT useful for synthesizing nucleic acids.  
 XX  
 PS Example 4; Page 89; 201pp; English.  
 XX  
 CC The invention relates to a new composition which comprises at least one  
 CC anti-DNA polymerases (anti-DNAp) antibody and/or at least one anti-  
 CC reverse transcriptase (anti-RT) antibody, and at least one single strand  
 CC binding protein (SSB) or at least two different SSBs. The compositions  
 CC are useful for nucleic acid synthesis reactions or are generated during  
 CC nucleic acid synthesis reactions. The methods are useful for synthesizing  
 CC one or more nucleic acid molecules. The compositions and methods are also  
 CC be used in amplifying nucleic acid molecules, in reverse transcription of  
 CC nucleic acid molecules and in coupled or uncoupled reverse  
 CC transcription/amplification. The present sequence is used in the  
 CC exemplification of the present invention.  
 XX  
 SQ Sequence 22 BP; 7 A; 5 C; 8 G; 2 T; 0 U; 0 Other;  
 Query Match 1.9%; Score 18.8; DB 1; Length 22;  
 Best Local Similarity 90.9%; Pred. No. 1.3e+03;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 670 TTGGCTCAGTCAACCTGTGCC 691  
 TTGGCTCAGTCAACCTGTGCC 691

DB 22 TTGGCTACTGTAGCCTGCC 1  
RESULT 719  
AAA37708  
ID AAA37708 standard; DNA; 23 BP.  
XX  
XX  
AC AAA37708;  
XX  
XX 22-NOV-2000 (first entry)  
XX  
XX Human Rad51 antisense inhibitor AS8.  
XX  
XX Antisense inhibitor; human; Rad51; cell proliferation; cancer survival;  
XX  
XX radiation sensitivity; therapy; AS8; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200047231-A2.  
XX  
XX 17-AUG-2000.  
XX  
XX 03-FEB-2000; 2000WO-US002881.  
XX  
XX 10-FEB-1999; 99US-0119578P.  
XX  
XX 06-DEC-1999; 99US-00454495.  
XX  
XX (PANG-) PANGENE CORP.  
XX  
XX Reddy G;  
XX  
XX WPI; 2000-506091/45.  
XX  
XX Inhibiting cell proliferation useful for cancer therapy, comprises  
XX  
XX administering Rad51 inhibitor in vivo.  
XX  
XX Claim 8; Page 26; 42pp; English.  
XX  
XX This sequence represents an antisense inhibitor of human Rad51,  
XX  
XX designated AS8 (also referred to as R51AS8). The antisense inhibitors can  
XX  
XX be used in a method of the invention, for inhibiting cell proliferation.  
XX  
XX They can also be used in methods for inducing sensitivity to radiation  
XX  
XX and DNA damaging chemotherapeutics in an individual and in a method for  
XX  
XX prolonging survival in an individual with cancer. The methods and  
XX  
XX antisense molecules are useful for inhibiting cell proliferation,  
XX  
XX especially cancerous cell proliferation, for inducing sensitivity to  
XX  
XX radiation and DNA damaging chemotherapeutics in individuals and for  
XX  
XX prolonging survival in an individual with cancer. Kits for carrying out  
XX  
XX the methods may be used to diagnose and/or treat cancer and for  
XX  
XX adjunctive therapy  
XX  
XX  
SQ Sequence 23 BP; 2 A; 13 C; 4 G; 4 T; 0 U; 0 Other;  
Query Match 1.9%; Score 18.8; DB 1; Length 23;  
Best Local Similarity 90.9%; Pred. No. 1.4e+03;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 837 GATCGCCTGCTCGGCTGCC 858  
DB 2 GATCCACTGCTCGGCTGCC 23  
RESULT 720  
AAS01201  
ID AAS01201 standard; cDNA; 23 BP.  
XX  
XX  
XX AAS01201;  
XX  
XX  
XX 04-JUL-2001 (first entry)  
XX  
XX Human RAD51 antisense oligonucleotide, AS8.  
XX  
XX Human; Rad51; antisense; drug screening; cancer; autoimmune disease;

KW arthritis; graft rejection; inflammatory bowel disease; surgery;  
XX angioplasty; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200119397-A1.  
XX  
XX 22-MAR-2001.  
XX  
XX 18-SEP-2000; 2000WO-US025838.  
XX  
XX 17-SEP-1999; 99US-0154616P.  
XX  
XX 06-DEC-1999; 99US-00455300.  
XX  
XX (PANG-) PANGENE CORP.  
XX  
XX Reddy G;  
XX  
XX WPI; 2001-244704/25.  
XX  
XX Inhibiting cell proliferation for treating arthritis, graft rejection,  
XX  
XX inflammatory bowel disease, cancer, proliferation induced after medical  
XX  
XX procedure, involves administering Rad51 antibody or its fragment to cell.  
XX  
XX Example 6; Fig 16C; 102pp; English.  
XX  
XX The sequence represents the human Rad51 antisense oligonucleotide, AS8.  
XX  
XX The antisense oligonucleotide is used to study down-regulation of Rad51  
XX  
XX protein in human brain, breast and prostate cells. Rad51 protein is  
XX  
XX defective in repair of damaged DNA, genetic recombination and the  
XX  
XX cancer. Inhibiting cell proliferation involves administering to a cell a  
XX  
XX Rad51 antibody or its fragment. The Rad51 antibody or its fragment is  
XX  
XX useful for inhibiting cell proliferation, for treating disease states  
XX  
XX such as cancer, autoimmune disease, arthritis, graft rejection,  
XX  
XX inflammatory bowel disease, proliferation induced after medical  
XX  
XX procedures such as surgery, angioplasty etc. in humans and animals  
XX  
XX  
SQ Sequence 23 BP; 2 A; 13 C; 4 G; 4 T; 0 U; 0 Other;  
Query Match 1.9%; Score 18.8; DB 1; Length 23;  
Best Local Similarity 90.9%; Pred. No. 1.4e+03;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 837 GATCGCCTGCTCGGCTGCC 858  
DB 2 GATCCACTGCTCGGCTGCC 23  
RESULT 721  
AAD43247  
ID AAD43247 standard; DNA; 23 BP.  
XX  
XX AAD43247;  
XX  
XX 14-NOV-2002 (first entry)  
XX  
XX Antisense oligonucleotide R51AS8.  
XX  
XX Tumour cell proliferation; Rad51 inhibitor; p53 protein; premature aging;  
XX  
XX hyperproliferative disorder; Hodgkin's disease; squamous cell carcinoma;  
XX  
XX leukaemia; autoimmune disease; cancer; graft rejection; angioplasty;  
XX  
XX inflammatory bowel disease; immunosuppressive; gene therapy; arthritis;  
XX  
XX antisense; phosphorothioate backbone; ss.  
XX  
XX Undifferentiated.  
XX  
XX  
XX Key Location/Qualifiers  
XX modified\_base 1..23  
XX FT /\*tag= a  
XX FT /mod\_base= OTHER  
XX FT /note= "Phosphorothioate backbone"



CC base -1569. They are used in a method for detecting cytochrome P4501A2  
CC gene polymorphism, in partic. for detecting a base substitution at  
CC position -1569 and may be used with primers for the detection of a T to G  
CC base substitution at position 2064 and a C to A substitution at position  
CC 2640. The method is easy, convenient and has a high degree of sensitivity  
CC and accuracy. Polymorphisms in the P4501A2 gene can lead to a  
CC modification of metabolism which may be beneficial or deleterious  
XX  
SQ Sequence 20 BP; 4 A; 8 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 1.9%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 721 GCCTCCTGAGTAGCTGGAC 740  
|||  
DB 20 GCGTCTGAGTAGCTGGAC 1

## RESULT 724

AAT66010  
ID AAT66010 standard; DNA; 20 BP.

AC AAT66010;

DT 25-MAR-2003 (revised)  
DT 18-JUN-1997 (first entry)

DE Primer #1 to amplify repeat sequence marker Mfd107.

XX Polymorphism; repeat sequence; genetic marker; primer; amplification;  
KW PCR; polymerase chain reaction; paternity; maternity; human; pedigree;  
KW linkage analysis; genetic disease; animal; plant; breeding; locus;  
KW hybridisation; chromosome; ds.

OS Synthetic.

XX US5582979-A.

PD 10-DEC-1996.

XX 04-APR-1994; 94US-00222177.

XX 21-APR-1989; 89US-00341562.

PR 05-SEP-1991; 91US-00754351.

XX (MARS-) MARSHFIELD CLINIC.

XX Weber JL;

DR WPI; 1997-042299/04.

PT Detection of polymorphic genetic markers of the form (dc-da)n(dg-dt)n -  
PT using novel nucleic acid mols. as primers.

XX Claim 7; Col 13-14; 186pp; English.

XX The invention relates to the isolation of polymorphic repeat sequences  
CC having the sequence (dc-da)n.(dg-dt)n which can be used as genetic  
CC markers. Primers based on these sequences can be used to detect these  
CC repeats, especially for use in e.g. paternity or maternity testing, human  
CC genetic analysis such as linkage analysis of genetic disease, commercial  
CC animal or plant breeding or pedigree analysis. Clones containing the  
CC repeat sequences were isolated by hybridisation of chromosome-specific  
CC phase libraries with a synthetic poly(dc-da).(dg-dt) probe. Over 100  
CC repeat blocks were isolated. The primers AAT65798-T66047 were used to PCR  
CC amplify the inserts from the isolated clones containing the repeat  
CC sequences. The primers AAT66010-1 were used to amplify the repeat  
CC sequence marker clone Mfd107 (AAT65778). (Updated on 25-MAR-2003 to  
CC correct PF field.)  
XX  
SQ Sequence 20 BP; 7 A; 5 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 1.9%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 386 CCCAAGTCTGGGATTACA 405  
|||  
DB 1 CCCAAGTCTGGGATTACA 20

## RESULT 725

AAT66017/c  
ID AAT66017 standard; DNA; 20 BP.

AC AAT66017;

DT 25-MAR-2003 (revised)  
DT 18-JUN-1997 (first entry)

DE Primer #2 to amplify repeat sequence marker Mfd110.

XX Polymorphism; repeat sequence; genetic marker; primer; amplification;  
KW PCR; polymerase chain reaction; paternity; maternity; human; pedigree;  
KW linkage analysis; genetic disease; animal; plant; breeding; locus;  
KW hybridisation; chromosome; ds.

OS Synthetic.

XX US5582979-A.

PD 10-DEC-1996.

XX 04-APR-1994; 94US-00222177.

XX 21-APR-1989; 89US-00341562.

PR 05-SEP-1991; 91US-00754351.

XX (MARS-) MARSHFIELD CLINIC.

XX Weber JL;

DR WPI; 1997-042299/04.

PT Detection of polymorphic genetic markers of the form (dc-da)n(dg-dt)n -  
PT using novel nucleic acid mols. as primers.

XX Claim 7; Col 13-14; 186pp; English.

XX The invention relates to the isolation of polymorphic repeat sequences  
CC having the sequence (dc-da)n.(dg-dt)n which can be used as genetic  
CC markers. Primers based on these sequences can be used to detect these  
CC repeats, especially for use in e.g. paternity or maternity testing, human  
CC genetic analysis such as linkage analysis of genetic disease, commercial  
CC animal or plant breeding or pedigree analysis. Clones containing the  
CC repeat sequences were isolated by hybridisation of chromosome-specific  
CC phase libraries with a synthetic poly(dc-da).(dg-dt) probe. Over 100  
CC repeat blocks were isolated. The primers AAT65798-T66047 were used to PCR  
CC amplify the inserts from the isolated clones containing the repeat  
CC sequences. The primers AAT66016-7 were used to amplify the repeat  
CC sequence marker clone Mfd110 (AAT65781). (Updated on 25-MAR-2003 to  
CC correct PF field.)  
XX  
SQ Sequence 20 BP; 4 A; 2 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 1.9%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 577 ACCACTACCTGGCTAATT 596  
|||  
DB 20 ACCACACACCTGGCTAATT 1

## RESULT 726

AAV85762;  
ID AAT94341 standard; DNA; 20 BP.  
XX  
AC AAT94341;  
XX  
DT 04-MAR-1998 (first entry)  
XX  
DE Human DPC4 sequence tagged site sense primer p0960-F5.  
XX  
KW DPC4; pancreatic cancer; deleted; locus 4; diagnosis; human;  
KW tumour suppressor gene; proliferative disease; bile duct; bladder;  
KW colorectal; cancer; Crohn's disease; colitis; PCR primer;  
KW sequence tagged site; STS; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN MO9766271-A1.  
XX  
PD 24-JUL-1997.  
XX  
PF 17-JAN-1997; 97MO-US000827.  
XX  
PR 19-JAN-1996; 96US-00588821.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
XX  
PI Kern SE, Hahn SA;  
XX  
PI WPI; 1997-385290/35.  
XX  
DR Deleted in Pancreatic Cancer locus 4 polypeptide - and related nucleic  
XX PT acids, used in diagnosis and treatment of proliferative diseases, e.g.  
XX PT cancer of pancreas or other organs.  
XX  
PS Example 2; Page 56; 104pp; English.  
XX  
XX The present sequence represents a sequence tagged site (STS) primer used  
XX in the isolation of cosmids from the DPC4 (deleted in pancreatic cancer,  
XX locus 4) region, and gene identification. DPC4 is a tumour suppressor  
XX gene. Detection of truncated DPC4 protein, or of homozygous deletions or  
XX intragenic mutations in the nucleic acid encoding it, is used to diagnose  
XX (in vivo or in vitro) proliferative diseases, especially pancreatic  
XX carcinoma, bile duct, bladder or colorectal cancer, Crohn's disease,  
XX colitis-associated neoplasia or chronic ulcerative colitis. These  
XX conditions, where associated with a homozygous deletion, can be treated  
XX by administering an agent that: (a) modulates DPC4 expression,  
XX specifically a sense DPC4 sequence (particularly in the form of a vector,  
XX i.e. by gene therapy), but also an antisense sequence where DPC4 protein  
XX is over expressed or (b) mimics the activity of DPC4. DPC4 nucleic acid  
XX is also used as hybridisation probes for detecting presence/absence of  
XX human chromosome 18q21.1 fragments. When a homozygous deletion is  
XX detected in this region, an agent can be administered that accumulates  
XX within, or kills, only cells which contain such a deletion. This agent  
XX exploits the absence of an enzyme (or other protein) encoded by a  
XX neighbouring gene and lost by the deletion, i.e. it has a highly  
XX selective action  
XX  
SQ Sequence 20 BP; 4 A; 5 C; 5 G; 6 T; 0 U; 0 Other;  
XX  
Query Match 1.9%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 385 TCCCAAGTCTGGGATTAC 404  
DB 1 TCCCAAGTCTGGGATTTC 20  
XX  
RESULT 727  
AAV85762/C  
ID AAV85762 standard; DNA; 20 BP.  
XX

AC AAV85762;  
XX  
XX 10-FEB-1999 (first entry)  
XX  
DE LRP5 exon primer 57-4 1r.  
XX  
KW LRP5; LDL-receptor related protein; LRP-3; IDDM; diagnosis; endocytosis;  
KW insulin dependent diabetes mellitus; autoimmune disease;  
KW glomerulonephritis; inflammation; viral infection; osteoporosis;  
KW hypercholesterolemia; Alzheimer's disease; low density lipoprotein;  
KW PCR primer; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN MO9846743-A1.  
XX  
PD 22-OCT-1998.  
XX  
PF 15-APR-1998; 98MO-GB001102.  
XX  
PR 15-APR-1997; 97US-0043553P.  
XX  
PR 05-JUN-1997; 97US-0048740P.  
XX  
PA (WELL ) WELLCOME TRUST LTD.  
XX  
PA (MERI ) MERCK & CO INC.  
XX  
PI Todd JA, Hess JW, Caskey CT, Cox RD, Gerhold D, Hammond H;  
PI Hey P, Kawaguchi Y, Merriman TR, Metzker ML, Nakagawa Y;  
PI Phillips MS, Twells RCJ;  
XX  
XX WPI; 1998-594573/50.  
XX  
XX New isolated LDL-receptor related protein - used to develop products for  
XX PT treating, e.g. elevated triglyceride levels, diabetes, autoimmune  
XX PT disorders, inflammation or Alzheimer's disease.  
XX  
XX Claim 12; Page 105; 200pp; English.  
XX  
XX The present invention describes LRP5 (low density lipoprotein (LDL)  
XX receptor related protein, previously designated LRP-3). AAV85587 to  
XX AAV85822 represent exon primers used for obtaining LRP5 cDNA. Nucleic  
XX acid molecules (NMs) encoding LRP5 can be used for determining if an  
XX individual is susceptible to insulin dependent diabetes mellitus (IDDM).  
XX The NMs or proteins can be used for reducing triglyceride levels in the  
XX serum of an individual. Therapies that affect LRP5 may also be useful in  
XX the treatment of autoimmune diseases such as glomerulonephritis, diseases  
XX and disorders involving disruption of endocytosis and/or antigen  
XX presentation, cytokine clearance and/or inflammation, viral infection,  
XX pathogenic bacterial toxin contamination, elevation of free fatty acids  
XX or hypercholesterolemia, type 2 diabetes, osteoporosis, Alzheimer's  
XX disease and cardiovascular disease. Products from the present invention  
XX can also be used for detection, diagnosis and drug screening  
XX  
SQ Sequence 20 BP; 5 A; 7 C; 3 G; 5 T; 0 U; 0 Other;  
XX  
Query Match 1.9%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 391 AGTCTGGGATTACAGCGT 410  
DB 20 AGTCTGGGATTACAGCGAT 1  
XX  
RESULT 728  
AAV85840/C  
ID AAV85840 standard; DNA; 20 BP.  
XX  
AC AAV85840;  
XX  
XX 10-FEB-1999 (first entry)  
XX

DE LRP5 SNP primer 57-4 1r.  
XX  
XX LRP5; LDL-receptor related protein; LRP-3; IDDM; diagnosis; endocytosis;  
KW insulin dependent diabetes mellitus; autoimmune disease;  
KW glomerulonephritis; inflammation; viral infection; osteoporosis;  
KW hypercholesterolemia; Alzheimer's disease; low density lipoprotein;  
XX PCR primer; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
XX WO9846743-A1.  
XX  
XX 22-OCT-1998.  
XX  
XX 15-APR-1998; 98WO-GB001102.  
XX  
XX 15-APR-1997; 97US-0043553P.  
XX PR 05-JUN-1997; 97US-0048740P.  
XX  
XX (WELL ) WELLCOME TRUST LTD.  
XX PA (MERT ) MERCK & CO INC.  
XX  
XX PI Todd JA, Hess JW, Caskey CT, Cox RD, Gerhold D, Hammond H;  
PI Hey P, Kawaguchi Y, Merriman TR, Metzker ML, Nakagawa Y;  
PI Phillips MS, Twells RCU;  
XX  
XX WPI; 1998-594573/50.  
XX  
XX New isolated LDL-receptor related protein - used to develop products for  
PT treating, e.g. elevated triglyceride levels, diabetes, autoimmune  
PT disorders, inflammation or Alzheimer's disease.  
XX  
XX Claim 12; Page 110; 200pp; English.  
XX  
XX The present invention describes LRP5 (low density lipoprotein (LDL)  
CC receptor related protein, previously designated LRP-3). AAV85823 to  
CC AAV85900 represent SNP primers used for obtaining LRP5 cDNA. Nucleic acid  
CC molecules (NMs) encoding LRP5 can be used for determining if an  
CC individual is susceptible to insulin dependent diabetes mellitus (IDDM).  
CC The NMs or proteins can be used for reducing triglyceride levels in the  
CC serum of an individual. Therapies that affect LRP5 may also be useful in  
CC the treatment of autoimmune diseases such as glomerulonephritis, diseases  
CC and disorders involving disruption of endocytosis and/or antigen  
CC presentation, cytokine clearance and/or inflammation, viral infection,  
CC pathogenic bacterial toxin contamination, elevation of free fatty acids  
CC or hypercholesterolemia, type 2 diabetes, osteoporosis, Alzheimer's  
CC disease and cardiovascular disease. Products from the present invention  
CC can also be used for detection, diagnosis and drug screening  
XX  
XX Sequence 20 BP; 5 A; 7 C; 3 G; 5 T; 0 U; 0 Other;  
SQ  
Query Match 1.9%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 391 AGNGCTGGATTACAGGCGT 410  
DB 20 AGTCTGGGATTACAGGCGAT 1  
RESULT 729  
AAV85801  
ID AAV85801 standard; DNA; 20 BP.  
XX  
XX AAV85801;  
XX  
XX 10-FEB-1999 (first entry)  
XX  
XX LRP5 exon primer 58-10 1r.  
XX  
XX LRP5; LDL-receptor related protein; LRP-3; IDDM; diagnosis; endocytosis;  
KW insulin dependent diabetes mellitus; autoimmune disease;  
KW

KW glomerulonephritis; inflammation; viral infection; osteoporosis;  
KW hypercholesterolemia; Alzheimer's disease; low density lipoprotein;  
XX PCR primer; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
XX WO9846743-A1.  
XX  
XX 22-OCT-1998.  
XX  
XX 15-APR-1998; 98WO-GB001102.  
XX  
XX 15-APR-1997; 97US-0043553P.  
XX PR 05-JUN-1997; 97US-0048740P.  
XX  
XX (WELL ) WELLCOME TRUST LTD.  
XX PA (MERT ) MERCK & CO INC.  
XX  
XX PI Todd JA, Hess JW, Caskey CT, Cox RD, Gerhold D, Hammond H;  
PI Hey P, Kawaguchi Y, Merriman TR, Metzker ML, Nakagawa Y;  
PI Phillips MS, Twells RCU;  
XX  
XX WPI; 1998-594573/50.  
XX  
XX New isolated LDL-receptor related protein - used to develop products for  
PT treating, e.g. elevated triglyceride levels, diabetes, autoimmune  
PT disorders, inflammation or Alzheimer's disease.  
XX  
XX Claim 12; Page 106; 200pp; English.  
XX  
XX The present invention describes LRP5 (low density lipoprotein (LDL)  
CC receptor related protein, previously designated LRP-3). AAV8587 to  
CC AAV85822 represent exon primers used for obtaining LRP5 cDNA. Nucleic  
CC acid molecules (NMs) encoding LRP5 can be used for determining if an  
CC individual is susceptible to insulin dependent diabetes mellitus (IDDM).  
CC The NMs or proteins can be used for reducing triglyceride levels in the  
CC serum of an individual. Therapies that affect LRP5 may also be useful in  
CC the treatment of autoimmune diseases such as glomerulonephritis, diseases  
CC and disorders involving disruption of endocytosis and/or antigen  
CC presentation, cytokine clearance and/or inflammation, viral infection,  
CC pathogenic bacterial toxin contamination, elevation of free fatty acids  
CC or hypercholesterolemia, type 2 diabetes, osteoporosis, Alzheimer's  
CC disease and cardiovascular disease. Products from the present invention  
CC can also be used for detection, diagnosis and drug screening  
XX  
XX Sequence 20 BP; 3 A; 8 C; 3 G; 6 T; 0 U; 0 Other;  
SQ  
Query Match 1.9%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 673 GCTCAGTCGACCTTGCGCT 692  
DB 1 GTTCACTGCAACCTTGCGCT 20  
RESULT 730  
AAV85879  
ID AAV85879 standard; DNA; 20 BP.  
XX  
XX AAV85879;  
XX  
XX 10-FEB-1999 (first entry)  
XX  
XX LRP5 SNP primer 58-10 1r.  
XX  
XX LRP5; LDL-receptor related protein; LRP-3; IDDM; diagnosis; endocytosis;  
KW insulin dependent diabetes mellitus; autoimmune disease;  
KW glomerulonephritis; inflammation; viral infection; osteoporosis;  
KW hypercholesterolemia; Alzheimer's disease; low density lipoprotein;  
XX PCR primer; ss.  
XX



OS Synthetic.  
 OS Homo sapiens.  
 XX MO9846743-A1.  
 XX 22-OCT-1998.  
 PD  
 XX 15-APR-1998; 98WO-GB001102.  
 XX  
 PF 15-APR-1997; 97US-0043553P.  
 PR 05-JUN-1997; 97US-0048740P.  
 XX  
 PA (WELL ) WELLCOME TRUST LTD.  
 PA (MERCK ) MERCK & CO INC.  
 XX  
 PI Todd JA, Hess JW, Caskey CT, Cox RD, Gerhold D, Hammond H;  
 PI Hey P, Kawaguchi Y, Merriman TR, Metzker ML, Nakagawa Y;  
 PI Phillips MS, Twells RCU;  
 XX  
 DR WPI; 1998-594573/50.  
 XX  
 PT New isolated LDL-receptor related protein - used to develop products for  
 PT treating, e.g. elevated triglyceride levels, diabetes, autoimmune  
 PT disorders, inflammation or Alzheimer's disease.  
 PT  
 PS Claim 12; Page 111; 200pp; English.  
 XX  
 CC The present invention describes LRP5 (low density lipoprotein (LDL)  
 CC receptor related protein, previously designated LRP-3). AAY85823 to  
 CC AAY85900 represent SNP primers used for obtaining LRP5 cDNA. Nucleic acid  
 CC molecules (NAMES) encoding LRP5 can be used for determining if an  
 CC individual is susceptible to insulin dependent diabetes mellitus (IDDM).  
 CC The NMs or proteins can be used for reducing triglyceride levels in the  
 CC serum of an individual. Therapies that affect LRP5 may also be useful in  
 CC the treatment of autoimmune diseases such as glomerulonephritis, diseases  
 CC and disorders involving disruption of endocytosis and/or antigen  
 CC presentation, cytokine clearance and/or inflammation, viral infection,  
 CC pathogenic bacterial toxin contamination, elevation of free fatty acids  
 CC or hypercholesterolemia, type 2 diabetes, osteoporosis, Alzheimer's  
 CC disease and cardiovascular disease. Products from the present invention  
 CC can also be used for detection, diagnosis and drug screening  
 CC  
 XX  
 SQ Sequence 20 BP; 3 A; 8 C; 3 G; 6 T; 0 U; 0 Other;  
 XX  
 QY Query Match 1.9%; Score 18.4; DB 1; Length 20;  
 Best Local Similarity 95.0%; Pred. No. 1.3e+03;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 Db 673 GCTCAGTCAACCTCTGCCT 692  
 1 GTTCACTGCAACCTCTGCCT 20  
 XX  
 RESULT 731  
 AAX90795/c  
 ID AAX90795 standard; DNA; 20 BP.  
 XX  
 AC AAX90795;  
 XX  
 DT 13-JAN-2000 (first entry)  
 XX  
 DE Human 7SL RNA specific PCR primer-1.  
 XX  
 KW PCR primer; human 7SL RNA; amplify; human staufen cDNA; hStau;  
 KW synthesised; random hexamer primer; Superscript II reverse transcriptase;  
 KM ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX MO9951255-A1.  
 FN  
 PD 14-OCT-1999.

XX  
 PF 06-APR-1999; 99WO-US007533.  
 XX  
 PR 06-APR-1998; 98US-0080783P.  
 XX  
 XX (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
 PA  
 PI Greider CW, Le S;  
 XX  
 DR WPI; 1999-620168/53.  
 XX  
 PF Human staufen polypeptide useful in methods for identifying telomerase  
 PF inhibitors.  
 PT  
 PS Example 1; Page 25; 50pp; English.  
 XX  
 CC The present sequence is a PCR primer specific to human 7SL RNA. It is  
 CC used to amplify human staufen (hStau) cDNA synthesised using random  
 CC hexamer primers and Superscript II reverse transcriptase  
 CC  
 XX  
 SQ Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 U; 0 Other;  
 XX  
 QY Query Match 1.9%; Score 18.4; DB 1; Length 20;  
 Best Local Similarity 95.0%; Pred. No. 1.3e+03;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 Db 730 GTAGCTGGGACTACAGGCGC 749  
 20 GTAGCTGGGACTACAGGCGC 1  
 XX  
 RESULT 732  
 AAX86546  
 ID AAX86546 standard; DNA; 20 BP.  
 XX  
 AC AAX86546;  
 XX  
 DT 04-OCT-1999 (first entry)  
 XX  
 DE Primer re617 used for amplification and sequencing of Rhd gene exons.  
 XX  
 KW Allele; Rheus D antigen; Rhd; weak D phenotype; blood transfusion;  
 KW PCR primer; ss.  
 KM  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO937763-A2.  
 XX  
 PD 29-JUL-1999.  
 XX  
 PF 18-DEC-1998; 98WO-EP008319.  
 XX  
 PR 23-JAN-1998; 98EP-00101203.  
 XX  
 PA (DRKB-) DRK BLUTSPENDEDIENST BADEN WUERTTEMBERG.  
 XX  
 PI Flegel WA, Wagner FF;  
 XX  
 DR WPI; 1999-469127/39.  
 XX  
 PF Nucleic acid sequences correlated with Rheus weak D phenotype, useful  
 PF for screening blood from donors and recipients for transfusion methods.  
 PT  
 PS Example; Page 33; 64pp; English.  
 XX  
 CC PCR primers AAX86523-62 were used for amplification and sequencing of  
 CC exons of the Rheus D (Rhd) antigen gene. The specification describes a  
 CC Rhd contributing to or indicative of the weak D phenotype, where the Rhd  
 CC polynucleotide carries at least one missense mutation as compared to the  
 CC wild-type Rhd, in its transmembrane and/or intracellular regions,  
 CC especially in amino acid positions 2-16, 114-149, 179-225 or/and 267-397,  
 CC with the proviso that the D antigen does not carry a single missense

CC mutation leading to a F233V or T283I substitution. The probes and  
CC antibodies are useful in the methods for detection of weak D phenotypes.  
CC Red blood cells, from probands, are useful for the assessment of the  
CC affinity, avidity and/or reactivity of monoclonal anti-D antibodies.  
CC polyclonal anti-D antisera or of anti-globulin or anti-human-globulin  
CC antisera. Detecting the presence of the Rhd associated with weak D  
CC phenotype is useful for determining that a patient in need of a blood  
CC transfusion is to be transfused with Rhd negative blood from a donor.  
CC Alternatively, testing for weak D phenotype Rhd in the blood of a donor  
CC is useful for determining whether the donor blood should be excluded for  
CC transfusion to patients having wild type Rhd or weak D types, other than  
CC that of the donor weak D type  
XX  
SQ Sequence 20 BP; 4 A; 9 C; 2 G; 5 T; 0 U; 0 Other;  
Query Match 1.9%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 968 TCTCGGCTCAGTCGCAACCTC 987  
DB 1 TCTCAGCTCAGTCGCAACCTC 20  
RESULT 733  
AAZ37738/C  
ID AAZ37738 standard; DNA; 20 BP.  
XX  
AC AAZ37738;  
XX  
DT 07-JAN-2000 (first entry)  
XX  
DE Human mdm2 phosphorothioate oligodeoxynucleotide #268.  
XX  
KM Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
KM antisense; modulation; oligonucleotide; expression; inhibition;  
KM hyperproliferation; blood cancer; brain cancer; breast cancer;  
KM lung cancer; soft tissue cancer; psoriasis; fibrosis; atherosclerosis;  
KM restenosis; ss.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Miragila LJ, Nero P, Graham MJ, Monia BP, Cowseert LM;  
PI WPI; 1999-610754/52.  
XX  
PT New antisense compounds used to treat eg. hyperproliferative conditions.  
XX  
PS Example 9, Page 55; 157pp; English.  
XX  
CC AAZ37473-237738 represent human mdm2 phosphorothioate oligonucleotides.  
CC AAZ37471, AAZ37472, AAZ37739, AAZ37740 and AAZ37741 are used in the  
CC exemplification of the present invention. The present invention describes  
CC novel nucleotide antisense compounds, targeted to the 5' untranslated,  
CC translation termination codon, or 3' untranslated region of a nucleic  
CC acid encoding human mdm2, that modulates expression of human mdm2. The  
CC oligonucleotides mediate their effect by antisense inhibition of  
CC hyperproliferative gene expression. The antisense compound is used to  
CC treat an animal having a disease or condition associated with mdm2,  
CC particularly a hyperproliferative condition, more particularly cancer,  
CC especially of the blood, brain, breast, lung or soft tissue, or  
CC psoriasis, fibrosis, atherosclerosis or restenosis

XX  
SQ Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;  
Query Match 1.9%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 868 GGATTACAGCGGTGAGCCAC 887  
DB 20 GGATTACAGCGGTGAGCCAC 1  
RESULT 734  
AAZ37716/C  
ID AAZ37716 standard; DNA; 20 BP.  
XX  
AC AAZ37716;  
XX  
DT 07-JAN-2000 (first entry)  
XX  
DE Human mdm2 phosphorothioate oligodeoxynucleotide #246.  
XX  
KM Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
KM antisense; modulation; oligonucleotide; expression; inhibition;  
KM hyperproliferation; blood cancer; brain cancer; breast cancer;  
KM lung cancer; soft tissue cancer; psoriasis; fibrosis; atherosclerosis;  
KM restenosis; ss.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Miragila LJ, Nero P, Graham MJ, Monia BP, Cowseert LM;  
PI WPI; 1999-610754/52.  
XX  
PT New antisense compounds used to treat eg. hyperproliferative conditions.  
XX  
PS Claim 4, Page 54; 157pp; English.  
XX  
CC AAZ37473-237738 represent human mdm2 phosphorothioate oligonucleotides.  
CC AAZ37471, AAZ37472, AAZ37739, AAZ37740 and AAZ37741 are used in the  
CC exemplification of the present invention. The present invention describes  
CC novel nucleotide antisense compounds, targeted to the 5' untranslated,  
CC translation termination codon, or 3' untranslated region of a nucleic  
CC acid encoding human mdm2, that modulates expression of human mdm2. The  
CC oligonucleotides mediate their effect by antisense inhibition of  
CC hyperproliferative gene expression. The antisense compound is used to  
CC treat an animal having a disease or condition associated with mdm2,  
CC particularly a hyperproliferative condition, more particularly cancer,  
CC especially of the blood, brain, breast, lung or soft tissue, or  
CC psoriasis, fibrosis, atherosclerosis or restenosis  
XX  
SQ Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 U; 0 Other;  
Query Match 1.9%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 668 TCTTGCTCAGTCGCAACCTC 687  
DB 20 TCTTGCTCAGTCGCAACCTC 1

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RESULT 735
AAA18013
ID AAA28013 standard; DNA; 20 BP.
XX
AC AAA28013;
XX
DT 29-AUG-2000 (first entry)
XX
DE Uncoupling protein isoform UCP5S1 nucleotide sequence PCR primer.
XX
KM Uncoupling protein 5; UCP5; metabolism; chromosome 10q23-25; H+ leak;
XX metabolic rate; obesity; stroke; trauma; burn trauma; sepsis; infection;
XX human; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN MO200032624-A2.
XX
PD 08-JUN-2000.
XX
PF 03-NOV-1999; 99WO-US025947.
XX
PR 30-NOV-1998; 98US-0110286P.
XX 16-APR-1999; 99US-0129583P.
XX 15-JUL-1999; 99US-0143886P.
XX
PA (GENTH ) GENTECH INC.
XX
PI Adams S, Pan J;
XX
DR WPI; 2000-412284/35.
XX
PT Isolated nucleic acid encodes human uncoupling protein 5 useful in
XX diagnostic assays and treatment of obesity, stroke, trauma, sepsis and
XX infection.
XX
PS Example 2; Page 37; 90pp; English.
XX
CC This sequence represents a PCR primer specific for the human uncoupling
XX protein 5 isoform hUCP5S1 encoding DNA sequence. UCP5 is involved in
XX metabolism, and it may be involved in catalysing H+ leak, and therefore
XX be involved in energetic inefficiency in vivo. The present invention
XX relates to human and murine UCP5 nucleotide and protein sequences. There
XX are three isoforms of human UCP5, hUCP5L, hUCP5S, and two
XX isoforms of murine UCP5, mUCP5L and mUCP5S. The human UCP5 gene is
XX located on chromosome 10q23-25. The nucleic acid encoding UCP5 can be
XX used as hybridization probes, in chromosome and gene mapping, for the
XX generation of antisense RNA and DNA and in the preparation of recombinant
XX UCP5 proteins. UCP5 nucleic acids can be used in gene therapy for
XX regulation of metabolic conditions. Upregulating or downregulating UCP5
XX activity in a mammal is used for modulating metabolic rate in the mammal,
XX in particular upregulation of UCP5 activity stimulates an increase in
XX metabolic rate in an obese mammal. Other therapeutic applications
XX associated with modulating UCP5 activity are treating symptoms associated
XX with stroke, trauma (e.g. burn trauma), sepsis and infection. Detecting
XX UCP5 activity can be used to assist predictions concerning metabolic
XX conditions or risk for onset of obesity and as UCP5 may control the
XX generation of reactive oxygen to diagnose impaired neural activity or
XX neural degeneration. Anti-UCP5 antibodies can be used in diagnostic
XX assays and for the affinity purification of UCP5 from recombinant cell
XX culture or natural sources
XX
SQ Sequence 20 BP; 5 A; 4 C; 7 G; 0 T; 0 U; 0 Other;
XX
Query Match 1.9%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 866 TGGGATTACAGCGGAGCC 885
DB 1 TGGGATTACAGCGGAGCC 20
```

```
RESULT 736
AAA11943
ID AAA11943 standard; DNA; 20 BP.
XX
AC AAA11943;
XX
DT 16-AUG-2000 (first entry)
XX
DE Human MDMX antisense oligonucleotide #31223.
XX
KM MDMX; human; antisense; inhibitor; anticarcinogen; antiinflammatory;
XX antineoplastic; modulation; treatment; disease; diagnosis; primer; ss.
XX
OS Homo sapiens.
XX
PN US6046320-A.
XX
PD 04-APR-2000.
XX
PF 09-APR-1999; 99US-00289267.
XX
PR 09-APR-1999; 99US-00289267.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Cowseert LM;
XX
DR WPI; 2000-282710/24.
XX
PT New antisense oligonucleotides targeting nucleic acids encoding human
XX MDMX useful for inhibiting MDMX expression and for treating diseases
XX associated with MDMX expression e.g. tumor formation, inflammation.
XX
PS Example 15; Col 97-98; 51pp; English.
XX
CC This invention describes a novel antisense compound (I), 8-30 nucleobases
XX in length, targeted to a nucleic acid encoding a human MDMX. (I)
XX specifically hybridizes with and inhibits the expression of human MDMX.
XX The products of the invention have anticarcinogen, antiinflammatory and
XX antineoplastic activity. Synthesized chimeric oligonucleotides targeted
XX to human MDMX, 20 nucleotides in length, composed of a central gap region
XX consisting of ten 2'-deoxynucleotides flanked on both sides by 5-
XX nucleotide wings were tested for antisense inhibition of MDMX expression.
XX Results of real-time quantitative polymerase chain reaction (PCR) showed
XX 71 out of the 159, 20 base pair sequences, all fully defined in the
XX CC specification, demonstrated at least 30% inhibition of MDMX expression.
XX The antisense oligonucleotides are useful for effective and specific
XX modulation, particularly inhibition of having or being prone to a
XX disease or condition associated with expression of MDMX. The antisense
XX oligonucleotides may also be used as research reagents or kits, and as
XX diagnostics, e.g. to elucidate the function of a particular gene or to
XX distinguish between functions of various members of a biological pathway,
XX and as prophylaxis, e.g. to prevent or delay infection, inflammation or
XX tumor formation. AAA11781-A11945 represent antisense oligonucleotides
XX described in the method of the invention
XX
SQ Sequence 20 BP; 4 A; 4 C; 8 G; 4 T; 0 U; 0 Other;
XX
Query Match 1.9%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 648 GCTGAGTGCAGTGGCGCAA 667
DB 1 GCTGAGTGCAGTGGCGCAA 20
```

```
RESULT 737
AAZ52253
ID AAZ52253 standard; DNA; 20 BP.
XX
AC AAZ52253;
XX
```

```
XX 18-JUN-2000 (first entry)
DT
XX
DE Primer ZC12502 for sequencing human stomach protein zsi928 cDNA.
XX
XX Human; stomach; zsi928 protein; chromosome 3q22.1-3q22.2; gene therapy;
XX claudin; oligodendrocyte-specific protein; OSP; apoptosis; RVP.1;
XX rat androgen-withdrawal apoptosis protein; growth factor receptor;
XX cell signalling molecule; cytosolic; antibacterial; food poisoning;
XX Botulism; diarrhoea; inflammation; cramping; cancer; gastric ulcer;
XX diagnosis; prevention; treatment; primer; ss.
XX
XX Homo sapiens.
XX
XX WO200015659-A2.
XX
XX 23-MAR-2000.
XX
XX 14-SEP-1999; 99WO-US021023.
XX
XX 16-SEP-1999; 98US-00154444.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Sheppard PO, Foley KP;
XX
XX WPI; 2000-271379/23.
XX
XX New isolated polynucleotide encoding a stomach zsi928 polypeptide used
XX for diagnosis, prevention and treatment of stomach disorders caused by
XX bacteria, gastric ulcers or cancer.
XX
XX Example 1; Page 121; 121pp; English.
XX
XX The present sequence is a primer ZC12502 used for sequencing a cDNA
XX corresponding to an expressed sequence tag identified in a human lung
XX library, to obtain full length clone of polynucleotide encoding stomach
XX protein zsi928. The zsi928 gene is located at 3q22.1-3q22.2 region of
XX human chromosome 3. The zsi928 protein shows homology to a diverse family
XX of receptor proteins containing e.g. human claudin 1 and 2, human and
XX murine oligodendrocyte-specific protein (OSP) and rat androgen-withdrawal
XX apoptosis protein RVP.1. It is thought to be a cell-cell signalling
XX molecule, a growth factor receptor or extracellular matrix associated
XX protein with growth factor hormone activity and may be involved in an
XX apoptotic cellular pathway. The protein may act as an anti-microbial
XX agent and may bind toxins produced by bacteria which cause food
XX poisoning, Botulism, severe diarrhoea, inflammation and cramping. zsi928
XX agonists are useful for promoting apoptosis in cells over-expressing
XX zsi928 e.g. in cancer cells. They are also useful for stimulating cell
XX growth or differentiation. Altered levels of zsi928 protein in a test
XX sample such as saliva, serum, sweat or biopsy can be monitored as an
XX indication of digestive function, gastric ulcer or cancer. zsi928
XX expression can be used as a differentiation marker to determine the stage
XX of tumour or cell maturity, particularly in epithelial cells.
XX Polynucleotides encoding zsi928 can be used in gene therapy applications
XX to increase or inhibit zsi928 activity
XX
XX Sequence 20 BP; 5 A; 3 C; 8 G; 4 T; 0 U; 0 Other;
SQ
Query Match 1.9%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 864 GCTGGGATTACAGCGCTGAG 883
DB 1 GCTAGGATTACAGCGCTGAG 20
RESULT 738
AAF31822/C
ID AAF31822 standard; DNA; 20 BP.
XX
XX AAF31822;
```

```
XX 10-APR-2001 (first entry)
DT
XX
DE Human RANK antisense oligonucleotide, SEQ ID NO: 80.
XX
XX Human; cytosolic; antiinflammatory; antisense oligonucleotide; cancer;
XX receptor activator of NF-kappaB; RANK; infection; inflammation; ss.
XX
XX Homo sapiens.
XX
XX US6171860-B1.
XX
XX 09-JAN-2001.
XX
XX 05-NOV-1999; 99US-00435296.
XX
XX 05-NOV-1999; 99US-00435296.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Baker BF, Cowsett LM;
XX
XX WPI; 2001-136876/14.
XX
XX Novel antisense compounds capable of modulating expression of human
XX receptor activator of NF-kappaB useful for diagnosis, prophylaxis and
XX treatment of diseases associated with expression of RANK.
XX
XX Claim 14; Col 44; 40pp; English.
XX
XX The present sequence is one of a number of antisense compounds of 8 to 30
XX nucleobases in length that have been designed to target a 5' untranslated
XX region, start codon, coding region or 3' untranslated region of the human
XX receptor activator of NF-kappaB (RANK). The antisense compounds
XX specifically hybridise with and inhibit the expression of RANK. The
XX antisense oligonucleotides are useful for inhibiting the expression of
XX human RANK in human cells or tissues. They can be utilised for
XX diagnostics, therapeutics for the treatment of diseases associated with
XX the expression of RANK, prophylaxis e.g. to prevent or delay infection,
XX inflammation or tumour formation, and as research reagent. The antisense
XX compounds are safely and effectively administered to humans
XX
XX Sequence 20 BP; 2 A; 4 C; 10 G; 4 T; 0 U; 0 Other;
SQ
Query Match 1.9%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 843 CCTGCTCGGCGCTCCCAAG 862
DB 20 CCAGCCTCGGCGCTCCCAAG 1
RESULT 739
AAF31823/C
ID AAF31823 standard; DNA; 20 BP.
XX
XX AAF31823;
XX
XX 10-APR-2001 (first entry)
XX
XX Human RANK antisense oligonucleotide, SEQ ID NO: 81.
XX
XX Human; cytosolic; antiinflammatory; antisense oligonucleotide; cancer;
XX receptor activator of NF-kappaB; RANK; infection; inflammation; ss.
XX
XX Homo sapiens.
XX
XX US6171860-B1.
XX
XX 09-JAN-2001.
XX
XX 05-NOV-1999; 99US-00435296.
XX
XX AAF31823;
```

```
XX 05-NOV-1999; 99US-00435296.
XX (ISIS-) ISIS PHARM INC.
XX Baker BP, Cowsett LM;
XX WPI; 2001-136876/14.
XX
XX Novel antisense compounds capable of modulating expression of human
XX receptor activator of NF-kappaB useful for diagnosis, prophylaxis and
XX treatment of diseases associated with expression of RANK.
XX
XX Claim 14; Col 44; 40pp; English.
XX
XX The present sequence is one of a number of antisense compounds of 8 to 30
XX nucleobases in length that have been designed to target a 5' untranslated
XX region, start codon, coding region or 3' untranslated region of the human
XX receptor activator of NF-kappaB (RANK). The antisense compounds
XX specifically hybridise with and inhibit the expression of RANK. The
XX antisense oligonucleotides are useful for inhibiting the expression of
XX human RANK in human cells or tissues. They can be utilised for
XX diagnostic, therapeutic for the treatment of diseases associated with
XX the expression of RANK, prophylaxis e.g. to prevent or delay infection,
XX inflammation or tumour formation, and as research reagent. The antisense
XX compounds are safely and effectively administered to humans
XX
XX Sequence 20 BP; 5 A; 8 C; 3 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 1.9%; Score 18.4; DB 1; Length 20;
XX Best Local Similarity 95.0%; Pred. No. 1.3e+03;
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 392 GTCCTGGATTACAGCGTG 411
XX |||||||||||||||
XX 20 GTACTGGATTACAGCGTG 1
XX
XX RESULT 740
XX AAD14819/C
XX ID AAD14819 standard; DNA; 20 BP.
XX
XX AC AAD14819;
XX
XX DT 01-NOV-2001 (first entry)
XX
XX Human glycogen synthase kinase 3 alpha antisense oligo ISIS #116660.
XX
XX Human; glycogen synthase kinase 3 alpha; antidiabetic; cytostatic;
XX antisense therapy; diabetes; hyperproliferative disorder; inflammation;
XX neurological disorder; tumour; haematopoietic disorder; infection;
XX hyperproliferative disorder; developmental disorder; antisense;
XX phosphorothioate backbone; ss.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX key Location/Qualifiers
XX modified_base 1..20
XX /tag= a
XX /mod_base= OTHER
XX /note= "Phosphorothioate backbone"
XX modified_base 1..5
XX /tag= b
XX /mod_base= OTHER
XX /note= "Methoxyethyl residues"
XX modified_base 2
XX /tag= d
XX /mod_base= m5c
XX modified_base 4
XX /tag= e
XX /mod_base= m5c
XX modified_base 5
XX
```

```
FT /tag= f
FT /mod_base= m5c
FT modified_base 6
FT /tag= g
FT /mod_base= m5c
FT modified_base 7
FT /tag= h
FT /mod_base= m5c
FT modified_base 14
FT /tag= i
FT /mod_base= m5c
FT modified_base 15
FT /tag= j
FT /mod_base= m5c
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "Methoxyethyl residues"
FT modified_base 16
FT /tag= k
FT /mod_base= m5c
FT modified_base 19
FT /tag= l
FT /mod_base= m5c
XX
XX WO200152865-A1.
XX
XX 26-JUL-2001.
XX
XX 16-JAN-2001; 2001WO-US001411.
XX
XX 21-JAN-2000; 2000US-00488856.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, McKay R, Butler MM, Wyatt JR;
XX WPI; 2001-442247/47.
XX
XX Antisense compound 8 to 30 nucleobases in length comprising a compound
XX that is targeted to a nucleic acid molecule encoding glycogen synthase
XX kinase 3 alpha, useful for the treatment of e.g. diabetes and
XX hyperproliferative disorders.
XX
XX Example 15; Page 84; 115pp; English.
XX
XX The invention relates to an antisense compound 8 to 30 nucleobases in
XX length targeted to a nucleic acid encoding glycogen synthase kinase 3
XX alpha. The antisense compound specifically hybridises with and inhibits
XX the expression of glycogen synthase kinase 3 alpha. The antisense
XX compound is useful for the treatment of a diseases associated with
XX glycogen synthase kinase 3 alpha such as diabetes, a neurological
XX disorder, a haematopoietic disorder, a hyperproliferative disorder or a
XX developmental disorder. The antisense compounds may also be used
XX prophylactically to prevent or delay infection, inflammation or tumour
XX formation. The present sequence is a phosphorothioate antisense
XX oligonucleotide targeted to human glycogen synthase kinase 3 alpha
XX genomic DNA
XX
XX Sequence 20 BP; 5 A; 9 C; 2 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 1.9%; Score 18.4; DB 1; Length 20;
XX Best Local Similarity 95.0%; Pred. No. 1.3e+03;
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 863 TGCTGGATTACAGGGTGA 882
XX |||||||||||||||
XX 20 TGCTGGATTACAGGGTGA 1
XX
XX RESULT 741
XX AAD14817/C
XX ID AAD14817 standard; DNA; 20 BP.
```

XX	AD14817;	
AC		
XX	01-NOV-2001 (first entry)	
DT		
XX		
DE	Human glycogen synthase kinase 3 alpha antisense oligo ISIS #116658.	
XX		
KW	Human; glycogen synthase kinase 3 alpha; antidiabetic; cytostatic; antisense therapy; diabetes; hyperproliferative disorder; inflammation; neurological disorder; tumour; haematopoietic disorder; infection; hyperproliferative disorder; developmental disorder; antisense; phosphorothioate backbone; ss.	
KW		
XX		
OS	Homo sapiens.	
OS	Synthetic.	
XX		
FH	Key	Location/Qualifiers
FT	modified_base	1..20
FT		/*tag= a
FT		/mod_base= OTHER
FT		/note= "Phosphorothioate backbone"
FT	modified_base	1..5
FT		/*tag= b
FT		/mod_base= OTHER
FT		/note= "Methoxyethyl residues"
FT	modified_base	8
FT		/*tag= d
FT		/mod_base= m5c
FT	modified_base	14
FT		/*tag= e
FT		/mod_base= m5c
FT	modified_base	15
FT		/*tag= f
FT		/mod_base= m5c
FT	modified_base	16..20
FT		/*tag= c
FT		/mod_base= OTHER
FT		/note= "Methoxyethyl residues"
FT	modified_base	16
FT		/*tag= g
FT		/mod_base= m5c
PN	WO200152865-A1.	
XX		
XX	26-JUL-2001.	
PD		
XX		
PF	16-JAN-2001; 2001WO-US001411.	
XX		
PR	21-JAN-2000; 2000US-0048856.	
XX		
PA	(ISIS-) ISIS PHARM INC.	
XX		
PI	Monia BP, McKay R, Butler MM, Wyatt JR;	
XX		
DR	WPI; 2001-442247/47.	
XX		
PT	Antisense compound 8 to 30 nucleobases in length comprising a compound that is targeted to a nucleic acid molecule encoding glycogen synthase kinase 3 alpha, useful for the treatment of e.g. diabetes and hyperproliferative disorders.	
PT		
XX		
PS	Example 15; Page 83; 115pp; English.	
XX		
CC	The invention relates to an antisense compound 8 to 30 nucleobases in length targeted to a nucleic acid encoding glycogen synthase kinase 3 alpha. The antisense compound specifically hybridises with and inhibits the expression of glycogen synthase kinase 3 alpha. The antisense compound is useful for the treatment of a diseases associated with glycogen synthase kinase 3 alpha such as diabetes, a neurological disorder, a haematopoietic disorder, a hyperproliferative disorder or a developmental disorder. The antisense compounds may also be used prophylactically to prevent or delay infection, inflammation or tumour formation. The present sequence is a phosphorothioate antisense	

CC oligonucleotide targetted to human glycogen synthase kinase 3 alpha  
CC genomic DNA  
XX  
SQ Sequence 20 BP; 5 A; 4 C; 8 G; 3 T; 0 U; 0 Other;

QY Query Match 1.9%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 968 TCTGGCTCACTGCACCTC 987  
20 TCTGGGTCACTGCACCTC 1

RESULT 742  
AAK95122/C  
ID AAK95122 standard; DNA; 20 BP.  
XX  
AC AAK95122;  
XX  
DT 06-NOV-2001 (first entry)  
XX  
DE Human cDNA clone-specific primer, SEQ ID NO: 4367.  
XX  
KW Human; full length cDNA; cDNA synthesis; oligo-capping; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN EP130094-A2.  
XX  
PD 05-SEP-2001.  
XX  
PF 07-JUL-2000; 2000EP-00114089.  
XX  
PR 08-JUL-1999; 99JP-00194486.  
PR 11-JAN-2000; 2000JP-00118774.  
PR 02-MAY-2000; 2000JP-00183765.  
XX  
XX (HELI-) HELIX RES INST.  
XX  
PA  
PI Ota T, Nishikawa T, Isogai T, Hayashi K, Iehi S, Kawai Y;  
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
PI  
DR WPI; 2001-524255/58.  
XX

830 Primers useful for synthesizing full length cDNA clones and their use  
in genetic manipulation.

Example 18; Page 131; 1380pp + Sequence Listing; English.

The invention relates to primers for synthesising full length cDNA  
clones. 830 cDNA molecules encoding a human protein have been isolated  
and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have  
been determined. Primers for synthesising the full length cDNA are useful  
for clarifying the function of the protein encoded by the cDNA. The full  
length clones were obtained by construction of full length enriched cDNA  
libraries that were synthesised by the oligo-capping method. The primers  
enable the production of the full length cDNA easily without any special  
methods. The present sequence is a primer used to amplify a human cDNA  
clone provided in the invention

Sequence 20 BP; 4 A; 5 C; 5 G; 6 T; 0 U; 0 Other;

QY Query Match 1.9%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 725 CCTGAGTAGCTGGGACTACA 744  
20 CCTGATAGCTGGGACTACA 1

RESULT 743

```
AAH02356
ID AAH02356 standard; DNA; 20 BP.
XX
AC AAH02356;
XX
DT 12-JUN-2001 (first entry)
XX
DE Human AKAP10 coding sequence PCR primer SEQ ID NO: 53.
XX
KM Database; polymorphism; SNP; human; genetic marker; disease; infection;
XX drug response; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200127857-A2.
XX
PD 19-APR-2001.
XX
PF 13-OCT-2000; 2000WO-US028413.
XX
PR 13-OCT-1999; 99US-0159176P.
PR 10-JUL-2000; 2000US-0217251P.
PR 10-JUL-2000; 2000US-0217658P.
PR 19-SEP-2000; 2000US-00663968.
XX
PA (SEQID-) SEQUENOM INC.
XX
PI Braun A, Koeser H, Van Den Boom D, Ping Y, Rodi C, He L;
PI Chin N, Jurinke C;
XX
DR WPI; 2001-273865/28.
XX
PT Producing a database for identifying polymorphic genetic markers,
PT comprises obtaining data relating to members of a healthy population and
PT entering the information into a database.
XX
PS Example 3; Page 293; 304pp; English.
XX
CC The present invention provides a database of human samples obtained from
CC healthy individuals which can be used to identify polymorphic genetic
CC markers. Data obtained for the database can be used to sort the samples
CC by parameters such as age, sex and ethnicity. This is useful in linking
CC markers with diseases, susceptibility to infection and drug responses.
CC The present primer was used in an assay to demonstrate the uses of the
CC database of the invention
XX
SQ Sequence 20 BP; 6 A; 5 C; 4 G; 5 T; 0 U; 0 Other;
XX
Query Match 1.9%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 385 TCCCAAGTCTGGGATTAC 404
Db 1 TCCCAAGTCTGGGATTAC 20
XX
RESULT 744
AAF92892/c
ID AAF92892 standard; DNA; 20 BP.
XX
AC AAF92892;
XX
DT 17-MAY-2001 (first entry)
XX
DE Human ABC1 transcription factor binding site #53.
XX
KM High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ds.
XX
OS Homo sapiens.
XX
PN WO200115676-A2.
XX
```

```
PD 08-MAR-2001.
XX
XX 01-SEP-2000; 2000WO-IB001492.
XX
PF 01-SEP-1999; 99US-0151977P.
XX
PR 15-MAR-2000; 2000US-00526193.
PR 23-JUN-2000; 2000US-0213958P.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX
PA (XENO-) XENON GENETICS INC.
XX
PI Hayden MR, Brooks-Wilson AR, Pimstone SN, Clee SM;
XX
DR WPI; 2001-244356/25.
XX
DT Treating a lower than normal high density lipoprotein-cholesterol (HDL-C)
XX level, a higher than normal triglyceride level, or a cardiovascular
XX disease, by administering a compound that modulates LXR- or RXR-mediated
XX PT transcriptional activity.
XX
PS Disclosure; Fig 3; 317pp; English.
XX
CC The present invention relates to a method for treating a patient
XX diagnosed as having a lower than normal high density lipoprotein-
XX cholesterol (HDL-C) level, a higher than normal triglyceride level, or a
XX cardiovascular disease, involving administering a compound that modulates
XX CC LXR- or RXR-mediated transcriptional activity or ABC1 expression or
XX CC activity. The LXR gene product may be used in an assay to identify
XX CC compounds useful for the treatment of a disease or condition selected a
XX CC lower than normal HDL cholesterol level, a higher than normal
XX CC triglyceride level, and a cardiovascular disease
XX
SQ Sequence 20 BP; 6 A; 6 C; 5 G; 3 T; 0 U; 0 Other;
XX
Query Match 1.9%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 485 GTGGTGATCAGCTCAC 504
Db 20 GTGGTGATCAGCTCAC 1
XX
RESULT 745
AAH28044
ID AAH28044 standard; DNA; 20 BP.
XX
AC AAH28044;
XX
DT 05-SEP-2001 (first entry)
XX
DE PCR primer for a minimal deletion in FRA16D oxidoreductase gene.
XX
KM Cancer associated protein; FOR gene; FRA16D; fragile site; aphidicolin;
XX KM chromosomal rearrangement; cancer; splice variant; DNA instability;
XX KM FRA16D oxidoreductase; neoplasia; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200144466-A1.
XX
DT 21-JUN-2001.
XX
PD 15-DEC-2000; 2000WO-AU001539.
XX
PF 16-DEC-1999; 99AU-00004711.
PR 19-APR-2000; 2000AU-00007025.
XX
XX (WOME-) WOMEN'S & CHILDREN'S HOSPITAL.
XX
PA Richards R, Ried K, Finnis M, Hobson L, Mangeltsdorf M, Dayan S;
XX PI Nancarrow J, Woollatt E, Baker E;
XX
```





XX 14-AUG-2001 (first entry)  
DT SNP specific lower PCR primer SEQ ID 1398.  
XX  
XX  
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
KW SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;  
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolemia;  
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
KW inflammation; forensic investigation; paternity analysis; PCR primer; ss.  
XX  
XX Homo sapiens.  
OS  
XX MO200129262-A2.  
PN  
XX 26-APR-2001.  
PD  
XX 13-OCT-2000; 2000MO-US028436.  
PF  
XX 15-OCT-1999; 99US-0160096P.  
PR  
XX (ORCH-) ORCHID BIOSCIENCES INC.  
PA  
XX Picoult-Newburg L, Pohl M;  
PI  
XX WPI; 2001-290930/30.  
DR  
XX  
XX New genotyping oligonucleotide, useful for detecting the presence,  
PT absence or identity of single polynucleotide polymorphism in a nucleic  
PT acid sample.  
XX  
XX  
PS Claim 1; Page 57; 83pp; English.  
XX  
XX Sequences AAH37205 - AAH0944 represent PCR primers, single nucleotide  
CC primer extension (SNPE) primers, and the sequences of regions flanking  
CC sites of single nucleotide polymorphisms SNPs. The present invention  
CC includes kits for determining the presence or absence of a SNP, using the  
CC oligonucleotides of the invention. The PCR primers are used to amplify a  
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.  
CC The oligonucleotides are useful for genotyping a nucleic acid sample by  
CC performing a single-nucleotide primer extension reaction. The  
CC oligonucleotides are useful for determining the presence, absence or  
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
CC assess by association analysis the genotype of an individual or group of  
CC individuals, having a pathological phenotypic trait suspected of being  
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular  
CC dystrophy, familial hypercholesterolemia, polycystic kidney disease,  
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
CC traits also include symptoms of or susceptibility to multifactorial  
CC disease of which a component is or may be genetic such as autoimmune  
CC diseases, including, rheumatoid arthritis, multiple sclerosis,  
CC inflammation, cancer, nervous system diseases and infection by pathogenic  
CC microorganism. The method is also useful in forensic investigations and  
CC paternity analysis. The present sequence represents a PCR primer specific  
CC for a human SNP containing DNA sequence  
XX  
SQ Sequence 20 BP; 6 A; 6 C; 5 G; 3 T; 0 U; 0 Other;  
XX  
XX Query Match 1.9%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
OY 869 GATTACAGCGCTGAGCCACC 888  
DB 1 GATTACAGCGCTGAGCCACC 20  
XX  
RESULT 749  
AAH37610/C  
ID AAH37610 standard; DNA; 20 BP.  
XX

AC AAH37610;  
XX 14-AUG-2001 (first entry)  
DT SNP specific lower PCR primer SEQ ID 406.  
XX  
XX  
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
KW SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;  
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolemia;  
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
KW inflammation; forensic investigation; paternity analysis; PCR primer; ss.  
XX  
XX Homo sapiens.  
OS  
XX MO200129262-A2.  
PN  
XX 26-APR-2001.  
PD  
XX 13-OCT-2000; 2000MO-US028436.  
PF  
XX 15-OCT-1999; 99US-0160096P.  
PR  
XX (ORCH-) ORCHID BIOSCIENCES INC.  
PA  
XX Picoult-Newburg L, Pohl M;  
PI  
XX WPI; 2001-290930/30.  
DR  
XX  
XX New genotyping oligonucleotide, useful for detecting the presence,  
PT absence or identity of single polynucleotide polymorphism in a nucleic  
PT acid sample.  
XX  
XX  
XX Claim 1; Page 52; 83pp; English.  
XX  
XX Sequences AAH37205 - AAH0944 represent PCR primers, single nucleotide  
CC primer extension (SNPE) primers, and the sequences of regions flanking  
CC sites of single nucleotide polymorphisms SNPs. The present invention  
CC includes kits for determining the presence or absence of a SNP, using the  
CC oligonucleotides of the invention. The PCR primers are used to amplify a  
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.  
CC The oligonucleotides are useful for genotyping a nucleic acid sample by  
CC performing a single-nucleotide primer extension reaction. The  
CC oligonucleotides are useful for determining the presence, absence or  
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
CC assess by association analysis the genotype of an individual or group of  
CC individuals, having a pathological phenotypic trait suspected of being  
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular  
CC dystrophy, familial hypercholesterolemia, polycystic kidney disease,  
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
CC traits also include symptoms of or susceptibility to multifactorial  
CC disease of which a component is or may be genetic such as autoimmune  
CC diseases, including, rheumatoid arthritis, multiple sclerosis,  
CC inflammation, cancer, nervous system diseases and infection by pathogenic  
CC microorganism. The method is also useful in forensic investigations and  
CC paternity analysis. The present sequence represents a PCR primer specific  
CC for a human SNP containing DNA sequence  
XX  
SQ Sequence 20 BP; 8 A; 7 C; 4 G; 1 T; 0 U; 0 Other;  
XX  
XX Query Match 1.9%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
OY 188 GGAGTTTCATGTTGTC 207  
DB 20 GGAGTTTCATGTTGTC 1  
XX  
RESULT 750  
AAH40090  
ID AAH40090 standard; DNA; 20 BP.  
XX



KW inflammation; cancer; autoimmune disease; graft rejection; amplify;  
KW graft versus host disease; systemic lupus erythematosus;  
KW polymerase chain reaction; ss.  
OS Synthetic.  
XX WO200146260-A2.  
XX PN 28-JUN-2001.  
XX PD 22-DEC-2000; 2000MO-US034963.  
XX PF 23-DEC-1999; 99US-0172025P.  
XX PR (BRIM ) BRISTOL-MYERS SQUIBB CO.  
XX PA Starling GC, Finger J;  
XX PI WPI; 2001-418044/44.  
XX DR Novel Antigen Presenting cell expression protein useful for treating  
XX PT asthma, arteriosclerosis, autoimmune diseases, AIDS, cirrhosis, Crohn's  
XX PT disease and atopic dermatitis.  
XX PS Claim 50; Page 83; 112PP; English.  
XX CC The sequences given in AAC86117-42 are primers which were used to isolate  
XX CC the cDNA sequences which encode antigen presenting cell expression (APEX)  
XX CC -1, APEX-2 and APEX-3 proteins. APEX-1 and APEX-2 comprise an  
XX CC extracellular domain having one immunoglobulin (Ig)-like structure and N-  
XX CC glycosylation site, a transmembrane domain, and a cytoplasmic domain  
XX CC having at least one SH2-binding motif. APEX proteins and antibodies are  
XX CC useful in the study, diagnosis, prevention and treatment of disease  
XX CC associated with the presence of an APEX protein e.g., asthma,  
XX CC atelectosclerosis, AIDS, cirrhosis, Crohn's disease, atopic dermatitis,  
XX CC autoimmune anaemia, bursitis, cholecystitis, diabetes mellitus,  
XX CC emphysema, atrophic gastritis, inflammatory bowel disease, multiple  
XX CC sclerosis, myasthenia gravis, myocardial or pericardial inflammation,  
XX CC osteoarthritis, osteoporosis, psoriasis, Reiter's syndrome, rheumatoid  
XX CC arthritis, inflammation, cancer, immune disorders, autoimmune diseases,  
XX CC graft rejections, graft versus host reaction and systemic lupus  
XX CC erythematosus. APEX proteins are useful as diagnostic and/or prognostic  
XX CC markers on APCs or APEX expressing cells, the ability to elicit the  
XX CC generation of antibodies and as targets for various therapeutic  
XX CC modalities. APEX proteins are also useful for identifying and isolating  
XX CC ligand that bind APEX  
XX CC  
XX Sequence 20 BP; 4 A; 8 C; 3 G; 5 T; 0 U; 0 Other;  
SQ  
Query Match 1.9%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 867 GGGATTACAGCGGTGAGCCA 886  
DB 20 GGGATTACAGCGGTGAGCCA 1  
RESULT 753  
AAH20704/C  
ID AAH20704 standard; DNA; 20 BP.  
XX  
XX AAH20704;  
AC  
XX 13-AUG-2001 (first entry)  
XX  
XX Human telomeric repeat binding factor 2 oligonucleotide 111432.  
DE  
XX Antisense; phosphorothioate; human; telomeric repeat binding factor 2;  
KW inhibitor; premature aging; hyperproliferative disorder; cancer;  
KW cytoskeletal; ss.  
XX  
XX Homo sapiens.  
OS

XX  
XX Key Location/Qualifiers  
XX FT modified\_base 1..20  
XX FT /\*tag= b  
XX FT /mod\_base= OTHER  
XX FT /note= "phosphorothioate backbone"  
FT modified\_base 1..3  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "2-O-methoxyethyl"  
FT modified\_base 13..20  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "2-O-methoxyethyl"  
XX  
XX WO200143752-A1.  
XX PN 21-JUN-2001.  
XX PD 14-DEC-2000; 2000MO-US033954.  
XX PF 17-DEC-1999; 99US-00467642.  
XX PR (ISIS-) ISIS PHARM INC.  
XX PA Monia BP, Cowseert LM;  
XX PI WPI; 2001-398071/42.  
XX DR Antisense compounds targeted to nucleic acid encoding telomeric repeat  
XX PT binding factor 2 useful for treating conditions such as premature aging  
XX PT and diseases such as cancer.  
XX PS Claim 3; Page 81; 108PP; English.  
XX CC This invention describes a novel antisense compound (I) 8-30 nucleobases  
XX CC in length targeted to a polynucleotide encoding human telomeric repeat  
XX CC binding factor 2 (II) which specifically hybridizes with, and inhibits  
XX CC the expression of (II). (I) is useful for treating a human having a  
XX CC disease or condition associated with (II) such as premature aging or a  
XX CC hyperproliferative disorder especially cancer. (I) is useful for  
XX CC expression of (II) in human cells or tissues. (I) is useful for  
XX CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.  
XX CC The products of the invention have cytostatic activity. This sequence  
XX CC represents an antisense oligonucleotide used to illustrate the method of  
XX CC the invention  
XX CC  
XX Sequence 20 BP; 5 A; 7 C; 3 G; 5 T; 0 U; 0 Other;  
SQ  
Query Match 1.9%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 863 TGCTGGGATTACAGCGGTGA 882  
DB 20 TGCTGGGATTACAGCGGTGA 1  
RESULT 754  
AAH20699/C  
ID AAH20699 standard; DNA; 20 BP.  
XX  
XX AAH20699;  
AC  
XX 13-AUG-2001 (first entry)  
XX  
XX Human telomeric repeat binding factor 2 oligonucleotide 111427.  
DE  
XX Antisense; phosphorothioate; human; telomeric repeat binding factor 2;  
KW inhibitor; premature aging; hyperproliferative disorder; cancer;  
KW cytoskeletal; ss.  
XX  
XX Homo sapiens.  
OS

Key	Location/Qualifiers
FT	1..20
FT	/*tag= a
FT	/mod_base= OTHER
FT	/note= "OTHER= All phosphorothioate linkages, additionally bases 1-6 and bases 15-20 are 2'-O-methoxyethyl bases, and bases 7-14 are deoxynucleotides"
XX	
XX	US2001016575-A1.
XX	
XX	23-AUG-2001.
XX	
XX	02-JAN-2001; 2001US-00752983.
PR	
PR	26-MAR-1998; 98US-00048810.
PR	26-MAR-1999; 99US-00280805.
PA	
PA	(MIRA/) MIRAGLIA L J.
PA	(NERO/) NERO P.
PA	(GRAH/) GRAHAM M J.
PA	(MONI/) MONIA B P.
PA	(COWS/) COWSERT L M.
PI	
PI	Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowsert LM;
DR	
DR	WPI; 2001-535565/59.
XX	
XX	An antisense compound, useful for treating e.g. cancer, comprises
PT	nucleobases targeted a region (e.g. translation termination codon region)
PT	of a nucleic acid encoding human mdm2.
XX	
XX	Example 9; Page 18; 81pp; English.
XX	
CC	The present invention relates to antisense compounds, 8-30 nucleobases in
CC	length targeted to the 5' untranslated region, translation termination
CC	codon region, 3' untranslated region, coding region or translation start
CC	site of a nucleic acid encoding human mdm2, where the antisense compound
CC	modulates the expression of human mdm2. The antisense oligonucleotides of
CC	the invention are useful for encoding human mdm2 and for inhibiting the
CC	expression of human mdm2. They may be used for treating an animal having
CC	a disease or condition associated with amplification of mdm2 gene or
CC	overexpression of mdm2 e.g. a hyperproliferative disorder such as cancer
CC	(blood, brain, breast, lung, or a soft tissue cancer) and psoriasis,
CC	fibrosis, atherosclerosis or restenosis, tumours, colorectal carcinoma
CC	and chronic myelogenous leukemia. The antisense compound may be
CC	administered with a chemotherapeutic agent to overcome drug resistance.
CC	The antisense compound reduces hyperproliferation of human cells. The
CC	method, which involves the use of the antisense compound, is also useful
CC	for detecting the role of mdm2 expression in various cell functions and
CC	physiological processes and useful in both clinical research and
CC	diagnostic tools. AAS29242-AAS29507 represent the human mdm2 antisense
CC	oligonucleotides of the present invention
XX	
XX	Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
XX	
XX	Query Match 1.9%; Score 18.4; DB 1; Length 20;
XX	Best Local Similarity 95.0%; Pred. NO. 1.3e+03;
XX	Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX	
QY	868 GGATTACAGCGGTGAGCCAC 887
Db	20 GGATTACAGCGGTGAGCCAC 1
XX	
XX	RESULT 756
XX	AAS29485/C
ID	AAS29485 standard; DNA; 20 BP.
XX	
XX	AAS29485;
XX	
XX	21-NOV-2001 (first entry)
XX	

DE Human mdm2 antisense oligonucleotide 31468.  
XX  
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;  
KW atherosclerosis; tumour; cytostatic; anti psoriatic;  
KW anti arteriosclerotic; vasotropic; antisense; phosphorothioate; ss.  
XX  
XX Homo sapiens.  
OS  
FH Key Location/Qualifiers  
FT modified\_base 1..20  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= All phosphorothioate linkages,  
FT additionally bases 1-6 and bases 15-20 are 2'-O-  
FT methoxyethyl bases, and bases 7-14 are deoxynucleotides"  
XX  
XX US2001016575-A1.  
XX  
XX 23-AUG-2001.  
XX  
XX 02-JAN-2001; 2001US-00752983.  
XX  
XX 26-MAR-1998; 98US-00048810.  
XX 26-MAR-1999; 99US-00280805.  
XX  
XX (MIRA/) MIRAGLIA L J.  
XX (NERO/) NERO P.  
XX (GRAM/) GRAHAM M J.  
XX (MONT/) MONIA B P.  
XX (COMS/) COMSERT L M.  
XX  
XX Miraglia LJ, Nero P, Graham MJ, Monia BP, Comsert LM;  
XX WPI; 2001-535565/59.  
XX  
XX An antisense compound, useful for treating e.g. cancer, comprises  
XX nucleobases targeted a region (e.g. translation termination codon region)  
XX of a nucleic acid encoding human mdm2.  
XX  
XX  
XX Claim 4; Page 18; 81pp; English.  
XX  
XX The present invention relates to antisense compounds, 8-30 nucleobases in  
XX length targeted to the 5' untranslated region, translation termination  
XX codon region, 3' untranslated region, coding region or translation start  
XX site of a nucleic acid encoding human mdm2, where the antisense compound  
XX modulates the expression of human mdm2. The antisense oligonucleotides of  
XX the invention are useful for encoding human mdm2 and for inhibiting the  
XX expression of human mdm2. They may be used for treating an animal having  
XX a disease or condition associated with amplification of mdm2 gene or  
XX overexpression of mdm2 e.g. a hyperproliferative disorder such as cancer  
XX (blood, brain, breast, lung, or a soft tissue cancer) and psoriasis,  
XX fibrosis, atherosclerosis or restenosis, tumours, colorectal carcinoma  
XX and chronic myelogenous leukemia. The antisense compound may be  
XX administered with a chemotherapeutic agent to overcome drug resistance.  
XX The antisense compound reduces hyperproliferation of human cells. The  
XX method, which involves the use of the antisense compound, is also useful  
XX for detecting the role of mdm2 expression in various cell functions and  
XX physiological processes and useful in both clinical research and  
XX diagnostic tools. AAS2242-AAS29507 represent the human mdm2 antisense  
XX oligonucleotides of the present invention  
XX  
XX Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 U; 0 Other;  
XX  
XX Query Match 1.9%; Score 18.4; DB 1; Length 20;  
XX Best Local Similarity 95.0%; Pred. No. 1.3e+03;  
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX 668 TCTTGCGTCACTGCAACCTC 687  
XX |||||||  
XX 20 TCTTGCGTCACTGCAAGCTC 1  
XX  
XX RESULT 757

AAD28754  
ID AAD28754 standard; DNA; 20 BP.  
XX  
XX AAD28754;  
AC  
XX  
XX 07-MAY-2002 (first entry)  
XX  
XX Target specific PCR primer #2 to amplify human AKAP10-1 target sequence.  
XX  
XX Human; polymorphic A-Kinase anchor protein; AKAP; disorder; neurological;  
XX bipolar; cardiovascular; cardiac; proliferative; neurodegenerative;  
XX cardiomyopathy; peripheral retinopathy; obesity; signal transduction;  
XX left ventricular function; Alzheimer's disease; retinitis pigmentosa;  
XX diabetes; PCR primer; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200204489-A2.  
XX  
XX 17-JAN-2002.  
XX  
XX 05-JUL-2001; 2001WO-US021308.  
XX  
XX 10-JUL-2000; 2000US-0217251P.  
XX 13-OCT-2000; 2000US-0240335P.  
XX 12-APR-2001; 2001US-00834700.  
XX  
XX (SEQU-) SEQUENOM INC.  
XX  
XX Braun A;  
XX  
XX WPI; 2002-154919/20.  
XX  
XX New polynucleotide encoding polymorphic A-Kinase anchor proteins for  
XX detecting an allelic variant of the human gene which is indicative of an  
XX alteration in signal transduction, and is related to a disorder e.g.  
XX Alzheimer's disease.  
XX  
XX  
XX Example 3; Page 90; 290pp; English.  
XX  
XX The present invention relates to a polynucleotide encoding polymorphic A-  
XX Kinase anchor protein (AKAP), with isoleucine residue at position 646  
XX replaced with valine, leucine or phenylalanine. AKAP is useful for  
XX detecting an allelic variant of a human AKAP10 gene which is indicative  
XX of an alteration in signal transduction, where the alteration is related  
XX to a disorder selected from cardiovascular, cardiac, proliferative,  
XX neurological, neurodegenerative disorders, obesity, diabetes and  
XX peripheral retinopathies, especially the disorders including Alzheimer's  
XX disease, altered left ventricular function, cardiomyopathies, bipolar  
XX disorder and retinitis pigmentosa. The method of the invention is useful  
XX for indicating susceptibility to morbidity and/or increased or early  
XX mortality of a subject, where the predominant allele comprises A at  
XX position corresponding to 2073 of AKAP, or a polymorphic region of AKAP10  
XX comprises a nucleotide other than A at position T corresponding to  
XX position 2073 of AKAP, or other than T of the complement of AKAP, and the  
XX detecting step is performed by allele specific hybridisation, primer  
XX specific extension, oligonucleotide ligation assay, restriction enzyme  
XX site analysis and single-stranded conformation polymorphism analysis, or  
XX the detection is by detecting a signal group from radioisotopes, enzymes,  
XX antigens, antibodies, spectrophotometric reagents, chemiluminescent  
XX reagents, fluorescent reagents and other light producing reagents. The  
XX present sequence is a target specific PCR primer used to amplify human  
XX AKAP10-1 target sequence  
XX  
XX Sequence 20 BP; 6 A; 5 C; 4 G; 5 T; 0 U; 0 Other;  
XX  
XX Query Match 1.9%; Score 18.4; DB 1; Length 20;  
XX Best Local Similarity 95.0%; Pred. No. 1.3e+03;  
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX 385 TCCCAAGTCTGGGATTAC 404  
XX |||||||  
XX 1 TCCCAAGTCTGGGAATTAC 20  
XX  
XX

```
RESULT 758
AAL40357
ID AAL40357 standard; DNA; 20 BP.
XX
AC AAL40357;
XX
DT 19-SEP-2002 (first entry)
XX
DE Human caspase 6 antisense inhibition related oligo SEQ ID No 76.
XX
KW Muscular; cytosolic; neurotropic; neuroprotective; ophthalmological;
KW anti-leukemic; osteopathic; caspase 6; Rieger's syndrome; bone metabolism;
KW ataxia telangiectasia; hyperproliferative disorder; cholesterol disorder;
KW haematopoietic disorder; cancer; neurological; Alzheimer's disease;
KW apoptotic; human; ds.
XX
XX Homo sapiens.
XX OS
XX WO200229066-A1.
XX PN
XX 11-APR-2002.
XX PD
XX 03-OCT-2001; 2001WO-US030871.
XX PF
XX 04-OCT-2000; 2000US-00679299.
XX PR
XX (ISIS-) ISIS PHARM INC.
XX PA
XX Brown-Driver VL, Zhang H, Watt AT;
XX PI
XX WPI; 2002-471315/50.
XX DR
XX An antisense oligonucleotide of 8 to 50 nucleotides in length that
XX PT inhibits caspase 6, is useful for treating Rieger's syndrome.
XX PS
XX Claim 3; Page 89; 141pp; English.
XX
CC The invention relates to an antisense oligonucleotide compound of 8 to 50
CC nucleotides in length that is targeted to a nucleic acid molecule
CC encoding caspase 6, where the oligonucleotide specifically hybridises
CC with and inhibits the expression of caspase 6. The oligonucleotide of the
CC invention specifically hybridises to and inhibits expression of caspase 6
CC in cells or tissues. The oligonucleotides can be administered
CC therapeutically or prophylactically to treat an animal having a disease
CC or condition associated with caspase 6, such as Rieger's syndrome or
CC ataxia telangiectasia, hyperproliferative disorder, a haematopoietic
CC disorder, a bone metabolism or cholesterol disorder, various types of
CC cancer, neurological conditions such as Alzheimer's disease and other de-
CC regulated apoptotic pathological conditions. This polynucleotide sequence
CC represents a human caspase 6 oligonucleotide relating to the invention.
CC NOTE: This phosphorothioate oligonucleotide sequence has 2'-MOE wings and
CC a deoxy gap
CC
XX SQ Sequence 20 BP; 5 A; 5 C; 6 G; 4 T; 0 U; 0 Other;
XX
Query Match 1.9%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 545 AGCCTCCCAAGTAGTGGA 564
DB 1 AGCCTCCCAAGTAGTGGA 20
XX
RESULT 759
ABK68939
ID ABK68939 standard; DNA; 20 BP.
XX
AC ABK68939;
XX
DT 02-JUL-2002 (first entry).
```

```
XX
DE Human phosphorylase kinase beta antisense oligonucleotide #52.
XX
XX Human; phosphorylase kinase beta; metabolic disorder; diabetes;
XX infection; inflammation; tumour formation; antidiabetic;
XX anti-inflammatory; cytosolic; phosphorothioate; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /tag= a
XX /mod_base= OTHER
XX /note= "OTHER= phosphorothioate internucleotide linkages,
XX optionally bases 1-5 and 16-20 are 2'-methoxyethoxy (2'-
XX MOE) bases, where the 2'-MOE cytidines are also
XX 5'-methylcytidines"
XX FT
XX
XX WO200222637-A1.
XX PN
XX 21-MAR-2002.
XX PD
XX 12-SEP-2001; 2001WO-US028586.
XX PF
XX 14-SEP-2000; 2000US-00662250.
XX PR
XX (ISIS-) ISIS PHARM INC.
XX PA
XX Monia BP, Wyatt JR;
XX PI
XX WPI; 2002-351873/38.
XX DR
XX
XX Novel antisense oligonucleotide which inhibits expression of
XX phosphorylase kinase beta, useful for treating metabolic disorder e.g.
XX diabetes, prevent or delay infection, inflammation or tumor formation.
XX PT
XX
XX Claim 3; Page 83; 132pp; English.
XX PS
XX
CC The present invention relates to antisense compounds and methods for
CC modulating the expression of human phosphorylase kinase beta. The
CC antisense compounds, particularly antisense oligonucleotides, target and
CC inhibit the expression of human phosphorylase kinase beta. The antisense
CC compounds are useful for inhibiting the expression of human phosphorylase
CC kinase beta in human cells or tissues and for treating an animal,
CC particularly a human suspected of having or being prone to a disease or
CC condition associated with expression of phosphorylase kinase beta such as
CC a metabolic disorder e.g. diabetes. The compounds are useful for
CC diagnostics, therapeutics and as research reagent, e.g. prophylactically
CC to prevent or delay infection, inflammation or tumour formation. The
CC antisense compounds are useful in the preparation of a pharmaceutical
CC formulation. They are highly specific, have an enhanced affinity for the
CC nucleic acid target, and are safely and effectively administered to
CC humans. ABK6888-ABK6895 represent human phosphorylase kinase beta
CC antisense oligonucleotides which comprise a phosphorothioate backbone
CC
XX SQ Sequence 20 BP; 2 A; 6 C; 6 G; 6 T; 0 U; 0 Other;
XX
Query Match 1.9%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 636 TCTGTCAACCAAGCTGAGT 655
DB 1 TCTGTCAACCAAGCTGAGT 20
XX
RESULT 760
AAL38181/C
ID AAL38181 standard; DNA; 20 BP.
XX
AC AAL38181;
XX
DT 29-AUG-2003 (revised)
```



XX	Human; thrombotic thrombocytopenic purpura; TTP; disintegrin;
KW	metalloproteinase; thrombospondin 1-like domains 13; ADAMTS13;
KM	thrombolytic; haemostatic; PCR; primer; R1-PCR; 5' RACE; 3' RACE; ss.
XX	
OS	Homo sapiens.
PN	W02003016492-A2.
XX	
PD	27-FEB-2003.
XX	
PF	16-AUG-2002; 2002MO-US026285.
XX	
PR	16-AUG-2001; 2001US-0312834P.
XX	
PR	16-AUG-2002; 2002US-00312834.
XX	
PA	(UNMI ) UNIV MICHIGAN.
XX	
PI	Ginsburg D, Levy G, Tsai H;
XX	
DR	WPI; 2003-268318/26.
XX	
PT	Identifying risk of developing thrombotic thrombocytopenic purpura
PT	disease, using a novel disintegrin and metalloproteinase containing
PT	thrombospondin 1-like domains genes and proteases.
XX	
PS	Example 1; Page 87; 98pp; English.
XX	
CC	The invention relates to a novel method for identifying subjects at risk
CC	of developing thrombotic thrombocytopenic purpura (TTP) disease,
CC	comprising providing nucleic acid having a disintegrin and
CC	metalloproteinase containing thrombospondin 1-like domains 13 (ADAMTS13)
CC	gene from a subject, and detecting the presence or absence of one or more
CC	variations in the ADAMTS13 gene. The method of the invention has
CC	thrombolytic and haemostatic activity. The methods and compositions of
CC	the present invention are useful for the diagnosis and treatment of,
CC	and/or analysing risks for thrombotic thrombocytopenic purpura. The
CC	present sequence is used in the exemplification of the invention
XX	
SO	Sequence 20 BP; 5 A; 3 C; 9 G; 3 T; 0 U; 0 Other;
XX	
Query Match	1.9%; Score 18.4; DB 1; Length 20;
Best Local Similarity	95.0%; Pred.No.1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	931 CTCACCTCTGTATCCAGGCT 950
DB	20 CTCACCTGTGATCCAGGCT 1
RESULT 764	
ABZ71056/C	
ID	ABZ71056 standard; DNA; 20 BP.
XX	
AC	ABZ71056;
XX	
DT	28-APR-2003 (first entry)
XX	
DE	Human HKR1 phosphorothioate antisense oligonucleotide SEQ ID NO:84.
XX	
KM	Human; HKR1; cytostatic; HKR1 inhibitor; hyperproliferative disorder;
KW	cancer; antisense oligonucleotide; 2'-O-methoxyethyl; 2'-MOE; control;
XX	phosphorothioate; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Location/Qualifiers
FT	modified_base 1..20
FT	/*tag= a
FT	/mod base= OTHER
FT	/note= "phosphorothioate linkages"
FT	1..5
FT	/*tag= b



```
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 16. .20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyl (2'-MOE) nucleotides"
XX
XX WO2003004513-A1.
XX
XX 16-JAN-2003.
XX
XX 02-JUL-2002; 2002WO-US021090.
XX
XX 03-JUL-2001; 2001US-00898556.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett FC, Freier SM;
XX
XX WPI; 2003-210336/20.
XX
XX New compounds, particularly antisense oligonucleotides targeted to a
XX nucleic acid encoding HKR1, useful for treating a disease/condition
XX associated with HKR1, such as hyperproliferative disorder, e.g. lung,
XX brain or breast cancer.
XX
XX Claim 3; Page 73; 105pp; English.
XX
XX The present invention describes a compound 8-50 nucleobases in length
XX targeted to, and which specifically hybridizes with a nucleic acid
XX molecule encoding HKR1, and inhibits the expression of HKR1. Also
XX described: (1) a compound 8-50 nucleobases in length that specifically
XX hybridizes with at least an 8-nucleobase portion of an active site on a
XX nucleic acid molecule encoding HKR1; (2) a composition comprising the
XX compound and a carrier or diluent; (3) a method for inhibiting the
XX expression of HKR1 in cells or tissues by contacting the cells or tissues
XX with the compound so that expression of HKR1 is inhibited; and (4) a
XX method of treating an animal having a disease or condition associated
XX with HKR1 by administering to the animal a therapeutic or prophylactic
XX amount of the compound so that expression of HKR1 is inhibited. HKR1
XX antisense oligonucleotides have cytostatic activities and can be used as
XX HKR1 inhibitors. The compound, composition and methods are useful for
XX treating a disease or condition associated with HKR1, such as a
XX hyperproliferative disorder, e.g. lung, brain or breast cancer, by
XX inhibiting the expression of HKR1. They are also useful in research and
XX diagnostics for modulating the expression of HKR1. The present sequence
XX represents a human HKR1 chimeric phosphorothioate oligonucleotide having
XX 2'-O-methoxyethyl (2'-MOE) wings and a deoxy gap, which is an antisense
XX oligonucleotide used in the inhibition of human HKR1 in an example from
XX the present invention
XX
XX Sequence 20 BP; 5 A; 4 C; 7 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 1.9%; Score 18.4; DB 1; Length 20;
XX Best Local Similarity 95.0%; Pred. No. 1.3e+03;
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 967 ATCTCGGCTCAGTCACACT 986
XX ||||||||||||||||
XX 20 ATCTCGGCTCAGTCACACT 1
XX
XX RESULT 765
XX ADA20921/c
XX ID ADA20921 standard; DNA; 20 BP.
XX
XX ADA20921;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human BAX chimeric phosphorothioate oligonucleotide SEQ ID NO:94.
XX
XX BCL2-associated X; BAX; neurotropic; neuroprotective; antiparkinsonian;
```

```
KW anticonvulsant; ophthalmological; antidiabetic; vitricide;
KW antisense therapy; BAX antagonist; BAX inhibitor;
KW familial amyotrophic lateral sclerosis; Alzheimer's disease;
KW Parkinson's disease; Hodgkin's disease; cartilage-hair hyperplasia;
KW diabetes-associated ocular disorder; scrapie infection;
KW aberrant apoptosis; human; phosphorothioate; ss.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX modified_base 1. .20
XX /tag= b
XX /mod_base= OTHER
XX /note= "phosphorothioate linkages, and all cytidine
XX residues are 5-methylcytidines"
XX
XX modified_base 1. .5
XX /tag= a
XX /mod_base= OTHER
XX /note= "2'-O-methoxyethyls"
XX
XX modified_base 16. .20
XX /tag= c
XX /mod_base= OTHER
XX /note= "2'-O-methoxyethyls"
XX
XX WO2003008543-A2.
XX
XX 30-JAN-2003.
XX
XX 13-JUL-2002; 2002WO-US022417.
XX
XX 17-JUL-2001; 2001US-00908147.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Zhang H, Watt AT;
XX
XX WPI; 2003-239321/23.
XX
XX New antisense compounds, useful for modulating the expression of BCL2-
XX associated X (BAX) protein or for treating a disease or condition
XX associated with BAX protein, e.g. Parkinson's disease, Hodgkin's disease
XX or Alzheimer's disease.
XX
XX Claim 3; Page 87; 139pp; English.
XX
XX The present invention describes a compound (1) 8-50 nucleobases in length
XX targeted to a nucleic acid molecule encoding BCL2-associated X (BAX)
XX protein, where the compound specifically hybridizes with the nucleic acid
XX molecule encoding BAX protein and inhibits the expression of BAX protein.
XX The compound specifically hybridizes with at least 8-nucleobase portion
XX of an active site on a nucleic acid molecule encoding BAX protein. Also
XX described: (1) a composition comprising (1) and a pharmaceutical carrier
XX or diluent; (2) inhibiting the expression of BAX protein in cells or
XX tissues comprising contacting the cells or tissues with (1); and (3)
XX treating an animal having a disease or condition associated with BAX
XX protein comprising administering to the animal (1) so that expression of
XX BAX protein is inhibited. (1) has neurotropic, neuroprotective,
XX antiparkinsonian, anticonvulsant, ophthalmological, antidiabetic and
XX vitricide activities, and can be used in antisense therapy, and as a BAX
XX antagonist. The antisense compounds (1) are useful for modulating the
XX expression of BAX protein, and for treating a disease or condition
XX associated with BAX protein, e.g. familial amyotrophic lateral
XX sclerosis, Alzheimer's disease, Parkinson's disease, Hodgkin's disease,
XX cartilage-hair hyperplasia, diabetes-associated ocular disorders or
XX scrapie infection, or a condition that arises from aberrant apoptosis.
XX The compounds are useful as research reagents and in diagnostics. The
XX present sequence represents a human BAX chimeric phosphorothioate
XX oligonucleotide, which is used in an example from the present invention.
XX
XX Sequence 20 BP; 5 A; 4 C; 8 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 1.9%; Score 18.4; DB 1; Length 20;
```

Best Local Similarity 95.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 672 GGGTCACTGCACCTCTGCC 691  
DB 20 GGTTCATCGCACCTCTGCC 1

RESULT 766  
ID ACF39682 standard; DNA, 20 BP.  
XX ACF39682;  
AC ACF39682;  
DT 29-SEP-2003 (first entry)

MHC class II transactivator antisense oligonucleotide SEQ ID NO:85.  
XX  
DE MHC class II transactivator complex class II transactivator;  
XX Human; major histocompatibility complex class II transactivator;  
XX MHC class II transactivator; antisense modulation; immunosuppressive;  
XX antimicrobial; antidiabetic; antirheumatic; antiarthritic; cytostatic;  
XX neuroprotection; immunomodulation; autoimmune disorder;  
XX MHC class II transactivator inhibitor; infection; transplant rejection;  
XX diabetes; rheumatoid arthritis; cancer; Alzheimer's disease;  
XX multiple sclerosis; severe combined immunodeficiency disease;  
XX phosphorothioate; antisense oligonucleotide; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.

Key Location/Qualifiers  
FH modified\_base 1..20  
FT /tag= a  
FT /mod\_base= OTHER  
FT /note= "phosphorothioate linkages; all cytidine residues  
FT modified\_base 1..5  
FT /tag= b  
FT /mod\_base= OTHER  
FT /note= "2'-O-methoxyethyls"  
FT modified\_base 16..20  
FT /tag= c  
FT /mod\_base= OTHER  
FT /note= "2'-O-methoxyethyls"

WO2003050247-A2.  
XX  
XX 19-JUN-2003.  
XX  
XX 04-DEC-2002; 2002WO-US038616.  
XX PF  
XX 05-DEC-2001; 2001US-00006366.  
XX PR  
XX (ISIS-) ISIS PHARM INC.  
XX PA  
XX Bennett FC, Dobie KW;  
XX PI  
XX WPI; 2003-577284/54.  
XX DR

New antisense oligonucleotides for modulating MHC class II transactivator  
PT gene expression, particularly useful for treating autoimmune disorders  
PT such as transplant rejection, Alzheimer's disease, or multiple sclerosis,  
PT or infection.  
XX  
XX Example 15; Page 84; 129pp; English.  
XX PS

The present invention describes a compound (I) that is 8-50 nucleobases  
CC in length: (a) targets a nucleic acid molecule encoding major  
CC histocompatibility complex (MHC) class II transactivator, and  
CC specifically hybridizes with the nucleic acid encoding the MHC class II  
CC transactivator, and inhibits the expression of MHC class II  
CC transactivator; or (b) specifically hybridizes with at least an 8-  
CC nucleobase portion of an active site on a nucleic acid molecule encoding

MHC class II transactivator. (I) has immunosuppressive, antimicrobial,  
CC antidiabetic, antirheumatic, antiarthritic, cytostatic, neuroprotection,  
CC neuroprotective and immunostimulant activities, and can be used as an MHC  
CC class II transactivator inhibitor. The MHC class II transactivator  
CC antisense oligonucleotides can be used for treating an animal having a  
CC disease or condition associated with MHC class II transactivator, e.g.,  
CC autoimmune disorder or infection. The antisense oligonucleotides can be  
CC used for inhibiting the expression of MHC class II transactivator in  
CC cells or tissues. In particular, these diseases include transplant  
CC rejection, diabetes, rheumatoid arthritis, cancer, Alzheimer's disease,  
CC multiple sclerosis, or severe combined immunodeficiency disease. The  
CC antisense compounds are useful for diagnostics, prophylaxis, or as  
CC research reagents or kits. The present sequence represents a human MHC  
CC class II transactivator chimeric phosphorothioate antisense  
CC oligonucleotide, which is used in an example from the present invention  
XX

SEQ Sequence 20 BP; 4 A; 6 C; 6 G; 4 T; 0 U; 0 Other;  
XX

Query Match 1.9%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1024 TCCCAAGCAGCTGGATTAC 1043  
DB 1 TCCCGAGCAGCTGGATTAC 20

RESULT 767  
ID ABT44432 standard; DNA, 20 BP.  
XX ABT44432;  
AC ABT44432;  
DT 06-NOV-2003 (first entry)

Chimeric antisense oligonucleotide ISIS 192407 to inhibit human ESRB.  
XX  
XX  
XX Oestrogen receptor beta; ESRB; steroid hormone; female sexual maturation;  
XX bone maintenance; cardiovascular system; ER beta; oestrogen receptor 2;  
XX ER52; Alzheimer's; uterine leiomyoma; cytostatic; kidney neoplasm; ss;  
XX cellular proliferation; cancer; human; antisense; chimeric.  
XX  
XX Chimeric - Homo sapiens.  
XX OS  
XX  
XX WO2003050133-A1.  
XX PN  
XX 19-JUN-2003.  
XX PD  
XX 06-DEC-2002; 2002WO-US039200.  
XX PF  
XX 07-DEC-2001; 2001US-00005058.  
XX PR  
XX (ISIS-) ISIS PHARM INC.  
XX PA  
XX Dobie KW, Roach MP, Koller E;  
XX PI  
XX WPI; 2003-577284/54.  
XX DR

New antisense oligonucleotides for modulating estrogen receptor beta gene  
PT expression, particularly useful for treating cancers, specifically  
PT leiomyoma, pancreatic cancer, prostate cancer, breast cancer, bone cancer  
PT or lymphoma.  
XX  
XX Claim 3; Page 82; 160pp; English.  
XX PS

This invention relates to a novel antisense compounds that modulate the  
CC expression of oestrogen receptor beta (ESRB). Oestrogen is a steroid  
CC hormone that exerts a wide range of effects throughout the human body  
CC being primarily involved in female sexual maturation. Additionally,  
CC however, oestrogen targets male reproductive tissues, is known to be  
CC important in bone maintenance and plays a protective role in the  
CC cardiovascular system. This hormone receptor, ESRB (also known as ER  
CC beta, oestrogen receptor 2 and ER52) has been mapped to chromosome 14q22-

CC q24, a region known to be associated with early onset of Alzheimer's  
CC disease, uterine leiomyomata and neoplasms of the kidney. Furthermore,  
CC ERBB has been localized to metastatic cells indicating an involvement in  
CC cellular proliferation. Accordingly, the selective inhibition of ERBB by  
CC the cytostatic antisense oligonucleotides of this invention could provide  
CC a therapeutic target for the treatment of cancer, as well as other ERBB-  
CC related disorders. This oligonucleotide sequence is the chimeric human  
CC antisense oligo used to inhibit expression of human ERBB, the aim of the  
CC invention. Note that it has two terminal five nucleotide 2'-methoxyethyl  
CC (2'-MOE) wings separated by a ten deoxynucleotide gap. The  
CC oligonucleotide backbone is phosphorothioate throughout  
XX  
SQ Sequence 20 BP; 4 A; 7 C; 3 G; 6 T; 0 U; 0 Other;  
XX  
Query Match 1.9%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
QY 1115 CTGCTCTCAAACTCTGACC 1134  
Db 1 CTGGTTCAAACTCTGACC 20  
XX  
RESULT 768  
ADD21681/c  
ID ADD21681 standard; DNA; 20 BP.  
XX  
AC ADD21681;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Human mdm2 antisense oligonucleotide #244.  
XX  
KW antisense oligonucleotide; human; mdm2; hyperproliferation;  
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;  
KW atherosclerosis; restenosis; apoptosis modulation; p21; ss;  
KW 2'-methoxyethoxy-residue; phosphorothioate backbone.  
XX  
OS Homo sapiens.  
XX  
PN WO2003048315-A2.  
XX  
PD 12-JUN-2003.  
XX  
PT 02-DEC-2002; 2002WO-US038281.  
XX  
PR 04-DEC-2001; 2001US-00005344.  
XX  
PS (ISIS-) ISIS PHARM INC.  
XX  
PI Miraglia LJ, Nero PS, Graham MJ, Monia BP, Koller E, Chiang MY;  
PI Manoharan M;  
XX  
DR WPI; 2003-577263/54.  
XX  
PT Novel antisense compound targeted to 5' untranslated region, coding  
PT region, or intron:exon junction of nucleic acid molecule encoding mdm2,  
PT useful for treating e.g. cancer, psoriasis or restenosis by inhibiting  
PT mdm2 expression.  
XX  
PS Claim 4; SEQ ID NO 246; 289pp; English.  
XX  
CC The invention comprises antisense oligonucleotides which are targeted to  
CC the human mdm2 gene. The antisense oligonucleotides of the invention are  
CC useful for reducing hyperproliferation of human cells. The antisense  
CC oligonucleotides are also useful for treating: hyperproliferative  
CC disorders (e.g. cancer), psoriasis, fibrosis, atherosclerosis, or  
CC restenosis. The antisense oligonucleotides are also useful for modulating  
CC apoptosis, and for increasing expression of p21. The present DNA sequence  
CC represents a human mdm2 gene antisense oligonucleotide of the invention.  
CC The present sequence contains 2'-methoxyethoxy-residues and has a  
CC phosphorothioate backbone.  
XX

SQ Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 U; 0 Other;  
XX  
Query Match 1.9%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
QY 668 TCTTGCTCAGCAGCAACCTC 687  
Db 20 TCTTGCTCAGCAGCAACCTC 1  
XX  
RESULT 769  
ADD21703/c  
ID ADD21703 standard; DNA; 20 BP.  
XX  
AC ADD21703;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Human mdm2 antisense oligonucleotide #266.  
XX  
KW antisense oligonucleotide; human; mdm2; hyperproliferation;  
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;  
KW atherosclerosis; restenosis; apoptosis modulation; p21; ss;  
KW 2'-methoxyethoxy-residue; phosphorothioate backbone.  
XX  
OS Homo sapiens.  
XX  
PN WO2003048315-A2.  
XX  
PD 12-JUN-2003.  
XX  
PT 02-DEC-2002; 2002WO-US038281.  
XX  
PR 04-DEC-2001; 2001US-00005344.  
XX  
PS (ISIS-) ISIS PHARM INC.  
XX  
PI Miraglia LJ, Nero PS, Graham MJ, Monia BP, Koller E, Chiang MY;  
PI Manoharan M;  
XX  
DR WPI; 2003-577263/54.  
XX  
PT Novel antisense compound targeted to 5' untranslated region, coding  
PT region, or intron:exon junction of nucleic acid molecule encoding mdm2,  
PT useful for treating e.g. cancer, psoriasis or restenosis by inhibiting  
PT mdm2 expression.  
XX  
PS Claim 4; SEQ ID NO 268; 289pp; English.  
XX  
CC The invention comprises antisense oligonucleotides which are targeted to  
CC the human mdm2 gene. The antisense oligonucleotides of the invention are  
CC useful for reducing hyperproliferation of human cells. The antisense  
CC oligonucleotides are also useful for treating: hyperproliferative  
CC disorders (e.g. cancer), psoriasis, fibrosis, atherosclerosis, or  
CC restenosis. The antisense oligonucleotides are also useful for modulating  
CC apoptosis, and for increasing expression of p21. The present DNA sequence  
CC represents a human mdm2 gene antisense oligonucleotide of the invention.  
CC The present sequence contains 2'-methoxyethoxy-residues and has a  
CC phosphorothioate backbone.  
XX  
SQ Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;  
XX  
Query Match 1.9%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
QY 868 GGATTACAGGCGTGAGCCAC 867  
Db 20 GGATTACAGGCGTGAGCCAC 1  
XX  
RESULT 770

AD43606/c  
ID ADE43606 standard; DNA; 20 BP.  
XX  
AC ADE43606;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Human KNSL1 sequencing primer, SEQ ID 211.  
XX  
KW Neurodegenerative disease; uPA; SNGG; IDE; KNSL1; LIPA; TNFRSF6;  
KM Alzheimer's disease; neuroprotective; nootropic; gene therapy;  
XX Chromosome 10; PCR; primer; 88.  
XX  
OS Homo sapiens.  
XX  
PN WO2003054143-A2.  
XX  
PD 03-JUL-2003.  
XX  
PF 25-OCT-2002; 2002WO-US034679.  
XX  
PR 25-OCT-2001; 2001US-0339525P.  
XX 08-NOV-2001; 2001US-0336929P.  
XX 08-NOV-2001; 2001US-0336910P.  
XX 09-NOV-2001; 2001US-0336363P.  
XX 04-DEC-2001; 2001US-0337052P.  
XX 28-MAR-2002; 2002US-0368919P.  
XX  
PA (NEUR-) NEUROGENETICS INC.  
XX (GEMO) GEN HOSPITAL CORP.  
XX  
PI Becker KD, Velicelbi G, Elliott KJ, Wang X, Tanzi RE, Bertram L;  
PI Saunders AJ, Mullin KM, Sampson AJ, Blacker DL;  
XX  
XX MPI; 2003-559131/52.  
XX  
DR Determining a predisposition for or the occurrence of neurodegenerative  
XX disease, e.g. Alzheimer's disease by detecting in a target nucleic acid  
XX the presence or absence of an allelic variant of one or more polymorphic  
XX regions.  
XX  
PS Example 3; Page 287; 848pp; English.  
XX  
CC The present invention relates to a method (M1) for determining a  
XX predisposition for or the occurrence of neurodegenerative disease in a  
XX subject. The method comprises detecting in a target nucleic acid obtained  
XX from the subject the presence or absence of an allelic variant of one or  
XX more polymorphic regions of one or more genes selected from uPA  
XX (Urokinase plasminogen activator), SNGG (gamma-synuclein), IDE (insulin-  
XX degrading enzyme), KNSL1 (Kinesin-like protein 1), LIPA (lysosomal acid  
XX lipase), and TNFRSF6 (Tumour Necrosis Factor Receptor-SF6), where the  
XX presence of at least one of the allelic variant of one or more  
XX polymorphic regions is indicative of a predisposition for or the  
XX occurrence of neurodegenerative disease. The genes are all located on  
XX chromosome 10. M1 is useful for determining a predisposition for or the  
XX occurrence of, and for treating neurodegenerative disease, particularly  
XX Alzheimer's disease. The present sequence is a PCR primer, which was used  
XX in the method of the invention.  
XX  
SQ Sequence 20 BP; 12 A; 2 C; 2 G; 4 T; 0 U; 0 Other;  
XX  
Query Match 1.9%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX  
AC ADE86781;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE GATC primer #1.  
XX  
KW 88; primer; molecular phenotyping; brain; lung; CD31+ cell;  
KM lineage committed cell; survival; proliferation; differentiation;  
KM haematopoietic stem cell; cancer; leukaemia; bone marrow;  
XX transplantation.  
XX  
OS Homo sapiens.  
XX  
PN WO2003089592-A2.  
XX  
PD 30-OCT-2003.  
XX  
PF 15-APR-2003; 2003WO-US011649.  
XX  
PR 16-APR-2002; 2002US-0373127P.  
XX  
PA (UNIV-) UNIV OREGON HEALTH SCI.  
XX  
PI Fleming WH, Li B;  
XX  
DR MPI; 2003-854104/79.  
XX  
XX  
PT A composition for promoting survival, proliferation and/or  
PT differentiation of hematopoietic stem cells useful in e.g. bone marrow  
PT transplantation, comprises in cells that express CD31, CD34 and CD105.  
XX  
PS Example 1; Page 27; 54pp; English.  
XX  
XX This sequence represents a primer which was used in the molecular  
XX phenotyping of brain and lung derived CD31+ cells. This primer was used  
XX to isolate cells which are CD31+ CD34+ CD45- CD105- c-kit- lin-. The  
XX isolated cells were used in the composition of the invention which  
XX comprises fewer than 20% of lineage committed cells. The composition of  
XX the invention is useful for reconstituting haematopoiesis, and therefore  
XX in promoting survival, proliferation and/or differentiation of  
XX haematopoietic stem cells which may be used in treating cancers (e.g.  
XX leukaemia) or in bone marrow transplantation as well as transplantation  
XX of other organs in association with the transplantation of bone marrow.  
XX  
SQ Sequence 20 BP; 5 A; 7 C; 3 G; 5 T; 0 U; 0 Other;  
XX  
Query Match 1.9%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 391 AGTGCTGGGATTACAGGCGT 410  
DB 20 AGTGCTGGGATTACAGGCGT 1

RESULT 772  
AD161628  
ID AD161628 standard; DNA; 20 BP.  
XX  
AC AD161628;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE Human SAP-1 gene targeted oligonucleotide ISIS 176450.  
XX  
KW cytostatic; antisense therapy; Serum response factor Accessory Protein;  
KM SAP-1; splice variant; hyperproliferative disorder; cancer; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers

```
FT modified_base 1..20
FT /tag= b
FT /mod_base= OTHER
FT /note= "contains phosphorothioate internucleotide
FT linkages; all C nucleotides are 5'-methylcytidine
FT nucleotides"
FT modified_base 1..5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyl nucleotide"
FT modified_base 15..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyl nucleotide"
PN WO2003011888-A1.
XX 13-FEB-2003.
XX 31-JUL-2002; 2002WO-US024369.
XX 01-APR-2001; 2001US-00920759.
XX (ISIS-) ISIS PHARM INC.
XX Baker BF, Freier SM;
XX WPI; 2003-248144/24.
XX
XX New antisense oligonucleotides targeted to nucleic acid encoding Serum
XX response factor Accessory Protein (SAP-1, for inhibiting the expression
XX of SAP-1 and for treating a disease or condition associated with the
XX expression of SAP-1.
XX
XX Example 15; SEQ ID NO 87; 143bp; English.
XX
XX The invention relates to a compound 8-50 nucleobases in length targeted
XX to a nucleic acid encoding Serum response factor Accessory Protein (SAP)-
XX 1 or a splice variant of SAP-1, where the compound specifically
XX hybridizes with and inhibits the expression of SAP-1, a splice variant of
XX SAP-1, or a truncated form of SAP-1, or hybridizes with an 8-nucleobase
XX portion of an active site on a nucleic acid encoding SAP-1. The compound
XX is used for inhibiting the expression of SAP-1 in cells or tissues, and
XX for treating an animal having a disease or condition associated with SAP-
XX 1. The disease or disorder is a hyperproliferative disorder, such as
XX breast, prostate or hematopoietic cancer. The antisense compounds may be
XX used as research reagents and diagnostics, as therapeutics, prophylaxis,
XX to elucidate the function of particular genes, to distinguish between
XX functions of various members of biological pathway, and in treatment
XX of regimens of cells, tissues, and animals. This sequence corresponds to an
XX oligonucleotide of the invention which is targeted to the human SAP-1
XX gene.
XX
XX Sequence 20 BP; 6 A; 7 C; 2 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 1.9%; Score 18.4; DB 1; Length 20;
XX Best Local Similarity 95.0%; Pred. No. 1.3e+03;
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 665 CAATCTTGCTCACTGCAAC 684
Db 1 CAATCTTGCTCACTGCAAC 20

```

```
XX human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiasthmatic;
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX Homo sapiens.
XX
XX WO200285308-A2.
XX 31-OCT-2002.
XX 23-APR-2002; 2002WO-US013135.
XX 24-APR-2001; 2001US-0286137P.
XX (EPIC-) EPIGENESIS PHARM INC.
XX Myce JW, Li Y, Sandrasegura A, Katz E, Pabalan J, Aguilar D;
XX Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
XX respiration, has oligo(s) antisense to specific gene(s) or its
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX ubiquinone.
XX
XX Disclosure; SEQ ID NO 13207; 872bp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
XX first active agent comprising an oligonucleotide antisense to the
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX junctions of genes encoding a polypeptide associated with lung and/or
XX nasal airway dysfunction and a second active agent comprising an
XX antiinflammatory steroid and ubiquinone. A composition of the invention
XX has antiinflammatory, antiasthmatic, hypotensive,
XX immunosuppressive, and cytostatic activity. The composition may have a
XX use in antisense gene therapy. The composition is useful for treating or
XX preventing a respiratory, lung or malignant disease or condition, also
XX for enhancing the prophylactic or therapeutic respiratory effect of an
XX antiinflammatory steroid in a subject, for reducing or depleting levels
XX of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or
XX receptor, producing bronchodilation, increasing levels of ubiquinone or
XX lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX lung inflammation, lung allergies, or a respiratory disease or condition.
XX Note: The sequence data for this patent is not represented in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 1.9%; Score 18.4; DB 1; Length 20;
XX Best Local Similarity 95.0%; Pred. No. 1.3e+03;
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 537 CCTGCTCAGCCCTCCCAAGT 556
Db 1 CTTGCTCAGCCCTCCCGAGT 20

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RESULT 773
AB297965
ID AB297965 standard; DNA; 20 BP.
XX
XX AB297965;
XX
XX 17-OCT-2003 (first entry)
XX
XX Human RANTES oligonucleotide sequence.
DE
```

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RESULT 774
AB289864/c
ID AB289864 standard; DNA; 20 BP.
XX
XX AB289864;
XX
XX 17-OCT-2003 (first entry)
XX
XX Human oligonucleotide sequence.
DE
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XX	Human; antisense; lung dysfunction; nasal airway dysfunction;
KM	antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KM	antiaesthetic; hypotensive; immunosuppressive; cytoskeletal; gene therapy;
KM	antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW	adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KV	lung inflammation; respiratory disease; ds.
XX	
OS	Homo sapiens.
XX	
PN	WO200285308-A2.
PD	31-OCT-2002.
XX	
PF	23-APR-2002; 2002WO-US013135.
XX	
PR	24-APR-2001; 2001US-0286137P.
XX	
PA	(EPIG-) EPIGENESIS PHARM INC.
PI	Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX	
PI	Miller S, Tang L, Shahabuddin S;
XX	
DR	WPI; 2003-229219/22.
XX	
PT	Pharmaceutical composition for treating ailments associated with impaired
PT	respiration, has oligo(s) antisense to specific gene(s) or its
PT	corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX	
PS	ubiquinone.
XX	
XX	Disclosure; SEQ ID NO 13206; 872pp; English.
XX	
CC	The invention relates to a novel pharmaceutical composition, which has a
CC	first active agent comprising an oligonucleotide antisense to the
CC	initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC	5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC	junctions of genes encoding a polypeptide associated with lung and/or
CC	nasal airway dysfunction and a second active agent comprising an
CC	antiinflammatory steroid and ubiquinone. A composition of the invention
CC	has antiinflammatory, antiallergic, antiaesthetic, hypotensive,
CC	immunosuppressive, and cytostatic activity. The composition may have a
CC	use in antisense gene therapy. The composition is useful for treating or
CC	preventing a respiratory, lung or malignant disease or condition, also
CC	for enhancing the prophylactic or therapeutic respiratory effect of an
CC	antiinflammatory steroid in a subject, for reducing or depleting levels
CC	of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC	receptor, producing bronchodilation, increasing levels of ubiquinone or
CC	lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC	lung inflammation, lung allergies, or a respiratory disease or condition.
CC	Note: The sequence data for this patent is not represented in the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences
XX	
SEQ	Sequence 20 BP; 2 A; 10 C; 2 G; 6 T; 0 U; 0 Other;
XX	
Query Match	1.9%; Score 18.4; DB 1; Length 20;
Best Local Similarity	95.0%; Pred. NO. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	532 ATCGTCCTGAGCTCAGCTCC 551
DB	1 ATTCCTCGCTCAGACTCC 20
RESULT 776	
AB297909	
ID	AB297909 standard; DNA; 20 BP.
XX	
AC	AB297909;
XX	
DT	17-OCT-2003 (first entry)
DE	Human RANTES oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiallergic; hypotensive; immunosuppressive; cytoskeletal; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.  
 XX Homo sapiens.  
 OS  
 XX WO200285308-A2.  
 PN  
 XX 31-OCT-2002.  
 PD  
 XX 23-APR-2002; 2002WO-US013135.  
 PF  
 XX 24-APR-2001; 2001US-0286137P.  
 PR  
 XX (EPIC-) EPIGENESIS PHARM INC.  
 PA  
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 PI  
 DR WPI; 2003-229219/22.  
 XX  
 PT Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.  
 PS  
 XX Disclosure; SEQ ID NO 13151; 872bp; English.  
 XX  
 CC The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiallergic, hypotensive,  
 CC immunosuppressive, and cytoskeletal activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at fep.wipo.int/pub/published\_pct\_sequences  
 CC  
 XX  
 SQ Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;  
 XX  
 XX Query Match 1.9%; Score 18.4; DB 1; Length 20;  
 XX Best Local Similarity 95.0%; Pred. No. 1.3e+03;  
 XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 QY 722 CCTCTGAGTAGTGGGACT 741  
 Db 1 CCTCCGAGTAGTGGGACT 20

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiallergic; hypotensive; immunosuppressive; cytoskeletal; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.  
 XX Homo sapiens.  
 OS  
 XX WO200285308-A2.  
 PN  
 XX 31-OCT-2002.  
 PD  
 XX 23-APR-2002; 2002WO-US013135.  
 PF  
 XX 24-APR-2001; 2001US-0286137P.  
 PR  
 XX (EPIC-) EPIGENESIS PHARM INC.  
 PA  
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 PI  
 DR WPI; 2003-229219/22.  
 XX  
 PT Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.  
 PS  
 XX Disclosure; SEQ ID NO 5103; 872bp; English.  
 XX  
 CC The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiallergic, hypotensive,  
 CC immunosuppressive, and cytoskeletal activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at fep.wipo.int/pub/published\_pct\_sequences  
 CC  
 XX  
 SQ Sequence 20 BP; 4 A; 4 C; 9 G; 3 T; 0 U; 0 Other;  
 XX  
 XX Query Match 1.9%; Score 18.4; DB 1; Length 20;  
 XX Best Local Similarity 95.0%; Pred. No. 1.3e+03;  
 XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 QY 970 TCGGCTCAGTCAACCTCTG 989  
 Db 20 TCGGCTCAGTCAACCTCTG 1

RESULT 777  
 AB289861/c  
 ID AB289861 standard; DNA; 20 BP.  
 AC  
 XX AB289861;  
 AC  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX  
 DE Human oligonucleotide sequence.

RESULT 778  
 AB297902  
 ID AB297902 standard; DNA; 20 BP.  
 AC  
 XX AB297902;  
 AC  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX  
 DE Human RANTES oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiasthmatic;  
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;  
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
XX lung inflammation; respiratory disease; ds.  
OS Homo sapiens.  
XX WO200285308-A2.  
XX 31-OCT-2002.  
XX 23-APR-2002; 2002WO-US013135.  
XX 24-APR-2001; 2001US-0286137P.  
XX (EPIC-) EPIGENESIS PHARM INC.  
XX  
XX Nyce JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
XX Miller S, Tang L, Shanabuddin S;  
XX WPI; 2003-229219/22.  
XX  
XX Pharmaceutical composition for treating ailments associated with impaired  
XX respiration, has oligo(e) antisense to specific gene(s) or its  
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
XX ubiquinone.  
XX  
XX Disclosure; SEQ ID NO 13144; 872pp; English.  
XX  
XX The invention relates to a novel pharmaceutical composition, which has a  
XX first active agent comprising an oligonucleotide antisense to the  
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,  
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
XX junctions of genes encoding a polypeptide associated with lung and/or  
XX nasal airway dysfunction and a second active agent comprising an  
XX antiinflammatory steroid and ubiquinone. A composition of the invention  
XX has antiinflammatory, antiasthmatic, hypotensive, immunosuppressive,  
XX and cytostatic activity. The composition may have a use in antisense  
XX gene therapy. The composition is useful for treating or preventing a  
XX respiratory, lung or malignant disease or condition, also for enhancing  
XX the prophylactic or therapeutic respiratory effect of an antiinflammatory  
XX steroid in a subject, for reducing or depleting levels of, or reducing  
XX sensitivity to adenosine, reducing levels of adenosine receptor,  
XX producing bronchodilation, increasing levels of ubiquinone or lung  
XX surfactant in a subject's tissue, or treating bronchoconstriction,  
XX lung inflammation, lung allergies, or a respiratory disease or condition.  
XX Note: The sequence data for this patent is not represented in the printed  
XX specification, but was obtained in electronic format directly from WIPO  
XX at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 20 BP; 4 A; 5 C; 8 G; 3 T; 0 U; 0 Other;  
SQ  
XX  
XX Query Match 1.9%; Score 18.4; DB 1; Length 20;  
XX Best Local Similarity 95.0%; Pred. No. 1.3e+03;  
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX 868 GGATTACAGCGTGGAGCCAC 887  
XX |||||  
XX 1 GGATTACAGCGTGGAGCCAC 20  
XX  
XX RESULT 779  
XX AB292724  
XX ID AB292724 standard; DNA; 20 BP.  
XX  
XX AB292724;  
XX  
XX 17-OCT-2003 (first entry)  
XX  
XX Human oligonucleotide sequence.  
DE

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiasthmatic;  
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;  
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
XX lung inflammation; respiratory disease; ds.  
OS Homo sapiens.  
XX WO200285308-A2.  
XX 31-OCT-2002.  
XX 23-APR-2002; 2002WO-US013135.  
XX 24-APR-2001; 2001US-0286137P.  
XX (EPIC-) EPIGENESIS PHARM INC.  
XX  
XX Nyce JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
XX Miller S, Tang L, Shanabuddin S;  
XX WPI; 2003-229219/22.  
XX  
XX Pharmaceutical composition for treating ailments associated with impaired  
XX respiration, has oligo(e) antisense to specific gene(s) or its  
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
XX ubiquinone.  
XX  
XX Disclosure; SEQ ID NO 7966; 872pp; English.  
XX  
XX The invention relates to a novel pharmaceutical composition, which has a  
XX first active agent comprising an oligonucleotide antisense to the  
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,  
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
XX junctions of genes encoding a polypeptide associated with lung and/or  
XX nasal airway dysfunction and a second active agent comprising an  
XX antiinflammatory steroid and ubiquinone. A composition of the invention  
XX has antiinflammatory, antiasthmatic, hypotensive, immunosuppressive,  
XX and cytostatic activity. The composition may have a use in antisense  
XX gene therapy. The composition is useful for treating or preventing a  
XX respiratory, lung or malignant disease or condition, also for enhancing  
XX the prophylactic or therapeutic respiratory effect of an antiinflammatory  
XX steroid in a subject, for reducing or depleting levels of, or reducing  
XX sensitivity to adenosine, reducing levels of adenosine receptor,  
XX producing bronchodilation, increasing levels of ubiquinone or lung  
XX surfactant in a subject's tissue, or treating bronchoconstriction,  
XX lung inflammation, lung allergies, or a respiratory disease or condition.  
XX Note: The sequence data for this patent is not represented in the printed  
XX specification, but was obtained in electronic format directly from WIPO  
XX at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 20 BP; 4 A; 0 C; 4 G; 12 T; 0 U; 0 Other;  
SQ  
XX  
XX Query Match 1.9%; Score 18.4; DB 1; Length 20;  
XX Best Local Similarity 95.0%; Pred. No. 1.3e+03;  
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX 768 TTTTGTATTTTGTAGTA 787  
XX |||||  
XX 1 TTTTGTATTTTGTAGTA 20  
XX  
XX RESULT 780  
XX AB298012  
XX ID AB298012 standard; DNA; 20 BP.  
XX  
XX AB298012;  
XX  
XX 17-OCT-2003 (first entry)  
XX  
XX Human RANFES oligonucleotide sequence.  
DE



XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiallergic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX  
OS Homo sapiens.  
XX  
PN MO200285308-A2.  
XX  
PD 31-OCT-2002.  
XX  
PF 23-APR-2002; 2002WO-US013135.  
XX  
PR 24-APR-2001; 2001US-0286137P.  
XX  
PA (EPIC-) EPIGENESIS PHARM INC.  
XX  
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
PI  
DR WPI; 2003-229219/22.  
XX  
PT Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
XX  
PS Disclosure; SEQ ID NO 13254; 872bp; English.  
XX  
CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antialsthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 2 A; 6 C; 7 G; 5 T; 0 U; 0 Other;  
XX  
Query Match 1.9%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 636 TCTGTGACCCAGGCTGAGT 655  
Db 1 TCTGTGCGCCGCGCTGAGT 20  
RESULT 781  
AB298015  
ID AB298015 standard; DNA; 20 BP.  
XX  
AC AB298015;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Human RANTES oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiallergic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX  
OS Homo sapiens.  
XX  
PN MO200285308-A2.  
XX  
PD 31-OCT-2002.  
XX  
PF 23-APR-2002; 2002WO-US013135.  
XX  
PR 24-APR-2001; 2001US-0286137P.  
XX  
PA (EPIC-) EPIGENESIS PHARM INC.  
XX  
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
PI  
DR WPI; 2003-229219/22.  
XX  
PT Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
XX  
PS Disclosure; SEQ ID NO 13257; 872bp; English.  
XX  
CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antialsthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 3 A; 4 C; 9 G; 4 T; 0 U; 0 Other;  
XX  
Query Match 1.9%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 651 GGAGTGCAGTGGCGCATCT 670  
Db 1 GGAGTGCAGTGGCGCGATCT 20  
RESULT 782  
AB297908  
ID AB297908 standard; DNA; 20 BP.  
XX  
AC AB297908;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Human RANTES oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasclastic; hypotensive; immunosuppressive; cyclostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX  
OS Homo sapiens.  
XX  
PN MO200285308-A2.  
XX  
PD 31-OCT-2002.  
XX  
PF 23-APR-2002; 2002WO-US013135.  
XX  
PR 24-APR-2001; 2001US-0286137P.  
XX  
PA (EP1G-) EPIGENESIS PHARM INC.  
XX  
PI Myce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX  
DR WPI; 2003-229219/22.  
XX  
PT Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
XX  
PS Disclosure; SEQ ID NO 13150; 872pp; English.  
XX  
XX The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasclastic, hypotensive,  
CC immunosuppressive, and cyclostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 3 A; 8 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 1.9%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 542 CTCAGCTCCCAAGTAGCTG 561  
DB 1 CTCAGCTCCCAAGTAGCTG 20

RESULT 783  
AB298003  
ID AB298003 standard; DNA; 20 BP.  
XX  
AC AB298003;  
XX  
AC 17-OCT-2003 (first entry)  
XX  
DT Human RANTES oligonucleotide sequence.  
XX  
DE

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasclastic; hypotensive; immunosuppressive; cyclostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX  
OS Homo sapiens.  
XX  
PN MO200285308-A2.  
XX  
PD 31-OCT-2002.  
XX  
PF 23-APR-2002; 2002WO-US013135.  
XX  
PR 24-APR-2001; 2001US-0286137P.  
XX  
PA (EP1G-) EPIGENESIS PHARM INC.  
XX  
PI Myce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX  
DR WPI; 2003-229219/22.  
XX  
PT Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
XX  
PS Disclosure; SEQ ID NO 13245; 872pp; English.  
XX  
XX The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasclastic, hypotensive,  
CC immunosuppressive, and cyclostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 5 A; 4 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 1.9%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 642 ACCCAGGCTGAGTAGAGTG 661  
DB 1 ACCCAGGCTGAGTAGAGTG 20

RESULT 784  
AB297903  
ID AB297903 standard; DNA; 20 BP.  
XX  
AC AB297903;  
XX  
AC 17-OCT-2003 (first entry)  
XX  
DT Human RANTES oligonucleotide sequence.  
XX  
DE

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiallergic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX  
OS Homo sapiens.  
XX  
PN MO200285308-A2.  
XX  
PD 31-OCT-2002.  
XX  
PF 23-APR-2002; 2002MO-US013135.  
XX  
PR 24-APR-2001; 2001US-0286137P.  
XX  
PA (EPIG-) EPIGENESIS PHARM INC.  
XX  
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
DR WPI; 2003-229219/22.  
XX  
PT Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
XX  
PS Disclosure; SEQ ID NO 13145; 872bp; English.  
XX  
CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end, genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiallergic, hypotensive,  
CC immunosuppressive, and cyrostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 4 A; 8 C; 7 G; 1 T; 0 U; 0 Other;  
XX  
Query Match 1.9%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 873 ACAGGCGTGAAGCCACACGCG 892  
Db 1 ACAGGCGTGAAGCCACACGCG 20  
RESULT 785  
ABZ99062  
ID ABZ99062 standard; DNA; 20 BP.  
XX  
AC ABZ99062;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Human PDE4C oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiallergic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX  
OS Homo sapiens.  
XX  
PN MO200285308-A2.  
XX  
PD 31-OCT-2002.  
XX  
PF 23-APR-2002; 2002MO-US013135.  
XX  
PR 24-APR-2001; 2001US-0286137P.  
XX  
PA (EPIG-) EPIGENESIS PHARM INC.  
XX  
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
DR WPI; 2003-229219/22.  
XX  
PT Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
XX  
PS Disclosure; SEQ ID NO 14304; 872bp; English.  
XX  
CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end, genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiallergic, hypotensive,  
CC immunosuppressive, and cyrostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 3 A; 10 C; 3 G; 4 T; 0 U; 0 Other;  
XX  
Query Match 1.9%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 538 CTGCTCAGCGCTCCACAGTA 557  
Db 1 CTGCTCAGCGCTCCACAGTA 20  
RESULT 786  
ABZ99105  
ID ABZ99105 standard; DNA; 20 BP.  
XX  
AC ABZ99105;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Human PDE4C oligonucleotide sequence.

XX	Human; antisense; lung dysfunction; nasal airway dysfunction;
KW	antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KM	anticholinergic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW	antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW	adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KV	lung inflammation; respiratory disease; ds.
XX	
OS	Homo sapiens.
PN	WO200285308-A2.
PD	31-OCT-2002.
PF	23-APR-2002; 2002WO-US013135.
PP	24-APR-2001; 2001US-0286137P.
PR	(EPIG-) EPIGENESIS PHARM INC.
PA	Myce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D; Miller S, Tang L, Shahabuddin S;
P1	WPI, 2003-229219/22.
XX	
PT	Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.
PS	Disclosure; SEQ ID NO 13255; 872pp; English.
XX	
CC	The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, anticholinergic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX	
Sequence	20 BP; 3 A; 6 C; 8 G; 3 T; 0 U; 0 Other;
Query Match	1.9%; Score 18.4; DB 1; Length 20;
Best Local Similarity	95.0%; Pred. No. 1.3e+03;
Matches	19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY	641 CACCCAGGCTGGAGTGCAGT 660       
Db	1 CGCCCAGGCTGGAGTGCAGT 20
RESULT 788	
ABZ99071	
ID	ABZ99071 standard; DNA; 20 BP.
AC	ABZ99071;
XX	
DT	17-OCT-2003 (first entry)
XX	
DE	Human PDE4C oligonucleotide sequence.

```
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX Homo sapiens.
XX WO200285308-A2.
XX 31-OCT-2002.
XX 23-APR-2002; 2002WO-US013135.
XX 24-APR-2001; 2001US-0286137P.
XX (EPIG-) EPIGENESIS PHARM INC.
XX NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
XX Pharmaceutical composition for treating ailments associated with impaired
XX respiration, has oligo(s) antisense to specific gene(s) or its
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX ubiquinone.
XX Disclosure; SEQ ID NO 14313; 872bp; English.
XX The invention relates to a novel pharmaceutical composition, which has a
XX first active agent comprising an oligonucleotide antisense to the
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX junctions of genes encoding a polypeptide associated with lung and/or
XX nasal airway dysfunction and a second active agent comprising an
XX antiinflammatory steroid and ubiquinone. A composition of the invention
XX has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
XX immunosuppressive, and cytostatic activity. The composition may have a
XX use in antisense gene therapy. The composition is useful for treating or
XX preventing a respiratory, lung or malignant disease or condition, also
XX for enhancing the prophylactic or therapeutic respiratory effect of an
XX antiinflammatory steroid in a subject, for reducing or depleting levels
XX of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or
XX receptor, producing bronchodilation, increasing levels of adenosine or
XX lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX lung inflammation, lung allergies, or a respiratory disease or condition.
XX Note: The sequence data for this patent is not represented in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX Sequence 20 BP; 2 A; 5 C; 7 G; 6 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.9%; Score 18.4; DB 1; Length 20;
XX Best Local Similarity 95.0%; Pred. No. 1.3e+03;
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 199 ATGTTGTCAGCGTGTCTC 218
Db 1 ATGTTGTCAGCGTGTCTC 20
RESULT 789
ABZ89844/C
ID ABZ89844 standard; DNA; 20 BP.
XX
XX ABZ89844;
XX
XX
XX 17-OCT-2003 (first entry)
XX
XX Human oligonucleotide sequence.
DE
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XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX Homo sapiens.
XX WO200285308-A2.
XX 31-OCT-2002.
XX 23-APR-2002; 2002WO-US013135.
XX 24-APR-2001; 2001US-0286137P.
XX (EPIG-) EPIGENESIS PHARM INC.
XX NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
XX Pharmaceutical composition for treating ailments associated with impaired
XX respiration, has oligo(s) antisense to specific gene(s) or its
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX ubiquinone.
XX Disclosure; SEQ ID NO 5086; 872bp; English.
XX The invention relates to a novel pharmaceutical composition, which has a
XX first active agent comprising an oligonucleotide antisense to the
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX junctions of genes encoding a polypeptide associated with lung and/or
XX nasal airway dysfunction and a second active agent comprising an
XX antiinflammatory steroid and ubiquinone. A composition of the invention
XX has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
XX immunosuppressive, and cytostatic activity. The composition may have a
XX use in antisense gene therapy. The composition is useful for treating or
XX preventing a respiratory, lung or malignant disease or condition, also
XX for enhancing the prophylactic or therapeutic respiratory effect of an
XX antiinflammatory steroid in a subject, for reducing or depleting levels
XX of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or
XX receptor, producing bronchodilation, increasing levels of adenosine or
XX lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX lung inflammation, lung allergies, or a respiratory disease or condition.
XX Note: The sequence data for this patent is not represented in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX Sequence 20 BP; 13 A; 2 C; 0 G; 5 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.9%; Score 18.4; DB 1; Length 20;
XX Best Local Similarity 95.0%; Pred. No. 1.3e+03;
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 766 ATTTTGTGATTTTACGA 785
Db 20 AATTTTGTGATTTTACGA 1
RESULT 790
ABZ92736
ID ABZ92736 standard; DNA; 20 BP.
XX
XX ABZ92736;
XX
XX
XX 17-OCT-2003 (first entry)
XX
XX Human oligonucleotide sequence.
DE
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```
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KM antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KM antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KM antisense gene therapy; respiratory; lung; adenosine sensitivity;
KM adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KM lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
OS
XX WO200285308-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013135.
XX
XX 24-APR-2001; 2001US-0286137P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX
XX Nlyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX Disclosure; SEQ ID NO 7978; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 20 BP; 4 A; 10 C; 2 G; 4 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.9%; Score 18.4; DB 1; Length 20;
XX Best Local Similarity 95.0%; Pred. No. 1.3e+03;
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KM antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KM antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KM antisense gene therapy; respiratory; lung; adenosine sensitivity;
KM adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KM lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
OS
XX WO200285308-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013135.
XX
XX 24-APR-2001; 2001US-0286137P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX
XX Nlyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX Disclosure; SEQ ID NO 14319; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 20 BP; 6 A; 2 C; 7 G; 5 T; 0 U; 0 Other;
SQ
XX
XX Query Match 1.9%; Score 18.4; DB 1; Length 20;
XX Best Local Similarity 95.0%; Pred. No. 1.3e+03;
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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